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1 MAMMEVQGGPSLGQTCVLIV......NEHLIDMDHEASFFGAFLVG 281
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Copyright (c) 1993 - 2004 Compugen Ltd.
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C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001
Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001
Species: Halobacterium sp. NRC-1
C;Accession: F84175
Sp. Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, Sp. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable Jung, K.H.; Alam, M.; Freitas, T. 2176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L. A;Reference number: A84160; MUID:205044483; PMID:11016950
A;Accession: F94175
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Gene 99, 127-132, 1991
AjTitle: Cloning of Toxoplasma gondii gene fragments encoding diagnostic antigens.
AjReference number: PS0423; MUID:91216437; PMID:2022319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Cross-references: GB: AE004437; NID: g10579798; PIDN: AAG18770.1; GSPDB: GN00138 C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H4 protein - Toxoplasma gondii (fragment)
N;Alternate names: diagnostic antigen H4
C;Species: Toxoplasma gondii
C;Species: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 09-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein Vng0151c [imported] - Halobacterium sp. NRC-1
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                                                                                                                                                                                                                                                                                     Length 51;
                                                                                                                              C;Keywords: hormone; pancreas Fil-30,31-51/Product: insulin #status experimental <MAT>Fil-30,000main: insulin chain B #status experimental <BCH>Fi31-51/Domain: insulin chain A #status experimental <ACH>Fi31-51/Domain: insulin chain A #status experimental <ACH>Fi31-51/Domain: insulin chain A #status experimental <ACH>Fi7-37,19-50,36-41/Disulfide bonds: #status predicted
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A;Molecule type: mRNA
A;Residues: 1-96 <400H>
A;Cross.references: GB:M57302; NID:g161914; PID:g161915
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                                                                                                                                                                                                                                                                                  2.5%; Score 7; DB 2;
100.0%; Pred. No. 8.5;
tive 0; Mismatches
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Best Local Similarity
Matches 7; Conserva
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                                                 A; Molecule type: protein
A; Residues: 31-51 <NOU1>
C; Superfamily: insulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-93 <STO>
A;Residues: 1-30 <NOU2>
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                           A;Accession: S63590
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C;Species: Ornithorhynchus anatinus (duckbill platypus)
C;Species: Ornithorhynchus anatinus (duckbill platypus)
C;Date: 19-Mar-1997 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: S63591; S63590
R;Nourse, A.; Treacy, G.B.; Shaw, D.C.; Jeffrey, P.D.
Biol. Chem. Hopper-Seyler 377, 147-153, 1996
A;Title: Platypus insulin: indications from the amino acid sequence of significant diffe A;Reference number: S63590; MuID:97021710; PMID:8868070
                                                                                                                                                                                                     C;Accession: G75599
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-643 <WHI>
A;Cross-references: GB:AE001862; GB:AE001825; NID:g6460468; PIDN:AAF12254.1; PID:g646054
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                 A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Accession: G75599
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A,Gene: cgl
                                                                                                                              probable drug transport protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
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100.0%; Pred. No. 6.9;
tive 0; Mismatches
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100.0%; Pred. No. 9.6
tive 0; Mismatches
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Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-950 <SUX>
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A;Molecule type: DNA
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EMBO J. 6, 3313-3316, 1987

A, Title: Molecular cloning of two CD7 (T-cell leukemia antigen) cDNAs by a COS cell exp A, Reference number: S03520; MUID: 88111517; PMID: 3501369

A, Accession: S03520
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R; Kucoda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
R; M.; A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A; Reference number: A89758; MUID:21311952; PMID:11418146
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A)Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein sarH2 [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Date: 10-May_2001 #sequence_revision 10-May_2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Keywords: glycoprotein; membrane protein; surface antigen; tandem repeat F1.25/Domain: signal sequence #status predicted <SIG> F;26-240/Product: T-cell surface glycoprotein CD7 #status predicted <MAT> F;145-180/Region: 9-residue repeats (X-P-P-X-A-S-A-L-P)
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A;Cross-references: BMBL:X06180; NID:g29819; PIDN:CAA29546.1; PID:g732757
                                                                                                                                           A;Cross-references: GB:M37271; NID:g180163; PIDN:AAA51953.1; PID:g180164
R;Aruffo, A.; Seed, B.
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R;Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1998
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Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches
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tive 0; Mismatches
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A;Map position: 17q25.2-17q25.3
A;Introns: 28/1
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Matches 7; Conservative
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A;Accession: T40807
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A;Molecule type: DNA
A;Residues: 1-247 <KUR>
                                                                                                                          A, Residues: 1-240 <SCH>
A,Accession: A39016
A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
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Cypothetical protein SSO1462 [imported] - Sulfolobus solfataricus
CySpecias Sulfolobus solfataricus
CySpecias Sulfolobus solfataricus
CySpecias Sulfolobus solfataricus
CyBate: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
CyAccession: C90304
RySth, Cy: Sindph, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Changong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Submitted to GenBank, April 2001
A; Description: Sulfolobus solfataricus complete genome.
A; Reference number: A99139
A; Accession: C90304
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-107 < KUR>
A; Conserved: Conserved: Conserved: CyConserved: CyConse
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T-cell surface glycoprotein CD7 precursor - human
N.Alternate names: T-cell leukemia antigen
N.Alternate names: T-cell leukemia antigen
C;Abterias: Homo sapiens (man)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 05-Nov-1999
C;Accession: A39016; S03520
C;Accession: A.B.; Fleenor, D.E.; Kurtzberg, J.; Haynes, B.F.; Kaufman, R.E.
Proc. Natl. Acad. Sci. U.S.A. 88, 603-607, 1991
A.Title: Isolation and characterization of the genomic human CD7 gene: structural simila A;Reference number: A39016; MUID:91110576; PMID:1703303
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C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C; Accession: G72549 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C; Accession: G72549 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C; Accession: C; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; R
awa, H.; Takamiya, M.; Yamazaki, J.; R
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A; Reference number: A72450; MUID:99310339; PMID:10382966
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A, Molecule type: DNA
A, Recule type: DNA
A, Cross-references: DDBJ:AP000062; NID:95105244; PIDN:BAA80676.1; PID:d1044462; PID:9510
A, Experimental source: strain K1
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100.0%; Pred. No. 16;
tive 0; Mismatches
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Matches 7; Conservative
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hes 7; Conservative
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A,Cross-references: GB:AE001509; CA,Experimental source: strain J99
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    R. Simpson, A. J. G.; Reinach, F. C.; Arruda, P.; Abreu, F. A.; Carraro, D.M.; Carrer, H Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H Briones, M.S.; Bueno, M.R.; Ferro, J.S.; Franco, D.M.; Carrer, H SAuthors: Ferreira, V. C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm C.D.; Junqueira, M.L.; Kanper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigt Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.W.; Martino, C.L.; Marques, M.V.; Martins, B.A; Muthors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
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R)anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A)Title: 406, 151-157, 2000
A)Title: A)Reference number: A82515; MUID: 20365717; PMID: 10910347
A)Reference number: A82515; MUID: 20365717; PMID: 10910347
A)Note: for a complete list of authors see reference number A59328 below
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A; Map position: 1
C; Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase
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A;Cross-references: EMBL:Z97209; PIDN:CAB10128.1; GSPDB:GN00066; SPDB:SPAC19G12.16c
A;Experimental source: strain 972h-; cosmid c19G12
                             A;Residues: 1-251 <BEC>
A;Cross-references: EMBL:AL032684; PIDN:CAA21798.1; GSPDB:GN00067; SPDB:SPBP8B7.13
A;Experimental source: strain 972h-; clone pl p8B7
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H82736
hypothetical protein XF0992 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cispecies: Schizosaccharomyces pombe
Cispecies: Schizosaccharomyces pombe
Cispecies: Schizosaccharomyces pombe
Cispecies: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 03-Nov-2000
Cispecies: 1738003
Rioliver, K.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
A;Reference number: 221760
A;Accession: T38003
A;
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C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPBP8B7.13
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100.0%; Pred. No. 36;
tive 0; Mismatches
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Matches 7; Conserv
                                                                                                                                                                                                                      A; Gene: SPDB: SPBP8B7.13
A; Map position: 2
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A; Status: preliminary
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A; Molecule type: DNA
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hypothetical protein CT839 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species: Chlamydia trachomatis
C;Decies: Chlamydia trachomatis
C;Decies: 08-001-1998
#sequence_revision 13-Sep-1998 #text_change 08-001-1999
C;Accession: G71465
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell
A;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia track, Reference number: A71570; MUID:99000809; PMID:9784136
Rodrigues, U.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasal A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A;Contents: annotation
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cjacession: D71887
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; J. Twes, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pat. A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: D71887
A;Accession: D71887
A;Molecule type: DNA
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-354 <ARN>
A;Cross-references: GB:AE001356; GB:AE001273; NID:g3329299; PIDN:AAC68436.1; PID:g33293:
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
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C;Keywords: isomerase
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A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 28-Jul-2000
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100.0%; Pred. No. ...
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Pred. No. 44;
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100.0%; Pred. No. 43;
tive 0; Mismatches
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Ribergez, P.; Doignon, F.; Crouzet, M. Yeast II, 967-974, 1995. Yeast II, 1967-974, 1995. A;Title: The sequence of a 44 420 bp fragment located on the left arm of chromosome XI A;Reference number: S58711; MUID:96021608; PMID:8533472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rishe, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chal Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A; Description: Sulfolobus solfataricus complete genome.
A; Reference number: A99139
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A; Residues: 1-420 <BER.>
A; Cross-references: EMBL:U12141; NID:g1314216; PIDN:AAA99645.1; PID:g994821
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
R; Bergez, P.; Doignon, F.; Crouzet, M.
submitted to the Protein Sequence Database, April 1996
A; Reference number: S62975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB: AE006641; NID: 913813800; PIDN: AAK40942.1; GSPDB: GN00155
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C;Date: 08-701-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
C;Date: 08-701-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
C;Accession: S33916; S58712; S62994; S62998; S63945
R;Poehlmann, R.; Philippsen, P.
submitted to the EMBL Data Library, April 1995
A;Reference number: S53896
A;Reference number: S53896
                                                                                                                                                                                                                                                                                              hypothetical protein purF-2 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: G90210
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A, Status: nucleic acid sequence not shown; translation not shown
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A; Residues: 1-420 < POB>
A; Cross-references: EMBL:X86470; NID:g791101; PID:g791122
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R;Poehlmann, R.; Philippsen, P.
submitted to the Protein Sequence Database, April 1996
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100.0%; Pred. No. 52;
ive 0; Mismatches
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Best Local Similarity 100.
Matches 7; Conservative
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    234 DAEYGLY 240
                                                                             157 DAEYGLY 163
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A;Residues: 1-420 <PC
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submitted to Genbank, June 2000, H.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Unqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigrado, M.A.; Madeira, A.M.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, E.M.P.; Matsukuma, A.Y.; Menork, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunse, L.R.; Oliveira, A.Y.; Menork, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunses, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.R. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors and Silva, A.C.R.; da Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zhira A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein XF1611 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: C82660
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717, PMID:10910347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE002289; GB:AE002160; NID:g7190254; PIDN:AAF39099.1; PID:g71902¢
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                                                                                                                                                                                                                                   Conserved hypothetical protein TC0227 [imported] - Chlamydia muridarum (strain Nigg)
Conserved hypothetical protein TC0227 [imported] - Chlamydia muridarum, Chlamydia trachomatis MoBn
C; Species : Chlamydia muridarum, Chlamydia trachomatis MoBn
C; Accession: A81728
R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Helson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A; Reference number: A81500; MUID:2015025; PMID:10684935
A; Status: preliminary
A; Molecule type: DNA
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100.0%; Pred. No.,46;
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                                                      150 KENDRIF 156
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251 KENDRIF 257
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-401 <SIM>
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A;Reference number: A71250; MUID:98332770; PMID:9665876

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Zinc metalloproteinase homolog [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: E84192
R;Ny W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, i. Fieithauser. B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl. Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: E84192
A;Scatus: preliminary
A;Molecule type: DNA
A;Status: Scroy.
                            A,Accession: G71272
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Molecule type: DNA
A,Ress: 1-427 <COL>
A,Cross-references: GB:AE001256, GB:AE000520; NID:g3323171; PIDN:AAC65826.1; PID:g33231.
A,Experimental source: strain Nichols
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R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelsen, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A; Reference number: A81500; MUID:20150255; PMID:10684935
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Reywords: phosphoprotein; pyridóxal phosphate; sulfurtransferase
F;232/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
F;374/Active site: Cys (cysteine persulfide intermediate) #status predicted
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100.0%; Pred. No. 55;
iive 0; Mismatches
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nes 7; Conservative
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B72109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein At2g38590 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001 C;Accession: H84806 R;Ath, X:; Kaul, S:; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
                                                                                                            A;Title: Sequencing a cosmid clone of Saccharomyces cerevisiae chromosome XIV reveals A;Reference number: S63925; MUID:96267764; PMID:8701611
A;Accession: S63945
                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X86470; NID:g791101; PIDN:CAA60196.1; PID:g791122
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
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AjTille: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84806
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A;Molecule type: DNA
A;Residues: 1-424 <STO>
A;Cross-references: GB:AE002093; NID:g3786013; PIDN:AAC67359.1; GSPDB:GN00139
C;Genetics:
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C;Keywords: mitochondrion
F;1-46/Domain: transit peptide (mitochondrion) #status predicted <TNP>F;46-420/Product: SUN4 protein #status predicted <MAT>
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A;Map position: 2
C;Superfamily: Arabidopsis thaliana hypothetical protein T1F15.9
                                                                                                                                                                                                                                                              A; Status: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A;Residues: 1-420 <POF>
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100.0%; Pred. No. 54;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: SGD:S0005010; MIPS:YNL066w
A, Experimental source: strain S288C
R, Poehlmann, R., Philippsen, P.
Yeast 12, 391-402, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 VAVITVY 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 14L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Genome: nuclear
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probable udp-n-acetylglucosamine pyrophosphorylase - fission yeast (Schizosaccharomyce: Schizosaccharomyces pombe C;Species Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T39359 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 shood, V: Rajandream, M.A.; Barrell, B.G.; Oliver, K.; Harris, D. submitted to the EMBL Data Library, March 1999 A;Reference number: Z21848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: EMBL:AL035675; PIDN:CAB38688.1; GSPDB:GN00067; SPDB:SPBC1289.08
A:Experimental source: strain 972h-; cosmid c1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:Z81041; PIDN:CAB02786.1; GSPDB:GN00023; CESP:C27A7.2 A;Experimental source: clone C27A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jan-1994 #sequence revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A47503; S17104; S19319
C;Accession: A47503; S17104; S19319
J. Shol. Chem. 268, 17623-17627, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein C27A7.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 26-May-2000
C;Accession: T19496
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A;Introns: 44/3; 87/2; 130/2; 164/3; 203/2; 273/3; 325/1; 369/2
C;Superfamily: Caenorhabditis elegans hypothetical protein F07G11.3
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A.Residues: 1-511 «MIL»
                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Accession: T39359
A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.5%; Score 7; DB 2;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches
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             Mismatches
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             7; Conservative
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A;Map position: 2
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                                                                  25 LLOSLCV 31
                                                                                                                 76 LLÓSLCV 82
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A; Residues: 1-475 < WOO>
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             Matches
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Accession: C86512
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: C86512
A;Accession: preliminary
A;Molecule type: DNA
A;Residues: 1-429 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: E81558
A;Molecule type: DNA
A;Residues: 1-429 <REB>
A;Coss.references: GB:AE002218; GB:AE002161; NID:g7189509; PIDN:AAF38415.1; PID:g718951
A;Experimental source: strain AR39, HL cells
C;Genetics:
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A;Cross-references: GB:AP003602; PIDN:BAB77244.1; PID:g17134686; GSPDB:GN00181
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:BA000008; NID:g8978544; PIDN:BAA98381.1; GSPDB:GN00142
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                                                                                                                                                                   A;Gene: guaA; CP0599
C;Superfamily: GMP Bynthase (glutamine-hydrolyzing); trpG homology
F;11-194/Domain: trpG homology <TRG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.5%; Score 7; DB 2; Length 429; 100.0%; Pred. No. 55; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                               Length 429;
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100.0%; Pred. No. 55;
tive 0; Mismatches
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Best Local Similarity 100.(
Matches 7; Conservative
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Best Local Similarity

Query Match

A; Genome: plasmid A; Gene: all7601

A, Status: preliminary A; Molecule type: DNA

155 ESSRSGH 161

A; Gene: guaA

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Gaps . 0

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conserved hypothetical protein Atu3866 [imported] - Agrobacterium tumefaciens (strain C: C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein AGR_L_1958 [imported] - Agrobacterium tumefaciens (strain C58, Cer. S.Speciess Agrobacterium tumefaciens
C;Speciess Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: G98253
R;Godher, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman A; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-233, 2011
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tur A,Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Accession: AE3032
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A;Molecule type: DNA
A;Residues: 1-801 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL44675.1; PID:g17742302; GSPDB:GN00187
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                                                                                                                                    A;Accession: T22360
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-710 < WILL>
A;Cross-references: EMBL: Z99171; PIDN:CAB16314.1; GSPDB:GN00019; CESP:F47G4.2
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C;Accession: T22360
R;White, S.
submitted to the EMBL Data Library, September 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Introns: 20/1; 131/3; 220/2; 273/1; 380/2; 577/2
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                                                                                                                                                                                                                                                                                                                         A; Experimental source: clone F47G4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: linear chromosome
                                                                                                          A; Reference number: Z19553
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A; Residues: 1-801 <KUR>
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A; Status: preliminary
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A;Gene: CESP:F47G4.2
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A,Reference number: S19319; MUID:92077134; PMID:1743286
                                                                                                                                                                                                                                                                         A,Note: sequence extracted from NCBI backbone (NCBIN:136329, NCBIP:136330)
R;Arand, M.; Knehr, M.; Thomas, H.; Zeller, H.D.; Oesch, F.
Submitted to the BMBL Data Library, September 1991
A;Description: The unusual bicompartimental distribution of cytosolic epoxide hydrolase A;Reference number: S17104
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A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: C82280
R;Heidelberg, U.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Title: Isolation and characterization of a cDNA encoding rat liver cytosolic epoxide ]
A;Reference number: A47503; MUID:93352557; PMID:8349641
A;Accession: A47503
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C;Superfamily: two-component sensor histidine kinase; sensor histidine kinase homology
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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                                                                                                   A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-554 <KMB-
A;Cross-references: GB:X65083; NID:g402631; PIDN:CAA46211.1; PID:g402632
A;Experimental source: liver
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A;Residues: 450-554 <ARA>
A;Cross-treferences: EMBL:X60328; NID:g55929; PIDN:CAA42898.1; PID:g55930
R;Arand, M.; Knehr, M.; Thomas, H.; Zeller, H.D.; Oesch, F.
FEBS Lett. 294, 19-22, 1991
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A;Residues: 448-554 <AR2>
C;Keywords: cytosol; ether hydrolase
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-565 <HEI>
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A,Gene: gp14
C;Superfamily: herpesvirus glycoprotein B
C;Superfamily: herpesvirus glycoprotein by S;Seywords: glycoprotein; transmembrane protein
F;1-66/Domain: signal sequence # status predicted <SIG>F;1-86/Domain: signal sequence # status predicted <WAT>F;87-979/Product: glycoprotein 14 #status predicted <WAT>F;831-871/Region: hydrophobic
F;831-871/Region: hydrophobic
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A;Title: Characterization of the gene and an antigenic determinant of equine herpesvir
A;Reference number: JH0109; MUID:90236317; PMID:1692002
A;Accession: JH0109
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Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome wustl.edu/gsc/C elegans/ and www sanger.ac.uk/Projects/C e. A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
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A;Molecule type: DNA
A;Roaddues: 1-926 <MLS.
A;Readdues: 1-926 <MLS.
A;Cross-references: EMBL:U40797; NID:g1065916; PID:g1065927; PIDN:AAB37553.1; GSPDB:GN-A;Experimental source: strain Bristol N2; clone C28C12
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A;Note: glycoprotein 14 is homologous to corresponding glycoprotein of pseudorabies,
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A;Introns: 18/3; 98/2; 173/2; 206/3; 298/3; 405/3; 488/3; 727/3; 761/1; 828/2
                                                                                 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T15683
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C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 26-Aug-1999
C;Accession: JH0109
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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: E88465
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                                                                                                                                                              Rimiller, N. submitted to the EMBL Data Library, November 1995 Ajbescription: The sequence of C. elegans cosmid C28C12. A; Accession: T15683
        Caenorhabditis elegans
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    hypothetical protein C28C12.10 - C
C;Species: Caenorhabditis elegans
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Matches 7; Conserv
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C;Specias: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: D90183
C;Accession: C;Acce
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A;Cross-references: GB:AE006641; NID:g13813545; PIDN:AAK40723.1; GSPDB:GN00155
C;Genetics:
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A;Introns: 49/3; 144/1; 319/2; 376/3; 484/2; 540/3; 573/2; 612/3; 720/3; 776/3
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A;Cross-references: EMBL:Z38112; PIDN:CAA86232.1; GSPDB:GN00021; CESP:E03A3.2
A;Experimental source: clone E03A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein E03A3.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20430
R;Gardner, A.
submitted to the EMBL Data Library, October 1994
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                                                                                                                                                              Length 801;
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A, Accession: T20430
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
                                                                                                                                                                  DB 2;
                                                                                                                                                              2.5%; Score 7; DB 2;
100.0%; Pred. No. 95;
tive 0; Mismatches
                                                                             A; Map position: linear chromosome
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Best Local Similarity 100...
7; Conservative
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                                                                                                                                                                                                                                                                                                                                 272 ASFFGAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                  216 ASFFGAF 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           756 EYGLYSI 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 ENDRIFU 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 517 ENDRIFY 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Gene: CESP:E03A3.2
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C;Genetics:
A;Gene: AGR_L_1958
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RESULT 34 T15683

Matches

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A;Map position: 1
A;Introns: 40/2; 70/1; 152/2; 318/2; 429/3; 494/2; 538/3; 564/3; 625/3; 654/3; 782/3; 8:
C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 5
A;Introns: 56/3; 76/1; 101/1; 161/1; 196/1; 226/3; 269/2; 318/1; 364/1; 475/3; 520/2; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlAccession: E64477
Ribult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Facily, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A. reach, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi A;Reference number: A64300; WuID:96337999; PMID:8688087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-1847 <BUL>
A;Cross-references: GB:U67583; GB:L77117; NID:g2826409; PIDN:AAB99433.1; PID:g1592072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AF067949; PIDN:AAC19236.1; GSPDB:GN00023; CESP:T10H9.2 A;Experimental source: strain Bristol N2; clone T10H9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cispecies: Caenorhabditis elegans
Cibate: 29-0c1-1999 #sequence_revision 29-0c1-1999 #text_change 29-0c1-1999
Cibacesion: T33236
RiGreco, T.; Bradshaw, H.; O'Brien, D.
submitted to the RMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid T10H9.
A;Reference number: Z21306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         replication factor C homolog - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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No. 1.5e+02;
0; Indels
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2.5%; Score 7; DB 2; Length 1414;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                      Length 1377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein T10H9.2 - Caenorhabditis elegans
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2.5%; Score 7; DB 2; L
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                  Query Match 2.5%; Score 7; DB 2
Best Local Similarity 100.0%; Pred. No. 1.5
Matches 7; Conservative 0; Mismatches
A;Experimental source: clone F26H9
C;Genetics:
A;Gene: CESP:F26H9.8
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A;Start codon: TTG
                                                                                                                                                                                                                                                                                                                                                                                                                                      1014 NIHLRNG 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1110 RGPORVA 1116
                                                                                                                                                                                                                                                                                                                                                                       166 NLHLRNG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 RGPQRVA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-1414 <GRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: CESP: T10H9.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Accession: T33236
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                    A;Cross-references: GB:chr_III; PIDN:AAA68379.1; PID:g861359; GSPDB:GN00021; CESP:B0244.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: T36031

R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, March 1999
A;Reference number: Z21581
A;Accession: T36031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AL035591; PIDN:CAB38148.1; GSPDB:GN00070; SCOEDB:SCC54.18c A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: uvrA; SCOEDB:SCC54.18c
C;Superfamily: excinuclease ABC chain A; ATP-binding cassette homology
C;Superfamily: bNA binding; bNA repair; hydrolase; nucleotide binding; P-loop
F;32-39/Region: nucleotide-binding motif A (P-loop)
F;645-652/Region: nucleotide-binding motif A (P-loop)
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A;Residues: 1-1377 <WIL>
A;Cross-references: EMBL:Z81467; PIDN:CAB03874.1; GSPDB:GN00019; CESP:F26H9.8
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A;Molecule type: DNA
A;Residues: 1-1377 <WI2>
A;Cross-references: EMBL:Z81516; PIDN:CAB04207.1; GSPDB:GN00019; CESP:F26H9.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 excinuclease ABC chain A SCC54.18c [similarity] - Streptomyces coelicolor N;Contains: excision endonuclease ABC (EC 3.1.-.-) chain A C. Species: Streptomyces coelicolor C: Species: Streptomyces coelicolor C: Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                 2.5%; Score 7; DB 2; Length 982; 100.0%; Pred. No. 1.16+02; tive 0; Mismatches 0; Indels
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Molecule type: DNA
A;Residues: 1-1014 <SEE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Experimental source: clone C12C8
R, Baynes, C.
submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                 Query Match 2.5
Best Local Similarity 100.
Matches 7; Conservative
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A;Accession: T21444
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                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-982 <STO>
      A; Accession: E88465
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RESULT 38

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A;Molecule type: genomic RNA
A;Residues: 1504-1778,'V',1780-3434 <LEE>
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Best Local Similarity 100...
7; Conservative
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Matches 7; Conservative
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                                                                                                           A Status: preliminary
A Molecule type: DNA
A Residues: 1-1995 <TET>
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                                                                                                                                                                                                                                                                       A; Gene: NMB1779
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                                                                                                                                                   calcium channel alpha-1 chain, L-type - Stylophora pietillata
C;Species: Stylophora pistillata
C;Species: Stylophora pistillata
C;Species: 1-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
C;Accession: T43352
R;Zoccola, D.; Tambutte, E.; Senegas-Balas, F.; Michiels, J.F.; Failla, J.P.; Jaubert, J Gene 227, 157-167, 1999
A;Title: Cloning of a calcium channel alphal subunit from the reef-building coral, Stylc A;Reference number: Z22375; MUID:99148007; PMID:10023047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Neiseeria meningitidis
C;Species: Neiseeria meningitidis
C;Species: Neiseeria meningitidis
C;Cpate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: B81192
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Bisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Reference number: Agl000; MUID:20175755; PMID:10710307
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GB1044

GB1044

GB1044

C;Bemagglutuinn/hemolysin-related protein NMB1779 [imported] - Neisseria meningitidis (str...)
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: GB1044

R;Tettellin, H; Saunders, N.J; Heidelberg, J; Jeffries, A.C; Nelson, K.E.; Bisen, J.A.Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B81192
hemagglutinin/hemolysin-related protein NMB0497 [imported] - Neisseria meningitidis (str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1975 <TET>
A;Residues: 1-1975 <TET>
A;Cross-references: GB:AE002406; GB:AE002098; NID:g7225720; PIDN:AAF40929.1; PID:g722572
C;Genetics:
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C,Genetics:
A,Gene: CACHL
C,Superfamily: voltage-dependent calcium channel protein alpha-1 chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7; DB 2; Dems-
; Pred, No. 2e+02;
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Best Local Similarity 100.0%; Pred. No. 2.1
Matches 7; Conservative 0; Mismatches
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Best Local Similarity 100.0
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557 AMHITGT 563
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                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
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                                                                                                      RESULT 41
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genome polyprotein - Murray Valley encephalitis virus (strain Australia)
N;Contains: capsid protein; envelope protein; membrane protein; nonstructural protein |
N;Contains: capsid protein NS4b; nonstructural protein NS5
C;Species: Murray Valley encephalitis virus
C;Date: 30-Jun-1988 #sequence_revision 17-Feb-1994 #text_change 19-Jan-2001
C;Accession: A24635; A60288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: B81989
R;Parkhill, J; Achtman, M; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mor. Holroyd, S; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandrea Mature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-2015 <PAR>
A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83974.1; PID:g7379
C;Genetics: serogroup A, strain Z2491
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J. Mol. Biol. 187, 309-323, 1986
A;Title: Partial nucleotide sequence of the Murray Valley encephalitis virus genome: C.
A;Reference number: A24635; MUID:86200215; PMID:3009829
                                                                                                                                                                                                                                           ....... seterences: GB:AE002527; GB:AE00209B; NID:g7227023; PIDN:AAF42119.1; PID:g7227
A;Experimental source: serogroup B, strain MC58
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein NMA0688 [imported] - Neisseria meningitidis (strain Z2491 serogro
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A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
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A,Residues: 1-1780 < DAL>
A,Cross-references: GB:X03467; NID:g59329; PIDN:CAA27184.1; PID:g755731
R,Lee, E.; Fernon, C.; Simpson, R.; Weir, R.C.; Rice, C.W.; Dalgarno, L.
Virus Genes 4, 197-213, 1990
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100.0%; Pred. No. 2.1e+02;
iive 0; Mismatches 0; Indels
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0

Gaps

.; 0

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C; Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. etrain PCC 7120
A;Note: Nostoc sp. etrain PCC 7120 is a synonym of Anabaena sp. etrain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AF2105
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch: Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, i DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                         A,Gene: atp8
A,Genome: mitochondrion
A,Genomeic code: SGC2
C,Superfamily: yeast H+-transporting ATP synthase protein 8
C,Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; ox:
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C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 03-Feb-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:BA000019; PIDN:BAB74096.1; PID:g17131489; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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R; Haandrikman, A.J.; van Leeuwen, C.; Kok, J.; Vos, P.; de Vos, W.M.; Venema, Appl. Environ. Microbiol. 56, 1890-1896, 1990
A; Title: Insertion elements on lactococcal proteinase plasmids.
A; Reference number: A60157; MUID:90343335; PMID:2166472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein as12397 [imported] - Nostoc sp. (strain PCC 7120)
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                                                                                                                                                                                                                                             DB 2;
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100.0%; Pred. No. 92;
tive 0; Mismatches
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 21 IFTVLL 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-55 < KUR>
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A; Residues: 1-56 < HAA>
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                    C;Genetics:
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C,Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 03-Jun-2002
C;Accession: S78202
R;Lang, B.F.
C;Superfamily: yellow fever virus genome polyprotein
C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;
T;1-125/Product: capsid protein; #status predicted <CLC>
F;126-292/Product: membrane protein precursor #status predicted <GLC>
F;126-292/Product: membrane protein precursor #status predicted <GLC>
F;126-292/Product: membrane protein #status predicted <GLM>
F;18-292/Product: membrane protein #status predicted <CLM>
F;293-791/Domain: transmembrane #status predicted <LN>
F;293-791/Domain: transmembrane #status predicted <LN>
F;293-791/Pomain: transmembrane #status predicted <LN2>
F;194-1055/Product: monstructural protein NS1 #status predicted <NS1>
F;1206-1372/Product: monstructural protein NS2 #status predicted <NS2>
F;1504-2122/Product: monstructural protein NS2 #status predicted <NS3>
F;1697-1104/Region: mucleotide-binding motif A (P-loop)
F;1784-1789/Region: mucleotide-binding motif A (P-loop)
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R.Kim, C.Y.; Jeong, S.Y.; Choe, M.S.; Cheong, Y.H.; Han, C.D.; Cho, M.J.
submitted to the EMBL Data Library, March 1997
A; Description: Isolation and characterization of early inducible rice genes by a fungal A; Reference number: Z15314
A; Accession: T04365
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A; Description: The mitochondrial genome of the fission yeast Schizosaccharomyces pombe:
A; Reference number: S78195
A; Accession: S78202
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A,Molecule type: mRNA
A,Residues: 1-47 <KIM>A,Residues: 1-47 <KIM>A,COSS-references: EMBL:U95216; NID:g2443456; PIDN:AAB71382.1; PID:g2443457
A,GORETICS:
A,GORETICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Species: Oryza sativa (rice)
C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;2123-2414/Product: nonstructural protein NS4a #status predicted <N4A>
F;2415-2529/Product: nonstructural protein NS4b #status predicted <N84b
F;2530-3434/Product: nonstructural protein NS5 #status predicted <NS5>
F;73,140,446/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A,Residues: 1-48 <LAN>
A;Cross-references: EMBL:X54421; NID:g13639; PID:g1334456
A;Experimental source: strain ad7-50h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
2.5%; Score 7; DB 1; Les
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 91;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 VIFTVLL 26
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Best Local Similarity
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hypothetical protein ECs4963 [imported] - Escherichia coli (strain O157:H7, substrain
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Cispecies: Escherichia coli
Cispecies: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
Ciscession: C91249
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, Gasawara, N.; Yasunaga, T.; Ruhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Ritle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gasaware, number: A99629; MUID:21156231; PMID:11258796
                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-65 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD02513.1; PID:g16503375; GSPDB:GN00176
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:BA000007; PIDN:BAB38386.1, PID:g13364439; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Species: Saccharomyces cerevisiae
C,Date: 15-Jan-1999 #sequence_revision 15-Jan-1999 #text_change 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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100.0%; Pred. No. 1.6e+02;
rative 0; Mismatches 0; Indels
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A;Description: The sequence of S. cerevisiae cosmid 9476.
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2.1%; Score 6; DB 2; Ler
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0;
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2.1%; Score 6; DB 2; Les
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0;
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A;Residues: 1-89 <DUZ>
A;Cross-references: EMBL:UZ8372; MIPS:YDR363w-a
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A;Cross-references: SGD:S0007235
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Best Local Similarity 100.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 IKENTK 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-85 < HAY>
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A; Accession: AC0774
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       hypothetical protein STV2363 [imported] - Salmonella enterica subsp. enterica serovar Typic (5)Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi (5)Accession: AC0774 #squence_revision 09-Nov-2001 #text_change 18-Nov-2002 (5)Accession: AC0774 #squence_revision 09-Nov-2001 #text_change 18-Nov-2002 (5)Accession: AC0774 #squence_revision 09-Nov-2001 #text_change 18-Nov-2002 (5)Accession: AC0774 #squence_revision N.R.; Pickard, D.; Wain, J.; Churcher, th. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
A; Moule, S.; O'Gaora, P.
A; Mature 413, 848-852, 2001
A; Authors: Assorbed and Acoustic and Action ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable bacterioferritin-associated ferredoxin bfd [imported] - Yersinia pestis (strain C;Species: Yersinia pestis (strain C;Species: Yersinia pestis (c;Date: O2-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 17-May-2002 C;Accession: AG0025 R;ParkHill, J: Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. Accession: A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
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C;Genetics:
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A;Map position: circular chromosome
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A; Residues: 1-64 < KUR>
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A; Status: preliminary
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A; Residues: 1-102 «KUR»
A; Residues: 1-102 «KUR»
A; Cross-references: GB: AE006469; PIDN: AAX65261.1; PID: g14523712; GSPDB: GN00165
A; Cross-references: STrain 1021, megaplasmid psyma
A; Experimental source: strain 1021, megaplasmid psyma
R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
Bela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
Science 293, 668-572, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K
A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. BDNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gench A;Reference number: A99629; MUID:21156231; PMID:11258796
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N;Alternate names: hypothetical protein Y (pbpF 5' region)

C;Species: Bacillus subtilis

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999

C;Accession: E69832; C40614

C;Accession: E69832; C40614

C;Accession: E69832; C40614

C;Bron, S; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch. Barte A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Exrington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable cytochrome C fragment [imported] - Sinorhizobium meliloti (strain 1021) magapl.
                                                                                                                                                                                                                                                                                          A;Cross-references: GB:BA000007; PIDN:BAB38382.1; PID:g13364435; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0;
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tes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 SFFGAF 20
                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <HAY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Riwood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein EC84959 [imported] - Bscherichia coli (strain O157:H7, substrain RI C;Species: Bscherichia coli (5) Pate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 (5) Accession: (6) 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE004139; GB:AE003852; NID:g9654953; PIDN:AAF93695.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                  conserved hypothetical protein VC0527 [imported] - Vibrio cholerae (strain N16961 serogr
                                                                                                                                                                                                                                       R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10352301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transposase inp [imported] - Agrobacterium tumefaciens (strain CS8, Dupont) plasmid AT C, Species: Agrobacterium tumefaciens C, Species: il-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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                                                                                                                                                                 C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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100.0%; Pred. No. 1.7e+02;
iive 0; Mismatches 0; Indels
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A;Molecule type: DNA
A;Residues: 1-96 <HEI>
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A;Molecule type: DNA
A;Residues: 1-96 <KUR>
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hi:
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans an
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                            pathogenic anti-mouse red blood cell autoantibod
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: A44887
R; Hogan, A.; Heyner, S.; Charron, M.J.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Development 113, 363-372, 1991
A; Title: Glucose transporter gene expression in early mouse embryos.
A; Reference number: A44887; MUID:92111400; PMID:1765007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glucose transporter isoform 1, GLUT 1 - mouse (fragment)
C,Species: Mus musculus (house mouse)
C,Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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                                                                                                                                                                                                                                                                   A; Cross-references: EMBL:X51852; NID:g55393; PIDN:CAA36145.1; PID:g930229
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                                                        A,Title: Variable region sequences of pathogenic anti-mc
A,Reference number: S09955, MUID:90269328; PMID:2347362
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2.1%; Score 6; DB 2; Ler
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0;
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                         Eur. J. Immunol. 20, 771-777, 1990
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A; Residues: 1-107 < HOG>
                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-107 <REI>
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A; Residues: 1-109 <STO>
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A; Status: preliminary
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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler jech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurta, K.; Lapidue, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadis, Y.; Sto, T.; Scanlon, A,Authors: Schleich, S.; Schroceter, R.; Scoffone, F.; Sediguchi, J.; Sekowska, A.; Seror A,Authors: Schleich, S.; Carnoter, R.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, R.; Minters, P.; Wipat, A.; Yamaneto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, R.; Tile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Accession: E69832
A;Accession: E69832
A;Accession: E69832
A;Accession: E69832
A;Accession: Schom, A.; Accession: Schom, A;Molecule type: DNA
A;Residues: 1-104 <KUN>
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C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C;Accession: S09964
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
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Best Local Similarity 100...
Loca 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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C; Genetics:
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Proc. Natl. Acad. Sci. U.S.A. 83, 9134-9138, 1986
A;Title: Structural differences in a single gene encoding the V-kappa-Ser group of ligh:
A;Reference number: A94141; MUID:87067464; PMID:3097643
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path, A;Reference number: A82950; MUID:20437337; PMID:10984043
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A, Status: preliminary
A, Molecule type: DNA
A, Molecule 116 < 25Tro>
A, Robertiues: 1-116 < 25Tro>
A, Cross-references: GB: AE004801; GB: AE004091; NID: g9950011; PIDN: AAG07229.1; GSPDB: GN00
A, Experimental source: strain PAO1
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Ciperate: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
Ciperate: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
Ciperate: 19-174
RNO1ling, U.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
.; Daly, M.J.; Bennett, G.N.; Xoonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl.
A;Reference number: A96900; MUID:21359325; PMID:21359325
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A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable chaperone PA3842 [imported] - Pseudomonas aeruginosa (strain PAO1)
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                                                                                                                                                                            A, Residues: 1-115 <BOX>
A, Cross-references: GB:M14360; NID:g197464; PIDN:AAA39034.1; PID:g197465
A, Experimental source: strain BALB/c
                                                                                                                                                                                                                                                                                                                       Aintrons: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Product: Ig kappa chain V region Ser-b #status predicted <MAT>
F;36-110/Domain: immunoglobulin homology <IMM>
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C;Superfamily: Yersinia pestis plasmid pCD1 hypothetical protein
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o. 2e+02;
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A;Molecule type: DNA
A;Residues: 1-117 <KUR>
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                                                                                                                                                                                                       Conserved hypothetical protein Atu2526 [imported] - Agrobacterium tumefaciens (strain C5 C5pecies: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #text_change 18-Nov-2002 C;Accession: AC2887 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I R;Wood, D.W.; Setubal, Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Science 294, 2317-2323, 2001 A;Athores: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein AGR C 4590 [imported] - Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium_tumefaciens
C; Species: Agrobacterium_tumefaciens
C; Species: Agrobacterium_tumefaciens
C; Accession: H97662
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:21608551; PMID:11741194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Accession: AC2887
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A,Reaidues: 1-112 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL43513.1; PID:g17741022; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
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A;Residues: 1-112 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK88257.1; PID:g15157717; GSPDB:GN00169
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RNGELV 43
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RESULT 65

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RESULT 66 B25924

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R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G. il, M.; Kutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AH0043
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-128 «KUR»
A;Cross_references: GB:AL590842; PIDN:CAC89211.1; PID:g15978450; GSPDB:GN00175
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Kreiware C. Stromb, J. F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R. Fromb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Khalak, H.G.; Glodek, A.; McKen son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidmann, J.M.; Fujii, C.; Bowman, C.; Matthey, M. Mature 388, 539-547, 1997

Ajauthors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A;Reference number: A64520; MUID: 97394467; PMID: 9252185
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A;Residues: 1-130 <TOM>
A;Cross-references: GB:AE000549; GB:AE000511; NID:g2313403; PIDN:AAD07385.1; PID:g2313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehr Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A;Reference number: A86625; WUDD:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE005176; PID:g12724648; PIDN:AAK05736.1; GSPDB:GN00146
A;Experimental source: strain IL1403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein HP0316 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
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100.0%; Pred. No. 2.2e+02;
rative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                         AjGene: YPO0352
C;Superfamily: Bscherichia coli hypothetical protein 0128
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Best Local Similarity 100...
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A;Molecule type: DNA
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A)Cross-references: GB:BA000018; PID:g13700285; PIDN:BAB41583.1; GSPDB:GN00149
A)Experimental source: strain N315
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001 C;Accession: AH0043
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
                                                                        2.1%; Score 6; DB 2; Length 117; 100.0%; Pred. No. 2e+02; trive 0; Mismatches 0; Indels
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Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                     6; Conservative
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                                                                                                                                                                    171 NGELVI 176
                                                                                              Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                 91 NGELVI 96
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A;Status: preliminary
A;Molecule type: DNA
                           A; Gene: CAC2228
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  C, Genetics:
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D89803
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0; Gaps

; Pred. No. 2.2e+02; 0; Mismatches 0; Indels

Best Local Similarity 100.0%; Matches 6; Conservative 0

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CjAccession: F70650

R/Cole S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Perkhill, M.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devies, R.; Devies, R.; Devies, R.; Devies, R.; Bernier, S.; Seeger, K.; Skelton, S.; Squares, S. Mature 393, 537-544, 1998

A) Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A) Attle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A) Reference number: A70500; MUID:98295987; PMID:9634230

A) Accession: F70650

A) Accession: F70650

A) Accession: P70650

A) And Park B. And B. An
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cjaccession: ACO885
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, H. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: ABO502; MUID:21534947; PMID:11677608
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A;Cross-references: GB:Z83866; GB:AL123456; NID:g3261691; PIDN:CAB06254.1; PID:g1781144
A;Experimental source: strain H37Rv
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A;Molecule type: DNA
A;Residues: 1-134 <PAR>
A;Residues: 1-134 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD06026.1; PID:g16503993; GSPDB:GN00176
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein Rv3069 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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A;Gene: Rv3069
C;Superfamily: hypothetical protein MJ1523
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194 EEIKEN 199
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A Botchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Brownstein M.J., Ugdin T.B., Ponaldo M.F., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

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A Nilalon D.K., Muzny D.M., Sodergren E.J., Iu X., Gibbs R.A., G.

A Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Butterfield Y.S.N., Krzywinski M.I., Skalska W., Smailus D.E.,

B Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

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                                                                                                                 01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
10-0cT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).
HOMEO SAPIOR (Human).
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J. Biol. Chem. 271:12687-12690(1996).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hymnwitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,
Relley R.F., Ashkenazi A., de Vos A.M.;
"Triggering cell death: the crystal structure of Apo2L/TRAIL in a complex with death receptor 5.";
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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TISSUE=Placenta;
MEDLINE=96278649; PubMed=8663110;
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                                            STANDARD;
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X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
       CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                        SUBCELLULAR LOCATION: Type II membrane protein (Potential).
TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG
                                                                                                                          COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00251; TNF 1; 1.

PROSITE; PS50049; TNF 2; 1.

Cytckine; Apoptosis; Transmembrane; Signal-anchor; Metal-binding; Zinc; 3D-structure.

DOMAIN

TRANSMEM

18

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTI
                                                                                                                                                                                        SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
ZINC.
                                                                                                                                                                                                                                                                                                                                                                                       GO, GO:0005887; C:integral to plasma membrane; TAS. GO; GO:0005625; C:soluble fraction; TAS. GO; GO:0005102; F:receptor binding; TAS. GO; GO:0007267; F:recell-cell signaling; TAS. GO; GO:0006917; F:induction of apoptosis; TAS. GO; GO:0006917; F:induction of apoptosis; TAS. GO; GO:0006917; F:induction of apoptosis; TAS. InterPro; IPR000652; TNF family.

InterPro; IPR0008983; TNF Tike.
Fram; PF00229; TNF 1.

ProDom; PF002012; TNF 2.

ProDom; PF002012; TNF 2.

SMART; SM00207; TNF; 1.
MEDLINE=99413670; PubMed=10485660;
                                                                                                                                                                                                                                                                                           EMBL, U37518; AAC50332.1; -.
EMBL, U57059; AAB01233.1; -.
EMBL, BC032722; AAH32722.1; -.
                                                                                                                                                                                                                                                                                                                                                                       HGNC:11925; TNFSF10.
                                                                                                                                              SUBUNIT: Homotrimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             induce apoptosis.
                                                                                                                                                                                                                                                                                                                            PDB; 1D0G; 22-OCT-99.
PDB; 1D4V; 01-NOV-99.
PDB; 1D2Q; 11-FEB-00.
PDB; 1DG6; 26-SEP-01.
                                                                                                                                                                             AND PROSTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:119
MIM; 603598; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNIHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDSYWDPNDEESMNSPCWQVKWQLRQLVRKWILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                         1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDITRE=96111955; PubMed=8777713;
Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
Wicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
Goodwin R.G.;
"Identification and characterization of a new member of the TNF
family that induces apoptosis.";
"Immunity 3:673-682(1995).
"INFRSTION-TRAILE1,
TNFRSTION-TRAILE1,
TNFRSTION-TRAILE2, TNFRSFION-TRAILE1,
may be modulated by binding to the decoy receptore
TNFRSFION-TRAILE3, TNFRSFION-TRAILE1,
TNFRSFION-TRAILE3, TNFRSFION-TRAILE1,
TNFRSFION-TRAILE3, TNFRSFION-TRAILE1,
TNFRSFION-TRAILE3, TNFRSFION-TRAILE1,
TNFRSFION-TRAILE3, TNFRSFION-TRAILE1,
TNFRSFION-TRAILE1,
TNFRSFION-TRAILE3, TNFRSFION-TRAILE1,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Homotrimer (By similarity).
SUBCELLULAR LOCATION: Type II membrane protein (Potential).
TISSUE SPECIFICITY: WIDESPREAD.
SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                   Length 281;
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 SIYQGGIFELKENDRIFYSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                    32509 MW; DDAAAF78DAAB2F6D CRC64;
                                                                                                                                                                                                                              100.0%; Score 281; DB 1; L 100.0%; Pred. No. 1.1e-294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 AA
                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                   281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nduce apoptosis.
                                                                                                                           281 AA;
                                                                                                                                                                                                                                                                    Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFSF10 OR TRAIL
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P50592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                               SEQUENCE
                                                                                                                                                                                                                     Query Match
Best Local
STRAND
                                                                                     STRAND
                                                                                                                                                                                                                                                                                                               Matches
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DR MGD; MGI:107414; Thref10.

DR MGD; MGI:107414; Thref10.

DR InterPro; IPR006052; TNF family.

DR InterPro; IPR008033; TNF like.

DR PR00202; TNF; 1.

DR PR001; P000202; TNF; 1.

DR PR051TE; PS00201; TNF; 1.

DR PR051TE; PS00201; TNF l; 1.

DR PR051TE; PS0049; TNF 2; 1.

DR PR051TE; PS0049; TNF 2; 1.

DR PR051TE; PS0049; TNF 2; 1.

TOTOPLASMIC (POTENTIAL).

NAMAIN 1 17 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

***CHOKING; TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
NCBI_TaxID=9258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 291; 4.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indele
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                                                                                                                                                                                                                                                                                                                                                                                   52 52 N-LINKED (GLCNAC. . .) (PC 291 AA; 33477 MW; 3FEACAB9F0D7D802 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0E4D30265D77EAA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DESCRIPTION STANDARD; PRT; 51 AA. (97077; 097078; 16-077-2001 (Rel. 40, Last sequence update) 10-077-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLUIAR LOCATION: Secreted.
-1- SIMILARITY: Belongs to the insulin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ornithorhynchus anatinus (Duckbill platypus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 7; DB 1;
Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INSULIN A CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. ...
o; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.0%; Score 14;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro, IPR004825; Ins/IGF/relax. PRINTS; PRO277; INSULINB. SMART; SMO078; IJGF; 1. PROSITE, PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Pancreas;
MEDLINE=97021710; PubMed=8868070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.5%; S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 VQYIYKYTSYPDPI 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217 VQYIYKYTSYPDPI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Conservative
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HSSP; P01308; 1MHJ.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                 MEDLINE=91216437; PubMed=2022319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nitrosomonadaceae; Nitrosomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 34 1
96 AA; 10853 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC 19718 / IFO 14298;
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M57302; AAA30139.1; -.
PIR; PS0423; PS0423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                  01-NOV-1997 (Rel. 35, I
Antigen H4 (Fragment).
                                                                                                                                                                                                                                                Gene 99:127-132(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nitrosomonas europaea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 FQEEIKE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                SEQUENCE FROM N.A.
                                                                    Poxoplasma gondii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 FOREIKE
                                                                                                                  NCBI_TaxID=5811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIPB OR NE1488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIPB NITEU
Q82UJ6;
                                                                                                      [oxop]asma
                                                                                                                                                                   STRAIN=RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                 antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIPB NITEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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      g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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     ö
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=9832472; PubMed=9662395;
Petrukhin K., Koisti M.J., Bakall B., Li W., Xie G., Marknell T.,
Sandgren O., Forsman K., Holmgren G., Andreasson S., Vujic M.,
Bergen A.A., McGarty-Dugan V., Figueroa D., Austin C.P., Metzker M.L.,
Caskey C.T., Wadellus C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of the gene responsible for Best macular dystrophy.";
Nat. Genet. 19:241-247(1998).
-!- FUNCTION: Forms calcium-sensitive chloride channels. May conduct
other physiologically significant anions such as bicarbonate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBUNIT: Tetramer or pentamers. May interact with PPP2CB and PPP2R1B (By similarity).
-1- SUBCELLULAR LOCATION: Integral membrane protein; plasma membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PD002802; Worm_fam 8, 1.
rt; Ion transport; Tonic channel; Chloride;
     Gaps
                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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0
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0
                                                                                                                                                                       15-UTL-1999 (Rel. 38, Created)
15-UTL-1999 (Rel. 38, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Bestrophin 1 (Vitelliform macular dystrophy protein 2 homolog)
   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.5%; Score 7; DB 1; Length 81;
100.0%; Pred. No. 5;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 AA; 9413 MW; 19FD94AB3D606178 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:1346332; Vmd2.
GO; GO:0016323; C:basolateral plasma membrane; ISS.
InterPro; IPR00615; Bestrophin.
Pfam; PF01062; Bestrophin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PTM: Phosphorylated by PP2A (By similarity).
-!- SIMILARITY: Belongs to the bestrophin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 AA.
                                                                                                                                                81 AA
 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transport, Ion transport, Tonic channel, Calcium, Transmembrane, Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF057171; AAC64345.1; -.
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Q27001;
01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
Les 7; Conservative
 7; Conservative
                                                                                                                                               STANDARD;
                                178 EKGFYYI 184
                                                                21 EKGFYYI 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 TVLLQSL 29
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                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81
                                                                                                                                                                                                                                                            OR BMD1.
                                                                                                                                          VMD2 MOUSE
088870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                              Fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                              RESULT 4
VMD2 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AH4_TOXGO
ID AH4_TO
AC Q2700:
DT 01-NO
Matches
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Chain P., Lamerdin J.B., Larimer F.W., Regala W., Lao V., Land M.,
Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
Complete genome sequence of the ammonia-oxidizing bacterium and
plaste chemolithroautotroph Nitrosomonas europaea.";
T. Bacteriol. 185:2759-2773 (2003).
T. FUNCTION: Involved in the attachment of lipoyl groups to proteins,
Dy creating an amide linkage that joins the free carboxyl group of
Dy creating an amide linkage that joins the free carboxyl group of
Inpoic acid to the epsilon-amino group of a specific lysine
residue in lipoylated proteins (By similarity).
T. PATHWAY: Liposynthesis.
T. STMILARITY: Belongs to the lipB family.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IS-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Lipoate-protein ligase B (EC 6....) (Lipoate biosynthesis protein
                                                                                                                                                                                                                                                                Johnson A.M., Illana S., "Cloning of Toxoplasma gondii gene fragments encoding diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.5%; Score 7; DB 1
100.0%; Pred. No. 5.9
Live 0; Mismatches
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X Strueberg Know N.A.

Tataubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

REDLINE=22388257; PubMed=12477932;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

R.Klauber R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Rischul S.F., Zeeberg B., Batcow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Cassavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muxry D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McGarry T.J., Kirschner M.W.; "Geminin, an inhibitor of DNA replication, is degraded during
                                                                                                                                                                                                                                                                                                                                                                                  2.5%; Score 7; DB 1; Length 204; 100.0%; Pred. No. 12; 0; Indels cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corby N.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                            204 AA; 22764 MW; A83F6EF5F0346E61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0754<u>3</u>6; Q9H121;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                           EMBL; BAJOLLOL,
HAMAP; MF 00013; -; 1.
InterPro; IPR004143; BPL Lipa LipB.
InterPro; IPR00544; Lipate B.
Pfam; PF03099; BPL Lipa LipB; 1.
ProDom; PD0066086; Lipoate B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98297356; PubMed=9635433;
                                                                                                                                                         EMBL; BX321861; CAD85399.1; -.
                                                                                                                                                                                                                                                                           TIGREAMS; TIGRO0214; lipB; PROSITE; PS01313; LIPB; 1. Ligase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mitosis.";
Cell 93:1043-1053(1998).
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
'-hes 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 ROLVRKM 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 ROLVRKM 91
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                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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               human and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-I- NATL Acad. Sci. U.S.A. 99:16899-16903(2002).

-I- FUNCTION: Inhibits DNA replication by preventing the incorporation of MCM complex into prereplication complex (pre-RC). It is degraded during the mitotic phase of the cell cycle. Its destruction at the metaphase-anaphase transition permits replication in the succeeding cell cycle.

-I- DEVELOPMENTAL STAGE: Absent during G1 phase, accumulates during S, G2, and M phases, and disappears at the time of the metaphase-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91110576; PubMed=1703303; Schanberg L.E., Kaufman R.E.; Schanberg L.E., Fleenor D.E., Kurtzberg J., Haynes B.F., Kaufman R.E.; "Isolation and characterization of the genomic human CD7 gene: structural similarity with the murine Thy-1 gene."; proc. Natl. Acad. Sci. U.S.A. 88:603-607(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
T-cell antigen CD7 precursor (GP40) (T-cell leukemia antigen) (TP41)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aruffo A., Seed B.;
"Molecular cloning of two CD7 (T-cell leukemia antigen) cDNAs by a COS cell expression system.";
EMBO J. 6:3313-3316(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0007050; P:cell cycle arrest; TAS.
GO; GO:0008156; P:negative regulation of DNA replication; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 AA; 23565 MW; 0BABE60F6F5AC252 CRC64;
                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the geminin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.5%; Score 7; DB 1
100.0%; Pred. No. 12;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF067855; AAC39787.1; -.
EMBL; AL133264; CAC21511.1; ALT_INIT.
EMBL; BC005185; AAH05185.1; -.
EMBL; BC005389; AAH05389.1; -.
Genew; HGNC:17493; GMNN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=88111517; PubMed=3501369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.00.
                                                                                                                                                                                      anaphase transition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 QEEIKEN 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GK; 075496; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell cycle.
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P09564;
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul, S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Latchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Raba S.S., Loquellano M.F., Perers G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Worlan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worlley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J.W., Scheurz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J.W., Schmutz J., Myers R.M.,

Rutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

human and mouse CDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lyman S.D., Escobar S., Rousseau A.-M., Armstrong A., Fanslow W.C.; "Identification of CD7 as a cognate of the human K12 (SECTM1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of the surface topography and putative tertiary structure of the human CD7 molecule."; J. Immunol. 143:3632-3640(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 205-240 FROM N.A.
MEDLINE=91267564; PubMed=1711009;
Yoshikawa K., Seto M., Ueda R., Obata Y., Notake K., Yokochi T.,
Takahashi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90063052; PubMed=2479685;
Ware R.E., Scearce R.M., Dietz M.A., Starmer C.F., Palker T.J.,
Haynes B.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning of the gene coding for the human T cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0. Biol. Chem. 275:3431-3437(2000).
-!- FUNCTION: Not yet known.
-!- SUBDINIT: Interacts with SECTM1.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SUBLINITY: Conteains 1 immunoglobulin-like domain.
-!- SIMILARITY: Conteains 1 immunoglobulin-like domain.
-!- DATABASE: NAME-EROW; NOTE=CD guide CD7 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd7.htm".
                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20119303; PubMed=10652336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M37271; AAA51953.1; -.
EMBL; BC009293; AAH09293.1; -
EMBL; BC013297; AAH13297.1; -
EMBL; D00749; BAA00646.1; JOINED.
EMBL; D00749; BAA00646.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         differentiation antigen CD7.";
Immunogenetics 33:352-360(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X06180; CAA29546.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERACTION WITH SECTM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew; HGNC:1695; CD7.
MIM; 186820; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A39016; A39016.
HSSP; P01607; IREI.
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GO; GO:0006955; P:immune response; TAS.
GO; GO:0042110; P:T-cell activation; TAS.
GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. ., NAS.
InterPro; IPR007110; Ig-like.
Fran; PF0047; Ig:
SWARY; SW0040; IG:
PROSITE; PS50835; IG-LIKE; I.
                                                                                                                                                                                                                                                                                                                                                                                                              4 X 9 AA TANDEM REPEATS, POTENTIAL SPACER FUNCTION.
                                                                                                                                                                                                        I-cell; Signal; Immune response; Antigen; Transmembrane; Glycoprotein; Immunoglobulin domain; Receptor; Lipoprotein; Palmitate; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE DUF23 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                     T-CELL ANTIGEN CD7.
EXTRACELLULAR (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EBBCE08279552108 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S-palmitoyl cysteine.
N-LINKED (GLCNAC. .).
N-LINKED (GLCNAC. .).
                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 2.5%; Score 7; DB 1; Local Similarity 100.0%; Pred. No. 14; les 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
28-FRE-2003 (Rel. 41, Last sequence update)
28-FRE-2003 (Rel. 41, Last annotation update)
Hypothetical protein C27A7.2 in chromosome V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                     PROBABLE
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InterPro; IPR008166; DUF23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
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181
202
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DISULFID
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CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                             SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96267764; PubMed=8701611;
Poehlmann R., Philippsen P.;
"Sequencing a cosmid clone of Saccharomyces cerevisiae chromosome XIV reveals 12 new open reading frames (ORFs) and an ancient duplication
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=SEY6210;
MEDLINE=98422453; PubMed=9748433;
Cappellaro C., Mrsa V., Tanner W.;
"New potential cell wall glucanases of Saccharomyces cerevisiae and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The 'SUN' family: yeast SUN4/SCW3 is involved in cell septation.";
Yeast 16,905-919(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20330540; PubMed=10870102;
Mouassite_M., Camougrand N.M., Schwob E., Demaison G., Laclau M.,
                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
SQUATION protein SUN4 precursor (Soluble cell wall protein 3).
SUN4 OR SCM3 OR YNLO66W OR N2411 OR YNL2411W.
SQUATOWINGS CEPEVISIAE (Baker'S yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bergez P., Doignon F., Crouzet M.; "The sequence of a 44 420 bp fragment located on the left arm of chromosome XIV from Saccharomyces cerevisiae.";
                                                                                                                                      .
0
                                                                                                      Length 362;
                                                                                                                                      0; Indels
                Pfam, PF01697; DUF23; 1. __
ProDom, PD04153; DUF23_C; 1.
Hypochetical protein.
SEQUENCE 362 Aa, 41854 MW; 76514AB25A1ECA14 CRC64;
                                                                                                Query Match 2.5%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                              420 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 25-35, AND SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- FUNCTION: Involved in cell septation.

-i- SUBCELLIGAR LOCATION: Cell wall.

-i- PTM: Glycosylated.

-i- SIMILARITY: BELONGS TO THE SUN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bergez P., Doignon F., Crouzet M.;
Yeast 12:297-297(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               their involvement in mating.";
J. Bacteriol. 180:5030-5037(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96021608; PubMed=8533472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97060022; PubMed=8904343;
InterPro; IPR008167; DUF23_C.
                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (east 12:391-402(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=S288c / FY1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=S288C / FY1676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast 11:967-974(1995)
                                                                                                                                                                  49 YSKSGIA 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of six ORFs.";
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                                                                                                                                                                                                                                                                        SUN4_YEAST
ID SUN4_YEAST
AC P53616;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaneko I., Nakamura Y., Wolk C.P., Kuritz I., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Mateumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Complete genomic sequence of the filamentous nitrogen-fixing DNA Res. 8:205-213 (2001).

-!-FUNCTION: H(+)-stimulated, highly selective, manganese uptake system (By similarity).
-!-SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                    .) (POTENTIAL)
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                                                                           EMBL; U12141; AAA99645.1; -.
EMBL; X86470; CAA60196.1; -.
EMBL; X21342; CAA55999.1; -.
EMBL; Z31342; CAA55999.1; -.
EMBL; Z31916; Z33916.
Germonline; 143072; -.
SGD; S0005010; SUN4.
GO; GO:0009277; C:cell wall (sensu Fungi); IDA.
InterPro; IPR005556; SUN.
Pfam; PF03856; SUN; 1.
Cell division; Septation; Cell wall; Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                  Score 7; DB 1; Length 420;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                           43442 MW; FIFB6CD46F2CDA13 CRC64;
                                                                                                                                                                                                                                                                      SEPTATION PROTEIN SUN4.
                                                                                                                                                                                                                                                                                     SER/THR-RICH.
POLY-SER.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable manganese transport protein mntH.
MNTH OR ALL7601.
                                                                                                                                                                                                                                                                                                                                                         2.5%; Scc...
V 100.0%; Pred. No. ...
O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the NRAMP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           442 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anabaena sp. (strain PCC 7120).
Plasmid pCC7120beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP003602; BAB77244.1; -.
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InterPro; IPR001046; Nramp.
                                                                                                                                                                                                                                                                                                                                                                                                       7; Conservative
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395
420 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 VAVTYVY 53
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=103690;
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                                                                                                                                                                                                                                                     SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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RA Wood V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,
R. Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
R. Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
R. Gollins M., Comnor R., Cronin A., Davis P., Feltwell T., Fraser A.,
R. Gollins M., Comnor R., Cronin A., Davis P., Feltwell T., Fraser A.,
R. Gontles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
R. Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J.,
R. Holroyd S., Mungall K., Murphy L., Niblett D., Odell C.,
R. Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
R. Mimens M., Squares R., Sanares S., Stevens K.,
R. Intherford K., Taylor R., Sanares D., Seeger K., Sharp S.,
R. Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
R. Taylor K., Taylor R. G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
R. Moodward J., Volckaert G., Art R., Robben J., Grymonprez B.,
Woldyen J., Volckaert G., Art R., Robben J., Grymonprez B.,
R. Woltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
R. Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
R. Borzym K., Candeu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
R. Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
R. Dominguez A., Revuelta J.L., Mocreno S., Armstrong J., Forsburg S.L.,
R. Sphkovski G.V., Ussery D., Barrell B.G., Nurse P.,
R. Shpkovski G.V., Ussery D., Barrell B.G., Nurse P.,
R. The genome sequence of Schizosaccharomyces pombe.",
R. Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                     ProDom; PD001861; Nramp; 1.
TIGRFAMs; TIGR01197; nramp; 1.
Transport; Symport; Manganese; Transmembrane; Inner membrane; Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable UDP-N-acetylglucosamine pyrophosphorylase (EC 2.7.7.23).
SPBC1289.08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 442; . 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A7CBADFAE628196B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast).
Bukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.5%; Scor.
100.0%; Pred. No. 2.,
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                475 AA
                                                                                                                                                                                                                                                                                                                               POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 40, Created)
(Rel. 40, Last seq
(Rel. 41, Last ann
                            PRINTS; PR00447; NATRESASSCMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
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Pfam; PF01566; Nramp; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 LLQSLCV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 LLQSLCV 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             442 AA;
                                                                                                                                                       Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- SUBCELLULAR LOCATION: Cytoplasmic and peroxisomal.
-!- INDUCTION: By compounds that cause peroxisome proliferation such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arand M., Knehr M., Thomas H., Zeller H.-D., Oesch F.,
"An impaired peroxisomal targeting sequence leading to an unusual
bicompartmental distribution of cytosolic epoxide hydrolase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Knehr M., Thomas H., Arand M., Gebel T., Zeller H.-D., Oesch F., "Isolation and characterization of a cDNA encoding rat liver cytosolic epoxide hydrolase and its functional expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Soluble epoxide hydrolase (SEH) (EC 3.3.2.3) (Epoxide hydratase)
= diphosphate + UDP-N-acetyl-D-glucosamine.
PATHWAY: UDP-GlcNAc biosynthesis from Fru-6-P; fourth (last)
                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                         2.5%; Score 7; DB 1; Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                              -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                               53121 MW; 3AF80295A682D7A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     levels of physiological mediators.
-!- CATALYTIC ACTIVITY: An epoxide + H(2)O = a glycol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 450-554 FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           554 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Sprague-Dawley, TISSUE-Liver;
MEDLINE-93352557; PubMed=8349641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Cytosolic epoxide hydrolase) (CEH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92077134; PubMed=1743286;
                                                                                                                                                                                                        EMBL; AL035675; CAB38688.1; -.
                                                                                                                                                                                                                                    GeneDB_SPombe, SPBC1289.08;
InterPro, IPR002618; UDPGP.
Pfam; PF01704; UDPGP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                 110
                                                                                                                                                                                                                                                                                                                                110
117
475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 TSEETIS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 rSEETIS 174
                                                                                                                                                                                                                       T39359; T39359
                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli
                                                                                                                                                                                                                                                                                                                                ACT_SITE
ACT_SITE
SEQUENCE
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P80299;
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamsatides P.C., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., MixLos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
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MYCROBODY TARGETING SIGNAL (POTENTIAL).
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                              SIMILARITY: Belongs to the AB hydrolase superfamily. Epoxide
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,

Beoptera, Endopterygota, Diptera; Brachycera; Muscomorpha;

Ephydroidea, Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2003 (Rel. 42, Last annotation update)
Probable cytochrome P450 306a1 (BC 1.14.-.-) (CYPCCCVIA1).
CYP306A1 OR CG6578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 554;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145FDCA53F582138 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          574 AA.
   clofibrate, tiadenol and fenofibrate
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100.0%; Pred. No. 31;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000073; A/b hydrolase. InterPro; IPR000073; A/b hydrolase. InterPro; IPR0000639; AB hydrolase. InterPro; IPR000639; Box hydrolase. InterPro; IPR006402; HAD-SF-IA-v3. InterPro; IPR005833; HIgnase/hydrlase. InterPro; IPR005834; Hydrolase. InterPro; IPR0005834; Hydrolase. InterPro; IPR000379; Ser_setrs. Pfam; PF00702; Hydrolase; 1. PRINTS; PR00112; ABHVDROLASE. PRINTS; PR00412; EPOXHYDRIASE. PRINTS; PR00412; HADHALOGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase, Peroxisome, Detoxification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIGRFAMS; TIGR01509; HAD-SF-IA-v3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           catabolism.
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                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X65083; CAA46211.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X60328; CAA42898.1; -. PIR; A47503; A47503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 7; Conservative
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495
523
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                                                               hydrolase family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKINTS; FKOUSES; FTSU.
PROSITE; PSEGORGE; CYTCHROME_P450; 1.
OXIGOTEGUCLESE; MGNDOXYGERBEE; Membrane; Heme; Microsome;
Endoplasmic reticulum; Hypothetical protein.
METAL 505 505 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
GROTTENCE 574 AA; 65177 MW; 9A8A3E1747101700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.5%; Score 7; DB 1; Length 574;
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    Last sequence update)
    Last annotation update)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Flyase; FBgn0030948; Cyp306al.
InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YFGG SCHPO STANDARD; E 013854; O42840; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last seq. 28-FEB-2003 (Rel. 41, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE003509; AAF48873.1; -. HSSP; P00179; 1DT6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 GGIFELK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 GGIFELK 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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670 AA; 68262 MW; 68E8D1CFB855F8A8 CRC64;

SEQUENCE

DB 1;

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                                                                                                                                                                    ARADINE-1848401; PubMed=11859360;

Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Squros V., Peat N., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Stoures V., Peat N., Hayles J., Batham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Gollins M., Connor R., Cronin A., Davis D., Hiddson G.,

RA Gollins M., Connor R., Cronin A., Davis D., Hiddson G.,

RA Gollins M., Connor R., Cronin M., Harris D., Hiddson G.,

RA Gollins M., Connor R., Murgall K., Murphy L., Niblett D., Odell C.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA Holroyd S., Moules M., Squares R., Seeger K., Sharp S.,

RA Nucherford K., Rutter S., Sauders D., Seeger K., Sharp S.,

RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Skelton J., Volckert G., Aert R., Robben J., Grymonprez B.,

Woodward J., Volckert G., Aert R., Robben J., Grymonprez B.,

Woodward J., Volckert G., Aert R., Robben J., Grymonprez B.,

RA Woodward J., Volckert E., Reeger M., Schaefer M., Meller S.,

RA Gabel C., Fuchs W., Fitze C., Holzer E., Mosell D., Hilbert H.,

RA Golfeau A., Cadieu E., Dreanc S., Gloux S., Lelaure V., Mottier S.,

RA Golfeau R., Cruzado L., Jimenez J., Hunt C., Moore K., Hurst S.M.,

Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Borzym K., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moren S.,

RA Galibert F., Necombie W.R., Paulsen I., Potashkin J.,

RA Gerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Sparkovski G.W., Ussery D., Barrell B.G., Nurse P.;

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C. I. Subscribert R., Rochential).
Hypothetical serine/threonine-rich protein C19G12.16c in chromosome I
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Schizosaccharomycetales; Schizosaccharomycetaceae;
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               precursor.
SPAC19G12.16C OR SPAC23A1.01C.
Schizosaccharomyces pombe (Fission yeast).
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EMBL; AL021813; CAA16975.1; -.
GeneDB_SPombe; SPAC19G12.16c;
                                                                                              Schizosaccharomyces.
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                              NCBI_TaxID=4896;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cyclic-AMP-dependent transcription factor ATF-6 beta (Activating transcription factor ATF-6 beta (Activating binding protein-like 1) (CAMP response element binding protein-like 1) (CAMP response element binding protein-related protein) (Creb-rp) (G13 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification of the G13 (cAMP-response-element-binding protein-related protein) gene product related to activating protein-related protein) gene product related to activating transcription factor 6 as a transcriptional activator of the mammalian unfolded protein response.";

Biochem. J. 355:19-28(2001).

-!- FUNCTION: TRANSCRIPTIONAL FACTOR THAT ACTS IN THE UNFOLDED PROTEIN RESPONSE (UPR) PATHWAY BY ACTIVATING UPR TARGET GENES INDUCED DURING ER STRESS. BINDS DNA ON THE 5'-CCAA(GA)-3' HALF OF THE ER STRESS RESPONSE ELEMENT (ERSE) (5'-CCAAT-N9-CCAC[GA]-3') WHEN NF-Y
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chapinn D.D.;
"A novel Creb family gene telomeric of HLA-DRA in the HLA complex.";
Genomics 30:149-156(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).

SROWEN L., Dankers C., Bankin D., Faust J., Loretz C., Ahearn M.B.,
Banta A., Schwartzell S., Smith T.M., Spies T., Hood L.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97081760; PubMed=8923003;
Speek M., Barry F., Miller W.L.;
"Alternate promoters and alternate splicing of human renascin-X,
gene with 5' and 3' ends buried in other genes.";
Hum. Mol. Genet. 15:1749-1758 (1996).
                                                                                                                                                                                                                                               Q99941; Q13269; Q14343; Q14345; Q99635; Q99637; Q9H3V9; Q9H3W1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Khanna A., Campbell R.D.;
"The gene G13 in the class III region of the human MHC encodes
potential DNA-binding protein.";
Biochem. J. 319:81-89(1996).
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MEDLINE-21157024; PubMed=11256944;
Haze K., Okada T., Yoshida H., Yanagi H., Yura T., Negishi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Min J., Shukla H., Kozono H., Bronson S.K., Weissman S.M., Chaplin D.D.;
                   Length 670;
                                                          0; Indels
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                                                                                                                                                                                                                               703 AA.
                   2.5%; Score 7; DB 1
100.0%; Pred. No. 37;
tive 0; Mismatches
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MEDLINE=97024424; PubMed=8870652;
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Query Match
Best Local Similarity 100...
7; Conservative
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                                                                                                                                 584 EETISTV 590
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EMBL; U52694; AAC14900.1; -.
EMBL; U52696; AAC50888.1; ALT_FRAME.
EMBL; U52633; AAC14898.1; ALT_FRAME.
EMBL; U52701; AAC50883.1; ALT_SEQ.
EMBL; AL049547; CAB892283.1; -.
Genew; HGNC:2349; CREBL1.
                                                                                                                                                                                                                                                                 (BY
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EMBL; X98053; CAA6663.1; -.
EMBL; X98054; CAA66664.1; -.
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Pfam; PF00170; bZIP; 1.
PROSITE; PS50217; BZIP; 1.
PROSITE; PS0036; BZIP_BASIC; 1.
Transcription regulation; DNA-binding; Activator;
Transcription regulation; Nuclear protein; Endoplasmic reticulum;
Unfolded protein response; Nuclear protein; Alternative splicing.
"""" Signal anchor; Glycoprotein; Alternative splicing.
""" SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
""" SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
""" NUCLEAR SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
""" NUCLEAR SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN IS
IS BOUND TO ERSE.
SUBDUIT: HOWODIMER AND HETERODIMER WITH ATF6-ALPHA. THE DIMER INTERACTS WITH THE NUCLEAR TRANSCRIPTION FACTOR Y (NF-Y) TRIMER THROUGH DIRECT BINDING TO NP-Y SUBUNIT C (NF-YC).
SUBCELLUIAR LOCATION: Type II membrane protein in the endoplasmic exteinlum. Under ER stress the cleaved N-terminal cytoplasmic domain translocates into the nucleus.
ALTERNAIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: N-glycosylated.

PTM: DURING UNFOLDED PROTEIN RESPONSE AN APPROXIMATIVE 60 KDA FRAGMENT CONTAINING THE CYTOPLASMIC TRANSCRIPTION FACTOR DOMAI SELEARED BY ROCITOLYSIS. THE CLEAVAGE IS PROBABLY PERFORMED SEQUENTIALLY BY SITE-1 AND SITE-2 PROTEASES.
SIMILARITY: Belongs to the bzip family. ATF subfamily.

GAUTION: SOME REF. 4 SEQUENCES DIFFER FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 600.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Isoid=Q99941-2; Sequence=VSP_000593;
Note=No experimental confirmation available;
NOTESNO ESPECIFICATE: Ubjultous.
DOMAIN: THE BASIC DOMAIN FUNCTIONS AS A NUCLEAR LOCALIZATION
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(GLCNAC. .) (POTENTIAL)
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N-LINKED (GLCNAC. . .) (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN: THE BASIC LEUCINE-ZIPPER DOMAIN IS SUFFICIENT FOR ASSOCIATION WITH THE NF-Y TRIMER AND BINDING TO ERSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMPORTANT FOR CLEAVAGE BY PS2
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GLQN -> D (in isoform 1).
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                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of the gene and an antigenic determinant of equine herpesvinus type-1 glycoprotein 14 with homology to gB-equivalent glycoproteins of cher herpesviruses."; Gene 87:249-255(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SIMILARITY: Belongs to the herpesviruses glycoprotein B family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
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         E -> D (IN REF. 2).

QQ -> HE (IN REF. 2).

Q -> HE (IN REF. 4).

V -> D (IN REF. 4; AAC50888).

BO4C7B23E7D83F82 CRC64;
                                                                                          2.5%; Score 7; DB 1; Length 703; 100.0%; Pred. No. 38; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 979;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLYCOPROTEIN B. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110331 MW; 9A19866B791C5B36 CRC64;
                                                                                                                                                                                                                                                                                                                             Equine herpesvirus type 1 (strain Kentucky D) (EHV-1). Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (P
/FTId=VSP 000593.
                                                                                                                                                                                                                                               P25218;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                     979 AA
                                                                                                                                                                                                                                                                                                       Glycoprotein B precursor (Glycoprotein 14). GB OR GP14 OR 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
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Pred. No.
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Pfam; PF00606; Glycoprotein_B; 1.
ProDom; PD000693; Glycoprot_B; 1.
Glycoprotein; Transmembrane; Signal.
SIGNAL 1 86 POTENTIAL.
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100.0%; Pre
0;
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                                                                 MW.
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         330
520
600
76709 M
                                                                                                      Local Similarity 100.
nes 7; Conservative
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497
514
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Best Local Similarity
Matches 7; Conserva
            3
329 3
520 5
600 6
703 AA;
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979 AA;
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870
165
275
380
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ID VGLB HSVEL
           CONFLICT
CONFLICT
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TRANSMEM
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                                                                                           Query Match
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STANDARD;
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744
                UVRA STRAW
Q829X3;
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 UVRA_STRAW
                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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InterPro; IPRO00276; GPCR Rhodpsn.
PROSITE; PSO0237; G_PROTEIN_RECEP_F1 1; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
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                                                                                                                                                                                                                                                                                                                                                              Favello A.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                 01-0cT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last Bequence update)
Putative G protein-coupled receptor B0244.6.
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N-LINKED (G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
                                                                                                                  STANDARD;
                                                                                                                                                                                                                                        Caenorhabditis elegans.
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                             839 SCIACFL 845
                                                                                                                                                                                                                                                                                                                                                                                                                                 Subfamily B0244.
SGIACFL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              982 AA;
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                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                           NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Slycoprotein.
TRANSMEM
                                                                                                                  YS96 CAEEL
25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lesions (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the ABC transporter family. UvrA subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003)
-!-FUNCTION: The UvrABC repair system catalyzes the recognition and processing of DNA lesions. UvrA is an ATPase and a DNA-binding processin. A damage recognition complex composed of 2 uvrA and 2 uvrB subunits scans DNA for abnormalities. When the presence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
PROSITE; PS50891; ABC_TRANSPORTER_2; 2.
SOS response; Excision nuclease; DNA repair; DNA recombination; DNA excision, ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
UVABC system protein A (UvrA protein) (Excinuclease ABC subunit A).
UVRA OR SAV6286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lesion has been verified by uvrB, the uvrA molecules dissociate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (By similarity). Surwing a heterotetramer with uvrB during the search for
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                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 1009;
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1009 AA; 110786 MW; CC90B4E219139700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
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100.0%; Pred. No. 54;
iive 0; Mismatches
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InterPro; IPR003435; ABC transporter.
InterPro; IPR003455; CytC heme_BS.
InterPro; IPR004602; UvrA.
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ProDom; PD000006; ABC_transporter; 1.
TIGREAMs; TIGR00630; uvra; 1.
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Best Local Similarity 100...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lesions (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the ABC transporter family. UvrA subfamily.
                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
UVYARG system protein A (UVYA protein) (Excinuclease ABC subunit A).
UVRA OR SCO1958 OR SCC54.18C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdemo-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Collins M., Eraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandram M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- FUNCTION: The UVTABC repair system catalyzes the recognition and processing of DNA legions. UVTA is an ATPase and a DNA-binding protein. A damage recognition complex composed of 2 uvrA and 2 uvrB subunits scans DNA for abnormalities. When the presence of lesion has been verified by uvrB, the uvrA molecules dissociate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00005; ABC tran; 2.
Probom: PD000006; ABC transporter; 1.
TIGRAMS: TIGRO630; uvra; 1.
PROSITE; PS00211; ABC TRANSPORTER 1; 2.
PROSITE; PS50893; ABC TRANSPORTER 2; 1.
SOS response; Excision nuclease; DNA repair; DNA recombination; DNA excision; AfP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: Forms a heterotetramer with uvrB during the search for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)."; Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 C4-TYPE.
110997 MW; 084D6B18692A792D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (POTENTIAL).
ATP (POTENTIAL).
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                                                                                                                                                                                                                                  PRT; 1014 AA
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HAMAP, MF_00205, -; .
InterPro; IPR003493; ABC_transporter.
InterPro; IPR004602; UvrA.
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NP BIND 32 39 AT
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                                                                                                                                                                                                                              STANDARD;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (By similarity).
111 SPLVRER 117
                                                           153 SPLVŘĚŘ 159
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744
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Q9Z507;
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Length 1014;

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RAPIERO DE SEQUENCE OF 208-1095 FROM N.A.

RAPEGUENCE OF 208-1095 FROM N.A.

RAPEGENCE OF 3. Barna N., Bastlen V., Boguslavkiy L., Boukhgalter B.,

RAPEGENCE OF Campopiano A., Chang J., Chazaro B.,

RAPEGENCE N., Dewar K., Diaz J.S., Dodge S., Farro S., Cook P.,

RAPEGENCE N., Collins S., Collymore A., Cook P.,

RAPETRIUGH W., Graham L., Grand-Pierre N., Hagos B., Heaford A.,

RAPEGENCE N., McLand T., Johnson R., Jones C., Kamat A.,

RATAGRAS A., Kells C., Landers T.,

RATAGRAS R., Kells C., Landers T.,

RATAGRAS R., McHews C., McCarthy M., McEwan P., McKernan K.,

RAPORT N., Matthews C., McCarthy M., McEwan P., McKernan K.,

RAPIOR J., Nguyen C., Norbu C., Norman C.H., O'Connor T.,

RAPIOR J., Nguyen C., Norbu C., Norman C.H., O'Connor T.,

RAPIOR J., Roman J., Rosetti M., Roy A., Santos R.,

RAPIOR S., Schubback R., Seaman S., Savery P., Spencer B.,

RAPIOR J., Testâpe S., Theodore J., Topham K., Travers M., Travis N.,

RAPIGE C., Rogov P., Seaman S., Severy P., Spencer B.,

RAPIGHAM S., Testâpe S., Theodore J., Topham K., Travers M., Travis N.,

RAPIGHAM S., Testâpe S., Theodore J., Topham K., Travers M., Travis N.,

RAPIGHAM S., Testâpe S., Theodore J., Topham R., Travers M., Travis N.,

RAPIGHAM S., Testâpe S., Theodore J., Zommer A., Zody M.;

RAPIGHAM S., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.;

RAPION S.,

RAPIGHAM S., Sommer M., Zembek L., Zimmer A., Zody M.;

RAPIGHAM S., Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Halleck M.S., Pradhan D., Blackman C.F., Berkes C., Williamson P.L.,
                                                                                                                                                                                                                                              043861; 060872;
30-MAY-2000 (Rel. 39, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Potential phospholipid-transporting ATPase IIB (EC 3.6.3.1) (HUSSY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yanamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma I., Sugano S., Nagahari K., Masulo Y., Magai K., Isogai T.; "NEDO human con A sequencing project.", Sugano S., Nagahari K., Masulo Y., Nagai K., Isogai T.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=21064499; PubMed=11124703;
Stanchi F., Bertocco B., Toppo S., Dioguardi R., Simionati B.,
Cannata N., Zimbello R., Lanfranchi G., Valle G.;
                              Indels
                              ;
                                                                                                                                                                                                                                  PRT; 1095 AA.
                            0; Mismatches
       Pred. No.
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       100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-420 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   ATP9B OR ATPIIB OR NEOLL.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                             STANDARD;
                                                                      111 SPLVRER 117
                                                                                                                153 SPLVRER 159
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Testis;
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                                                                          Unpublished observations (JUL-2002).
-!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the cation transport ATPases family (P-type ATPases). Subfamily IV.
"Characterization of 16 novel human genes showing high similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                             TIGREAMS; TIGRO1652; ATPase-Plipid; 1.
PROSITE; PS00154; ATPASE E1 E2; 1.
Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
                                                                                                                                                                                                                                                                                                                       GO; GO:0016011; C:integral to membrane; NAS.
GO; GO:0015247; F:aminophospholipid transporter activity; NAS.
GO; GO:0015249; F:AFP binding; NAS.
GO; GO:0019829; F:AFP binding; NAS.
GO; GO:0015917; P:aminophospholipid transport; NAS.
ThterPro; IPRO01797; ATPase E1-E2.
InterPro; IPRO06139; Filippase.
PRINTS; PR00119; CATATPASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
PHOSPHOKYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
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2 -> K (IN REF. 3).
3 -> I (IN REF. 3).
3 -> D (IN REF. 3).
5 -> D (IN REF. 3).
5 -> M (IN REF. 3).
7 -> N (IN REF. 3).
7 -> N (IN REF. 3).
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                                                                                                                                                                                                                                                          EMBL, AK097757; -; NOT_ANNOTATED_CDS.
EMBL; AC104423; -; NOT_ANNOTATED_CDS.
EMBL; U78978; AAC05243.13; -.
EMBL; AJ006268; CAA06934.1; -.
                                                                                                                                                                                                                                                                                                              Genew; HGNC:13541; ATP9B.
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1043
1051
                                                  CONCEPTUAL TRANSLATION.
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1015
1036
1053
1078
1095
416
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1116
121
121
122
328
349
349
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878
                          Teast 18:69-80(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multigene family.
             yeast sequences.
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                                                               Axelsen K.B.;
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TRANSMEM
DOMAIN
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DB 1; Length 1095;

58:

2.5%; Score 7; D 100.0%; Pred. No.

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and the statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Found in most tissues except spleen and muscle. Most abundant in testis. Also detected in fetal tissues.
-!- SIMILARITY: Belongs to the cation transport ATPases family (P-type ATPases). Subfamily IV.
                                                                                                                                                                                                                                                                                            STRAIN=ICR; TISSUE=Brain;
MEDLINE=20473714; PubMed=11015572;
Halleck M.S., Lawler J.F. Jr., Blackshaw S., Gao L., Nagarajan P.,
Hacker C., Pyle S., Newman J.T., Nakanishi Y., Ando H., Weinstock D.,
Williamson P., Schlegel R.A.;
"Differential expression of putative transbilayer amphipath
  Gaps
                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 .
                                                                                                                              P981<u>95;</u> Q99L13;
P-MAX-2000 (Rel. 39, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Potential phospholipid-transporting ArPase IIB (EC 3.6.3.1).
  Indels
  .;
0
 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:1354757; Atp9b.
Interpro; IPR001757; ATPase E1-E2.
InterPro; IPR008250; E1-E2_ATPase_reg.
                                                                                                                                                                                                                                                                                                                                                                                         Physiol. Genomics 1:139-150(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF155913; AAF08476.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC003246; AAH03246.1; -.
7; Conservative
                                                                                                                      STANDARD;
                          241 SIYQGGI 247
                                                     968 SIYQGGI 974
                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                            transporters.";
                                                                                                                    AT9B MOUSE
                                                                                           RESULT 22
AT9B_MOUSE
 Matches
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01-NOV-1988 (Rel. 09, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
6enome polyprotein (Contenins: Capsid protein C (Core protein); Matrix protein (Envelope protein M); Major envelope protein B, Nonstructural proteins NS1, NS2A, and NS2B; Protease/helicase (EC 3.4.21.98) (NS3)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE=86200215; PubMed=3009829;
Dalgarno L., Trent D.W., Strauss J.H., Rice C.M.;
Partial nucleotide sequence of the Murray Valley encephalitis virus genome. Comparison of the encoded polypeptides with yellow fever virus structural and non-structural proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murray valley encephalitis virus.
Viruses, ssRNA positive-strand viruses, no DNA stage, Flaviviridae,
Flavivirus.
                                                                                                                                                                                Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYDRATES-LINKAGE SITES OF NS1, AND DISULFIDE BONDS.
MEDLINE-21405829; PubMed-11514736;
Blitvich B.J., Scanlon D., Shiell B.J., Mackenzie J.S., Pham K.,
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MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
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EXTRACELLULAR (POTENTIAL)
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100.0%; Pred. No. 58;
iive 0; Mismatches
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            InterPro) PR005834; Hydrolase.
Pfam; PF00122; E1-E2 ATPase; 1.
Pfam; PF00702; Hydrolase; 1.
PRINTS, PR00119; CATATPASE.
TIGRPAMs; TIGRO1652; ATPASE-Plipid; 1.
TIGRFAMS; TIGRO164; ATPASE_E1_E2; 1.
PROSITE; PS00154; ATPASE_E1_E2; 1.
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InterPro; IPR006539; Flippase.
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nes 7; Conserv
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       "Determination of the intramolecular disulfide bond arrangement and blochemical identification of the glycosylation sites of the nonstructural protein NS1 of Murray Valley encephalitis virus.";
J. Gen. Virol. 82:2251-2256(2001).
-!- FUNCTION: The small proteins NS2A, NS2B, NS4A and NS4B are hydrophobic, suggesting a possible membrane-related function. NS3 and NS5 may play a role in the viral RNA replication.
-!- CATANYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral precursor polyprotein, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1.
-!- SUBNUIT: The virion of this virus is a nucleocapsid covered by a lipoprotein envelope. The envelope consists of two proteins: protein RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R Pfam; PF00103; Flavi_capsid; 1.

R Pfam; PF00103; Flavi_capsid; 1.

R Pfam; PF00103; Flavi_capsid; 1.

R Pfam; PF00869; Flavi_capsid; 1.

R Pfam; PF00849; Flavi_dlycop.cf; 1.

R Pfam; PF00949; Flavi_M; 1.

R Pfam; PF01004; Flavi_NS1A; 1.

R Pfam; PF01002; Flavi_NS2A; 1.

R Pfam; PF01570; Flavi_MS2B; 1.

R Pfam; PF01570; Flavi_dropep; 1.

R Pfam; PF01570; Flavi_dropep; 1.

R Pfam; PF01570; Flavi_dropep; 1.

R Pfam; PF01570; Flavi_MS2B; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NONSTRUCTURAL PROTEIN NSI.
NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
PROTEASE/HELICASE (NS3).
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                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                         Cys. Ser. trypsin.
Flavi capsidc.
Flavi glycoprote.
Flavi Ms.
Flavi NS.
Flavi NS.
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Ig-like.
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217
292
793
1207
1372
1503
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InterPro; IPR001157; F
InterPro; IPR000752; F
InterPro; IPR000487; F
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InterPro; IPR001122;
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InterPro; IPR007110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000336;
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MEROPS; S07.001; -.
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POTENTIAL

Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hiracka Y.;
"Large-scale screening of intracellular protein localization in living fission yeast cells by the use of a GFP-fusion genomic DNA library."; genes Cells 5:169-190(2000).
-!-FUNCTION: This is one of the chains of the nonenzymatic component (CF(0) subunit) of the mitochondrial ATPase complex.
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(IN) = ADP + phosphate +
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                    (GLCNAC. . .).
(GLCNAC. . .) (HIGH MANNOSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ding D.-O., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
                                                                                                                           (POTENTIAL) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                       ATP8_SCHPO STANDARD; PRT; 48 AA.
P21536; Q9UU72;
01-MAY-1991 (Rel. 18, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (AGL).
                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                     DB 1; Length 1780;
                                                                                                                                                                                                                      1780 AA; 194866 MW; ODGAA7FF0FB706DE CRC64;
                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lang B.F.;
Submitted (AUG-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the ATPase protein 8 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
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(GLCNAC.
                                                                                                                          (GLCNAC.
           SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                  2.5%; Score 7; DB 1, 100.0%; Pred. No. 92; ive 0; Mismatches
SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H(+)(Out).
-!- SUBCELLULAR LOCATION: Membrane-bound
                                                                                                                          N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
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BY
BY
BY
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BY
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EMBL; AB027775; BAA87079.1; -.
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SEQUENCE OF 1-43 FROM N.A.
                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                         20 VIFTVLL 26
                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                          1780
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Lang B.F.;
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SEQUENCE
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DISULFIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STAIN=C2A / ATCC 35395 / DSM 2834;

MEDLINE=21929760; bubMed=1193238;

MEDLINE=21929760; bubMed=1193238;

A alagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

A lalen N., Naylor V., Stange-Thomann N., DeArellano K., Johnson R.,

Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

A inner A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

A dederich R., Innaram-Smith C., Kuettner H.C., Krzycki J.A.,

M. Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

Rerry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,

Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

Metcalf W.W., Birren B.;

The genome of Methanosarchia acetivorans reveals extensive metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 12:532-542(2002).
-!- SIMILARITY: Belongs to the L29P family of ribosomal proteins.
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                                                                                         0; Indels
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                                                       Length 48;
 8 32. POTENTIAL.
48 AA; 5636 MW; 36B3BF480A5FB803 CRC64;
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100.0%; Pred. No. 50;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
55.0S ribosomal protein L29P.
RPL29P OR MA1079.
                                                       DB 1;
                                                                                                                                                                                                                                                         67 AA.
                                                                100.0%; Pred. No. --
                                                         Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ribosomal protein; Complete proteome
SEQUENCE 67 AA; 7612 MW; 232230E:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF 00374; -; 1.
InterPro; IPR001854; Ribosomal L29.
Pfam, PF00831; Ribosomal L29; 1.
IGRFAMS; TIGR0012; L29; 1.
PROSITE; PS00579; RIBOSOMAL L29; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and physiological diversity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE010775; AAM04504.1; -.
                                                       2.1%;
                                                                                                                                                                                                                                                                                                                                                                                     Methanosarcina acetivorans.
                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                           21 IFTVLL 26
                                                                      Best Local Similarity
                                                                                                                                                              19 iFTVLL 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=2214;
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TRANSMEM
SEQUENCE
                                                     Query Match
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RESULT 26

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Natl. Acad. Sci.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 NLHLRN 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid ColK-K235
                                                                                                                                                                                                                                                     similarity).
                                                                                            CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CKI OR CFI.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=562;
                            Praser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMK ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
SEQUENCE
                                                      cholerae
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                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-GOE1 / GO1 / ATCC BAA-199 / DSM 3647 / OCM 88;
STRAIN-GOE1 / GO1 / ATCC BAA-199 / DSM 3647 / OCM 88;
MEDLINE-22120807; PubMed-12125824;
Deppenmeter U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C.,
Brueggemenn H., Lienard T., Christmann A., Boemecke M., Steckel S.,
Fritz H.-J., Gottschalk G.,
Fritz H.-J., Gottschalk G.,
"The genome of Methanoarcina mazzi: evidence for lateral gene
transfer between Bacteria and Archaea.";
J. Mol. Microbiol Biotechnol 4:453-461(2002).
-: SIMILARITY: Belongs to the L29P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=El Tor Ni6961 / Serotype Ol;
STRAIN=El Tor Ni6961 / Serotype Ol;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                  Methanosarcina mazei (Methanosarcina frisia).
Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribosomal protein; Complete proteome. SEQUENCE 67 AA; 7612 MW; 232324E450A236B8 CRC64;
                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
50s ribosomal protein L29P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 6; DB 1;
100.0%; Pred. No. 50;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
FUSH division protein ftsB.
Vibrio
             67 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF_00374; -; 1.
InterPro; IPR001854; Ribosomal_L29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00831; Ribosomal L29; 1.
TIGRFAMs; TIGR00012; L29; 1.
PROSITE; PS00579; RIBOSOMAL L29; 1.
             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09KUJ3;
28-FEB-2003 (Rel. 41, Created)
10-OCT-2003 (Rel. 42, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE013454; AAM31827.1; -.
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hes 6; Conservative
          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 ILRTSE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 ILRTSE 8
                                                                                                                                        NCBI_TaxID=2209;
                                                                                       RPL29P OR MM2131
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          RL29 METMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
RL29_METMA
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FTSB VIBCH
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McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Strong function-related homology between the pore-forming colicins K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDILINE=21980622; PubMed=11972052;
Buddelmeijer N., Judson N., Boyd D., Mekalanos J.J., Beckwith J.;
"YgbQ, a cell division protein in Escherichia coli and Vibrio
cholerae, localizes in codependent fashion with FtsL to the division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: Required for the cell division process.
-!- SUBUNIT: May interact with ftsL (By similarity).
-!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane (Potential). Colocalizes with ftsL to the division site (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                   'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COILED COIL (POTENTIAL).
CE7DF6651369821D CRC64;
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 AA.
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100.0%; Pred. No. 69;
cive 0; Mismatches
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STRAINEME449, and ECORS;
MEDLINE=96074330; PubMed=7592493;
Pilel H., Braun V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterobacteríaceae; Escherichia.
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4 21 PP 22 2 94 PP 32 76 PP 24 PP 25 2 94 PP 25 27 
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                                                                                                                                                                                                                                                                                            Nature 406:477-483(2000).
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Q05122;
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                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., A Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., A Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier I., Brans A., Braun M., Brignell S.C., Bron S., A Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., A Bohiac F., Devine K.M., Dusterhôft A., Ehrlich S.D., Emmerson P.T., Brian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Pujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., A Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guiseppi G., Guy B.J., Hajech J., Harvod C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
                                                                                                                                                                                                                                                                                                                                 Gaps
                                 SECUENCE FROM N.A.

IZATG J., Chartier M., Baty D.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: THIS PROTEIN IS ABLE TO PROTECT A CELL, WHICH HARBORS

THE PLASMID COLK ENCODING COLICIN K, AGAINST COLICIN K.
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0
                                                                                                                                                                                                                                                    Bacteriocin immunity; Plasmid; Transmembrane; Inner membrane.
                                                                                                                                                                                                                                                                                                    2.1%; Score 6; DB 1; Length 96; 100.0%; Pred. No. 71; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                          96 AA; 11498 MW; E82853239597A5CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0cT-1994 (Rel. 30, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-0cT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                   POTENTIAL
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           Bacteriol. 177:6973-6977(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98240224; PubMed=9579061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microbiology 144:859-875(1998).
                                                                                                                                                                                                              EMBL; X87834; CAA61100.1; -. EMBL; X87835; CAA61103.1; -. EMBL; U27452; AAB41289.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein yhgB.
                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YHGB OR BSU10090
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YHGB BACSU
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Rurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Rarro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Rieger M., Rivolta C., Rocha E., Rapoport G., Rey M., Raynolds S.,
Rieger M., Rivolta C., Schleich S., Schroeter R., Scoffone F.,
Sato T., Sanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi J., Sekowska A., Seros S.J., Serror P., Shin B.S.,
Sorokin A., Tarakoshi T., Tarkanshi H., Tarkansur K.,
Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein B., Yoshikawa H., Danchin A.;
subtilis "."
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Hypothetical 13.4 kba protein in ubiquitin 3'region (Lambda 208).
Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; daDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 104;
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SEQUENCE 104 AA; 11998 MW; 6844CD77B52FD968 CRC64;
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5. 76;
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100.0%; Pred. No. 76;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y14083; CAA74515.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 390:249-256(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme A to a Ser of acyl-carrier protein (By similarity).

CATALYTIC ACTIVITY: COA + apo-[acyl-carrier protein] = adenosine 3', 5'-bisphosphate + holo-[acyl-carrier protein].

COPACTOR: Magnesium (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

SIMILARITY: Belongs to the P-Pant transferase superfamily. AcpS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
14-0CT-2003 (Rel. 42, Last annotation update)
(4'_phosphopantetheinyl transferase acps).
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=RIMD 2210633 / Serotype O3:K6;
MEDLINE=22508454; PubMed=12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iljima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                       Length 119;
                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                 PIR; JQ2032; JQ2032.
Hypothetical protein.
SEQUENCE 119 AA; 13415 MW; 8B35F990F5BD9678 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C565E0E2812C3A3C CRC64;
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MAGNESIUM (BY SIMILARITY)
                                                                                                                                                                                                                                                                   Query Match 2.1%; Score 6; DB 1;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches
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Interbro; IPR008278; 4-PPT_transf.
Pfam; PP01648; ACPS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP005082; BAC60831.1; -.
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                                                                                                                                                                EMBL; D13375; BAA02641.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            parahaemolyticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vibrionaceae, Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 AA;
                                                                                                                                                                                                                                                                                                                                                83 QLRQLV 88
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCES "Luberculosis; STRAIN=H37Rv;

MEDLINE=98295987; PubMed=9534230;

A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., A Hornaby T., Jagels K., Kroph A., McLean J., Moule S., Murphy L., Oliver S., Seeger K., Skelton S., Squares R., Seeger K., Skelton S., Squares S., Squares R., Sulston J.B., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES—M.tuberculosis, STRAIN-CDC 1551 / Oshkosh,
MEDLINE-2220644; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Kolonay J.F., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Folcher A., Utterback T., Weidman J.A., Ermolaeva M., Salzberg S.L.,
Pelcher A., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=M.bovis; STRAIN=AF2122/97; MEDLINE=22709107; PubMed=12788972; Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Garnier T., Eiglmeier K., Camus J.-C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; "The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100:7377-7882(2003).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
      Length 126;
                                             Indels
                                                                                                                                                                                                                                                                                                                                  Protein crcB homolog 1.
CRCBI OR RV3069 OR WT3153.1 OR WTCY22D7.12C OR MB3096.
Mycobacterium tuberculosis, and
Mycobacterium bovis.
                                                                                                                                                                                                                                                                   16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
    DB 1;
/ Match 2.1%; Score 6; DB 1 Local Similarity 100.0%; Pred. No. 91; Nes 6; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . Bacteriol. 184:5479-5490(2002).
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                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TaxID=1773, 1765;
                                                                                     144 EKALGR 149
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                                                                                                                          17 EKALGR 22
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P95089;
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    Query Match
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CRB1 MYCTU
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Matches
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129 WQLRQL 134
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P30024;
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Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hiyosuchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Matanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136 (1996).

-I. SUBCELJULAR LOCATION: Integral membrane protein (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001129; MAPEG.
Pfam; PF01124; MAPEG; 1.
Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 5 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 129 POTENTIAL.
137 AA; 15414 MW; 9741232427529924 CRC64;
                                                                                                                                                                                                                                                                                      132 AA; 14301 MW; CA9B283379B0174E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Cyanobacteria, Chroococcales, Synechocystis.
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                      2.1%; Score 6; DB 1
100.0%; Pred. No. 95;
ative 0; Mismatches
                                                                                                                                                                                                                 POTENTIAL. POTENTIAL.
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                                                                                           HAMAP; MF 00454; -; 1.
InterPro; IPR003691; Camphor_CrcB.
Pfam; PF02537; CRCB; 1.
                                                                                                                                                                    Complete proteome.
EMBL; BX248344; CAD96783.1; -. PIR; F70650.
TIGR: MT3153.1; -. TIGR: MT3153.1; -. Tuberculist; Rv3069; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein sll1147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D90909; BAA17849.1; -
                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S74888; S74888.
                                                                                                                                                                                                                                                                                                                                                                                                                                   276 GAFLVG 281
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 GAFLVG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                    Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YB47 SYNY3
ID YB47 SYNY3
AC P73795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
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  ARORAN ANTIFIES
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MEDLINE=96337999; PubMed=868887;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDIINE=22148942; PubMed=1310766;
Geng Y., Chandran B., Josephs S.F., Wood C.;
"Identification and characterization of a human herpesvirus 6 gene segment that trans activates the human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Virol. 66:1564-1570(1992).
-!- FUNCTION: MAY BE RESPONSIBLE FOR MOST OF THE TRANS-ACTIVATING ACTIVITY ON THE HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 PROMOTER BY HHV-6. IT MAY FUNCTION BY DIRECTLY BINDING TO THE NF-KAPPAB SITE OR MAY INVOLVE CELLULAR FACTORS, SUCH AS NF-KAPPAB, EITHER DIRECTLY OR INDIRECTLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ٠;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation; Trans-acting factor; Activator. SEQUENCE 143 AA; 16385 MW; DOCE4D7C2422AAD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
14-0CT-2001 (Rel. 40, Last annotation update)
Human herpesvirus (type 6 / strain GS) (HHV6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ1483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 AA.
           143 AA.
PRT;
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PIR; A42186; WMBE6H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Betaherpesvírinae; Roseolovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanococcus jannaschii.
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           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10369;
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Matches

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Gaps

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0; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mood V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A., Rocoks K., Brown D., Baker S., Basham D., Bowman S., Bouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Rocoks K., Brown D., Eromin A., Davis P., Feltwell T., Fraser A., Gollins M., Connor R., Hamilin N., Harris D., Hidalgo J., Hodgson G., Hornbby T., Howarth S., Huckle E.J., Hunt S., Jagels K., Jones L., Jones M., Leather S., McDonald S., McLean J., Anoney P., Moule S., Mongall K., Murphy L., Nibbett D., Odell C., Anoney P., Moule S., Mangall K., Murphy L., Nibbett D., Odell C., Anoney P., Moule S., Murder S., Saunders B., Stevens K., Starps K., Starps S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Relton J., Simmonds M., Squares R., Schaefer M., Mueller-Auer S., Anodward U., Volckaert G., Aert R., Robben J., Grymonprez B., Baylis B., Langer M., Fritzc C., Holzer E., Noestl D., Hilbert H., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Goffeau A., Cadleu E., Dreano S., Gloux S., Lelaure V., Mottier S., Golioux S., Lelaure V., Mottier S., Lucas M., Rochet M., Gallardin C., Tallada V.A., Galzon R., Thode G., Lucas M., Rochet M., Gallardin C., Tallada V.B., Garzon A., Thode G., Bominguez A., Revuelta J.L., Moreno S., Armstrong J., Prorsburg S.L., Reruttti L., Lowe T., Moreno S., Armstrong J., Prorsburg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Bordoveky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 7 27 27 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 AA; 17659 MW; 90227132448E8802 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetacese,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 6; DB 1; Le:
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Adaptin complex small chain homolog C30D11.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.1%; Scc...
100.0%; Pred. No. ...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                    EMBL; U67589; AAB99498.1; -. PIR; B64485; B64485.
                                                                                                                                  Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 KNEKAL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 KNEKAL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             TIGR; MJ1483; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YAJS SCHPO
009905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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YAJS SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Umbilical vein;
MEDLINE=99091541; PubMed=9872942;
Zhai Y., Ni J., Jiang G.-W., Lu J., Xing L., Lincoln C., Carter K.C., Janat F., Kozak D., Xu S., Rojas L., Aggarwal B.B., Ruben S.,
Li L.-Y., Gentz R., Yu G.-L.;
"VEGI, a novel cytokine of the tumor necrosis factor family, is an angiogenesis inhibitor that suppresses the growth of colon carcinomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: Homotrimer (Potential).
-!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
-!- TISSUE SPECIFICITY: Specifically expressed in endothelial cells.
Detected in placenta, lung, kidney, skeletal muscle, pancreas, spleen, prostate, small intestine and colon.
-!- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                095150;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 15 (Vascular
endothelial cell growth inhibitor) (TNF ligand-related molecule 1).
TNFSFIS OR VEGI OR TL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PASEB J. 13:181-189(1999).
-!- FUNCTION: Inhibits vascular endothelial growth and anglogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                           -!- SIMILARITY: Belongs to the adaptor complexes small subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                 General Sponde, SPAC30D11.05; -.
InterPro; IPR000804; Clat adaptor s.
Pfam; PF01217, Clat adaptor s; 1.
PROSITE: PS00989; CLAT ADAPTOR S; 1.
Hypothetical protein; Coated pits.
SRQUENCE 165 AA; 18642 MW; 9EA796AD34C40FF3 CRC64;
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 6; DB 1; Ler
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.1%; Score 6; UB 1.
Best Local Similarity 100.0%; Pred. No. 1.2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                EMBL; Z67961; CAA91891.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 SNTLSS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 SNTLSS 138
                                                                                                                                                                                                                                                                                                               PIR; T38594; S62563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                     family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAINSJAL-1 / DSM 2661 / ATCC 43067;

STRAINSJAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Karlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

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Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                            SMART; SM00207; 1NF 2; 1.

PROSITE; PS50049; TNF 2; 1.

CYCOKine; Transmembrane; Glycoprotein; Signal-anchor.

CYTOKine; Transmembrane; Glycoprotein; Signal-anchor.

DOMAIN 1 2 CYTOPIASMIC (POTENTIAL).

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 273:1058-1073(1996).
-!- COFACTOR: Binds 1 zinc ion per molecule (Potential).
-!- SIMILARITY: Belongs to the aldolase class II family. AraD/fucA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.1%; Score 6; DB 1; Length 174; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 AA; 20131 MW; CCB83BA7EE673B98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                       MIM; 604052; -.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005102; F:receptor binding; TAS.
GO; GO:00074; F:receptor binding; TAS.
InterPro; IPR006053; TNF_abc.
InterPro; IPR006053; TNF Tamily.
InterPro; IPR006983; TNF Tamily.
InterPro; IPR006983; TNF Tabc.
InterPro; IPR006983; TNF Tabc.
InterPro; IPR0060536; TNF Tabc.
InterPro; IPR0060536; TNF Tabc.
InterPro; IPR006051; TNF Tabc.
InterPro; IPR006051; TNF Tabc.
ProDom; PR00201; TNF Tabc.
ProDom; PR002012; TNF Tabc.
SWART; SM00207; TNF; T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical aldolase class II protein MJ1418
                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                EMBL; AF039390; AAD08783.1; -. HSSP; P50591; 1D0G.
                                                      Genew; HGNC;11931; TNFSF15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 FFGAFL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 FFGAFL 173
                                                                                                                                                                                                                                                                                                                                                                                                                 26
85
56
152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YE18 METUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            058813;
                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 38
YE18 METJA
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAINER / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed=7542800;
MEDLINE-95350630; PubMed=7542800;
MERDLINE-95350630; PubMed=7542800;
Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., Mcrlavage A.R., Sutron G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Ulterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Probable).
-!- SIMILARITY: BELONGS TO THE B.COLI NLPC / LISTERIA P60 FAMILY.
                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                          DB 1; Length 181; . 1.3e+02;
                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                               68 68 ZINC (BY SIMILARITY).

87 87 ZINC (BY SIMILARITY).

89 89 ZINC (BY SIMILARITY).

147 147 ZINC (BY SIMILARITY).

181 AA; 20470 MW; E5F3BF13722145B0 CRC64;
                                                                                                                        Interpro; IPR001303; Aldolase II N.
Pfam; PF00596; Aldolase II; 1.
Hypothetical protein; Zīnc; Complete proteome.
Hypathetical 68 68 ZINC (BY SIMILARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-DAD Inpoprotein nlpC homolog precursor.
NLPC OR HI1652.
                                                                                                                                                                                                                                                                                          2.1%; Score 6; DB 1
100.0%; Pred. No. 1.3
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000064; Peptidase C40.
InterPro; IPR000437; Prok lipoprot_S.
Pfam; PF00877; NLPC_P60; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U32838; AAC23297.1; -.
                                                   EMBL; U67582; AAB99428.1; -. PIR; A64477; A64477. HSSP; PIISSO; IDZX. TIGR; MJ1418; -.
                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; H64173; H64173.
MEROPS; C40.UPW; -.
                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  57 FLKEDD 62
                                                                                                                                                                                                                                                                                                                                                                                                      45 FLKEDD 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rigr; Hi1652; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLPC HAEIN
ID NLPC HAEIN
AC P45296;
                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                        METAL
                                                                                                                                                                                                                                      METAL
                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUTAGENESIS OF CYS-85.
MUTAGENESIS OF CYS-85.
MEDLINE=22004684; PubMed=1660887;
Sullivan M.L., Vierstra R.D.;
"Cloning of a 16-kDa ubiquitin carrier protein from wheat and
Arabidopsis thaliana. Identification of functional domains by in
vitro mutagenesis.";
J. Biol. Chem. 266:13878-23885(1991).
-!- FUNCTION: Catalyzes the covalent attachment of ubiquitin to other
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
                                                                   N-palmitoyl cysteine (Potential).
S-diacylglycerol cysteine (Potential).
772BE57F79452E38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diphosphate + protein N-ubiquityllysine.
PATHWAY: Ubiquitin conjugation; second step.
MISCELLANEOUS: A cysteine residue is required for ubiquitin-
                                  POTENTIAL.
PROBABLE LIPOPROTEIN NLPC HOMOLOG.
                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Augusta;
MEDLINE=90099364; PubMed=2557633;
Sullivan M.L., Vierstra R.D.;
"A ubiquitin carrier protein from wheat germ is structurally an
functionally similar to the yeast DNA repair enzyme encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP
              Membrane; Lipoprotein; Sīgnal; Complete proteome; Palmitate. SIGNAL 17 POTENTIAL.
                                                                                                                                      2.1%; Score 6; DB 1; Length 183; 100.0%; Pred. No. 1.3e+02;
                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1990 (Rel. 15, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
Ubiquitin-conjugating enzyme E2-23 kDa (EC 6.3.2.19)
(Ubiquitin-protein ligase) (Ubiquitin carrier procein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 86:9861-9865(1989).
                                                                                                                                                                                                                                                                                                                                  184 AA
                                                                                                                                                                        0; Mismatches
 PROSITE; PS00013; PROKAR LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, PF00179; UQ con; 1.
ProDom; PD000461; UBQ conjugat; 1.
SMART; SM00212; UBCc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000608; UBQ_conjugat.
                                                                                                     20585 MW;
                                                                                                                                                                                                                                                                                                                                                               01-AUG-1990 (Rel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M28059; AAA34309.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Priticum aestivum (Wheat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thiolester formation.
                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                  183
18
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                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                           121 LGRKIN 126
                                                                                                                                                                                                         147 LGRKIN 152
                                                                                                   183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteins.
                                                                                                                                                                                                                                                                                                                             UBC4 WHEAT
P16577;
                                                                                                 SEQUENCE
                                                                    LIPID
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UBC4_WHEAT
                                                    CHAIN
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RATAIN-BERTALL-SETEMBLY;

RATAIN-BERTALL-SETEMBLAGE-10731132;

RADIANIS-20196006; PubMed=10731132;

RADIANIS-20196006; PubMed=10731132;

RADIANIS-20196006; PubMed=10731132;

RADIANIS-20196006; PubMed=10731132;

RADIANIS-20196006; Richards S.B., Lib P.W., Hookerins R.W., Henderson S.N., George R.A., Calards S.D., Ashburner M., Henderson S.N., RADIANIS G.W., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Raderson G.G., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Radia M., Basul A., Baxerdale J., Bayraktaroglu L., Beasley E.M., Radia W., Barandon R.Y., Benos P.V., Berman B.P., Bhandari D., Bolakovo S., Radeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolakovo S., Radeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolakovo S., Radeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolakovo S., Radeson K.Y., Benos P.V., Berman B.P., Brander A., Cawley S., Dahlke C., Davenport L.B., Daviez S.M., Radeson K.J., Bolcher A., Deng Z., Maya A.D., Dew I., Dietz S.M., A. Double L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Rodson K.J., Evangelista C.C., Ferraz C., Ferriara S., Fleischmann W., Rodson K.J., Brownes M., Dugan-Rocha S., Dunkov B.C., Dunn R., Andonk F., Karpen G.H., Ke Z., Kennison J.A., Heuris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Alush B., McIntosh T.C., McLeod M.P., McIndon D.R., Nelson D.L., Radiacon M., Pittman G.S., Pan S., Pollard J., Wolfneria N., Radishon M., Murphy B., Murphy L., Murphy D., Shen H., Rainston M., Skupski M.P., Shen H., Shen B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Shen H., Shen B.C., Siden-Kiamos I., Shene H., Shene R. Shier E., Spiradling A.C., Stapleton M., Skupski M.P., Shier P., Spier E., Spiradling A.C., Stapleton F., Shier P., Shier F., Spiradling A.C., Stapleton F., Stapleton M., Strong R., Shier S., Shier B., Shier E., Spiradling A.C., St
                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schmidt A., Hollmann M., Schaefer U., A. newly identified Mintle locus, M(2)32D, encodes the ribosomal protein L9 in Drosophila melanogaster.", Mol. Gen. Genet. 251:381-387(1996).
                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI TaxID=7227;
                                                                                                                                                                                Length 184;
                                                                                                                                                                                                                             0; Indels
                                                                                   141 176 ASP/GLU-RICH (ACIDIC).
85 85 C->S: LOSS OF ACTIVITY.
184 AA; 21125 MW; AA479C4E42C893B7 CRC64;
PROSITE; PS00183; UBIQUITIN_CONJUGAT_1; 1.
PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
Ubl conjugation pathway; Ligase; Multigene family.
BINDING 85 85
                                                                                                                                                                                Score 6; DB 1; Ler
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                            P50882; Q9VKL6; Q9VKL7;
01-0CT-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
RPL9 OR M(2)32D OR CG6141.
                                                                                                                                                                                                                                                                                                                                                                                                                           190 AA
                                                                                                                                                                                                                          0; Mismatches
                                                                   UBIQUITIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96262192; PubMed=8676882;
                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD:
                                                                                                                                                                                                                                                                  241 SIYOGG 246
                                                                                                                                                                                                                                                                                                                42 SIYOGG 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                           RL9 DROME
                                                                                      DOMAIN
MUTAGEN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of Encsophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                               Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.B., Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
                                                                                                                                                                                                                                                                                                                                                                           "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                              systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
-!- SIMILARITY: Belongs to the L6P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Dephospho-CoA kinase (EC 2.7.1.24) (Dephosphocoenzyme A kinase).
COAE OR SC01996 OR SC7H2.10C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 6; DB 1; Length 190; 100.0%; Pred. No. 1.3e+02; trive 0; Mismatches 0; Indels
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689B2520ACDA12D3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; ASTOLOGIO, ARFS3048.2; -. AB003630; ARFS3048.2; -. PIK; JC6062. JC6062. RlyBase; FBgn0015756; Rpl9. InterPro; IPR000702; Ribosomal_L6. InterPro; IPR002359; Ribosomal_L6_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00347; Ribosomal L6; 2.
PROSITE; PS00700; RIBOSOMAL L6_2; 1.
Ribosomal protein.
                                                                                                                                                                                                              MEDLINE=22426069; PubMed=12537572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT 37 37 SEQUENCE 190 AA; 21392 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X94613; CAA64319.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nicotiana tabacum (Common tobacco).
Bukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLUTAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: EXPRESSED MAINLY IN FLORAL ORGANS AND, WITHIN THE FLOWER, EXPRESSION IS RESTRICTED TO PETALS AND STAMENS.
-!- MISCELLANEOUS: MUTATIONS IN GLO CAUSE TRANSFORMATION OF PETALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitesch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                        "Complete genome sequence of the model actinomycete Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01294; COAE; 1.
Transferase; Kinase; ATP-binding; Coenzyme A biosynthesis;
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 6; DB 1; Length 200; 100.0%; Pred. No. 1.4e+02; tive 0; Mismatches 0; Indels
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01-0CT-1993 (Rel. 27, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (POTENTIAL)
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InterPro; IPR01977; Depp_CoAkinase.
Prodom, PP003329; Depp_CoAkinase; 1.
TIGREAMS; TIGR00152; TIGR00152; 1.
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                                                                                                                                                                                                                                                                                                                                  EMBL; AL939111; CAB52052.1; -. PIR; T35741; T35741.
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210 AA;
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"Cloning, sequencing, and mutagenesis of the cytochrome c4 gene from Azotobacter vinelandii: characterization of the mutant strain and a proposed new branch in the respiratory chain.";
Biochim. Biophys. Acta 1230:119-129(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ambler R.P., Daniel M., Melis K., Stout C.D.,
"The amino acid sequence of the dihaem cytochrome c4 from the
Bacterium Azotobacter vinelandii.";
Biochem. J. 222:137-227 [1984].
-!- FUNCTION: DIHEME, HIGH POTENTIAL CYTOCHROME C BELIEVED TO BE AN
INTERMEDIATE ELECTRON DONOR TO TERMINAL OXIDATION SYSTEMS.
-!- SUBCELLULAR LOCATION: Periplasmic.
-!- PTM: Binds 2 heme groups per molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00350; MADS BOX 1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
Transcription regulation; DNA-binding; Activator; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
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100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0; Indels
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209 AA; 24691 MW; 5661F9C1640E1A47 CRC64;
                             SIMILARITY: Contains 1 K-box dimerization domain. SIMILARITY: Contains 1 MADS-box domain.
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01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
   INTO SEPALS AND STAMINA INTO CARPELS.
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STRAIN-ATCC 13705 / OP1;
MEDLINE-84307416; PubMed=6089759;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002487; TF Kbox.
InterPro; IPR002100; TF_MADSbox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01486; K-box; 1.
Pfam; PF00119; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
                                                                                                                                                                                                                                                                                                                                                                   EMBL; X67959; CAA48142.1; -. PIR; S35226; S35226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytochrome C4 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Azotobacter vinelandii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Developmental protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P11746; 1MNM.
TRANSFAC; T01779; -.
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P43302;
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Gockel G., Hachtel W., Baier S., Fliss C., Henke M.;
"Genes for components of the chloroplast translational apparatus are
conserved in the reduced 73-kb plastid DNA of the nonphotosynthetic
euglenoid flagellate Ascasia longa.";
Curr. Genet. 26:256-262(1994).
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P34778; P58144;
01-FEB-1994 (Rel. 28, Created)
42-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DNA-directed RNA polymerase alpha chain (EC 2.7.7.6) (PEP) (Plastid-
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MEDLINE=21080522; PubMed=11212895;
MCDKINE=21080522; PubMed=11212895;
MCDKPLET G. Hachrel W.;
"Complete gene map of the plastid genome of the nonphotosynthetic euglenoid flagellate Astasia longa.";
Protist 151:347-351(2000).
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HEME I (COVALENT).
IRON (HEME I AXIAL LIGAND).
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HEME 2 (COVALENT).
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100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam, PF00034; cytchrome_c; 1.
PRINTS; PR0605; CYTCHROMECIC.
ProDom; PD004020; Cyt C bact; 2.
PROSTIE; PS00190; CYTOTHROME C; 2.
PROSTIE; PS00190; CYTOTHROME C; 2.
SIGNAL 1 20
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HSSP, Q52369; IETP.
InterPro; IPR008169; Cyt_C_Dact.
InterPro; IPR003089; Cyt_CT.
InterPro; IPR008168; Cyt_CT.
InterPro; IPR000345; Cyt_CT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21687 MW;
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                                                                                            Nucleic Acids Res. 30:1247-1254 (2002).
-!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as
                          MEDLINE=21851312; PubMed=11861918;
Sheveleva E.V., Giordani N.V., Hallick R.B.;
"Identification and comparative analysis of the chloroplast
"Igha-subunit gene of DNA-dependent RNA polymerase from seven Euglena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S38600; S38600.

HAMAP; ME 00055; atypical; 1.

InterPro; IPR009025; RBP11-like RNApo.

InterPro; IPR001070; RNA_polA bac org.

Transferase; Transcription; DNA-directed RNA polymerase; Chloroplast.

SEQUENCE 220 AA; 26287 MW; D221F70D995BB5AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                          similarity).
-!-SUBCELLULAR LOCATION: Chloroplast.
-!-SIMILARITY: Belongs to the RNA polymerase alpha chain family.
-!- CAUTION: Ref.1 and Ref.2 sequences differ from that shown due to erroneous game model prediction.
-!- CAUTION: The C-terminal domain thought to be required for interaction with some regulatory factors is missing from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92164783; PubMed=1537407;
Bulant M., Richter K., Kuchler K., Kreil G.;
Bulant M., Richter K., Kuchler K., Kreil G.;
Bulant M., Richter K., Kuchler K., Kreil G.;
thyrotropin-releasing hormone.";
FEBS Lett. 296:292-26(1992).
-: SUBCELLULAR LOCATION: Secreted.
-: MISCELLANBOUS: This precursor contains seven copies of
                                                                                                                                                      CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                               -!- SUBUNIT: In chloroplasts the minimal PEP RNA polymerase is composed of four subunits: alpha, beta, beta', and beta'' (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
10-OCT-2003 (Rel. 42, Last samotation update)
Thyroliberin precursor 2 (Thyrotropin releasing hormone) (TRH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.1%; Score 6; DB 1; Length 220; 100.0%; Pred. No. 1.5e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ294725; CAC24589.1; ALT_SEQ.
EMBL; AJ294725; CAC24588.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
 [3]
IDENTIFICATION OF GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 EEIKEN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 EEIKEN 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=8355;
                                                                                                                                          substrates.
                                                                                                                                                                     RNA) (N).
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                                                                                                                                                                                                                                                                                                            protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THY2 XENLA
Q00643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                  species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THY2_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its word non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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"Two preursors of thyrotropin-releasing hormone from skin of Xenopus
Jaevis. Bach contains seven copies of the end product.";
J. Biol. Chem. 265:11731-11733(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMIDATION (G-108 PROVIDE AMIDE GROUP). PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMIDATION (G-122 PROVIDE AMIDE GROUP).
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AMIDATION (G-154 PROVIDE AMIDE GROUP).
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AMIDATION (G-194 PROVIDE AMIDE GROUP).
                     -!- MISCELLANEOUS: There are at least two genes for TRH in Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYRROLIDONE CARBOXYLIC ACID.
AMIDATION (G-92 PROVIDE AMIDE GROUP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYRROLIDONE CARBOXYLIC ACID.
AMIDATION (G-78 PROVIDE AMIDE GROUP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
Thyroliberin precursor 1 (Thyrotropin releasing hormone) (TRH).
Xenopus laevis (African clawed frog).
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100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                                                                                               Pfam, PF05438; TRH; 1.
Amidation; Hormone, Repeat, Signal;
Cleavage on pair of basic residues; Multigene family;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
PROTHYROLIBERIN
                                                                                                                                                                                                                                                                                                                                                                                                      THYROLIBERIN.
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                                                                                                                                                                                                                      EMBL; X64056; CAA45412.1; -.
PIR; S20382; S20382.
InterPro; IPR008857; TRH.
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NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 AA;
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thyroliberin
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151
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153
168
191
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THY1 XENLA
ID THY1 XENLA
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MOD_RES
SEQUENCE
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PEPTIDE
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MOD_RES
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Query Match
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Matches
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     SOW KWAN TO THE PROPERTY OF TH
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                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                        Richter K., Kawashima E., Egger R., Kreil G.; "Blosynthesis of thyrotropin releasing hormone in the skin of Xenopus laevis: partial sequence of the precursor deduced from cloned cDNA."; EMBO J. 3:617-621(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMIDATION (G-110 PROVIDE AMIDE GROUP).
PYRROLIDONE CARBOXYLIC ACID.
AMIDATION (G-124 PROVIDE AMIDE GROUP).
PYRROLIDONE CARBOXYLIC ACID.
AMIDATION (G-156 PROVIDE AMIDE GROUP).
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PYRROLIDONE CARBOXYLIC ACID.
AMIDATION (G-196 PROVIDE AMIDE GROUP).
                                                                                                                                                                                      thyroliberin.
-!- MISCELLANEOUS: There are at least two genes for TRH in Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYRROLIDONE CARBOXYLIC ACID.
AMIDATION (G-78 PROVIDE AMIDE GROUP).
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDATION (G-92 PROVIDE AMIDE GROUP). PYRROLIDONE CARBOXYLIC ACID.
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0
                                                                                                                                                                  MISCELLANEOUS: This precursor contains seven copies of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISSING.
7DEC001E3154CD47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M34699; AAA49974.1; -..
EMBL; X00770; CAA25345.1; ALT_TERM.
EMPL; X37061; RHXLT.
INTERPO; IPRO08857; TRH.
Pfam; PF05438; TRH; 1.
Amidation; Hormone; Repeat; Signal;
Cleavage on pair of basic residues; Multigene family;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTHYROLIBERIN 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THYROLIBERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.1%; Score 6;
                                                                                                                                       SUBCELLULAR LOCATION: Secreted.
                                                      MEDLINE=84182535; PubMed=6425056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 M
26336 MW;
                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M34699; AAA49973.1; -.
                 SEQUENCE OF 1-123 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 AA;
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SEQUENCE
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à
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HIS9 THEMA STANDARD; PRT; 233 AA Q9WZR1; 20071-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update)

THEMA

RESULT 48 HIS9_THEMA

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                                                                                                                                                                                                MEDLINE-9287316; PubMed=10360571;
MEDLINE-99287316; PubMed=10360571;
Melon K.E., Clayton K.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutron G.G., Fleischmann R.D., Eisen J.A., White O.,
"Exidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: L-histidinol-phosphate + H(2)0 = L-histidinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               + phosphate.
-!- PATHWAY: Histidine biosynthesis; eighth step.
-!- SIMILARITY: BELONGS TO THE PHP FAMILY OF HYDROLASE, HISK FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang W., Wan T., Yuan Z., He L., Cao X.;
"A novel regulator of G-protein signaling.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
15-WAR-2004 (Rel. 43, Last annotation update)
Probable histidinol-phosphatase (EC 3.1.3.15) (HolPase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Histidine biosynthesis; Hydrolase; Complete protecme. SEQUENCE 233 AA; 27144 MW; E0CE3D245E0EDA30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
RGS18 OR RGS13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF02811, PHP C; 1.
Pfam, PF02231, PHP N; 1.
SMART; SM00481; POLIIIAc; 1
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InterPro; IPR004013; PHP_C.
InterPro; IPR003141; PHP_N.
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                                                                             Thermotoga maritima.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 KNEKAL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 KNEKAL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEOUENCE FROM N.A.
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                                                                                                                                                                                SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                HISK OR TM0804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGSI HUMAN
Q9NS28;
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156 SSRSGH 161

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REDLINE=22388257; PubMed=12477932;

REDLINE=22388257; PubMed=12477932;

Retausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ratusper R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Bhetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschul S.F., Zeeberg B., Bonaldo M.F., Casvant T.L., Scheetz F.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rabers S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rabers S., McMan A., Young A.C., Shewchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rutterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO THEIR INACTIVE GDP-BOUND FORM. BINDS TO G(I)-ALPHA AND G(Q)-ALPHA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Generation and construction and sequences,";
human and mouse cDNA sequences,";
Proc. Natl. Acad. Sci. US.A. 99.16899-16903 (2002).

-!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
-!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION THEREBY DRIVING THEM INTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- TISSUE SPECIFICITY: Expressed in peripheral leukocytes, bone marrow, spleen and fetal liver.
-!- SIMILARITY: Contains 1 RGS domain.
Gagnon A.W., Murray D.L., Leadley R.J. Jr.; "Cloning and characterization of a novel regulator of G-protein signaling in human platelets."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                          Park I.K., Klug C.A., Li K., Jerabek L., Li L., Nanamori M., Neubig R.R., Hood L., Weissman I.L., Clarke M.F.; "Molecular cloning and characterization of a novel regulator of G-protein signaling from mouse hematopoietic stem cells."; J. Biol. Chem. 276:915-923(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 227 DV -> ML (IN REF. 3).
235 AA; 27582 MW; 973ABDE8EC7DE3D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000342; Regl Gprotein.
Pfam; PF00615; RGS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01301; RGSPROTEIN.
ProDom; PD001580; Regl_Gprotein; 1.
SMART; SM00315; RGS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE, PS50132, RGS, 1.
Signal transduction inhibitor.
DOMAIN 86 202 R
                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                 "Cloning and expression of a yeast ubiquitin-protein cleaving activity in Escherichia coli.";
                                                                               01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ubiquitin carboxyl-terminal hydrolase YUH1 (EC 3.4.19.12) (Ubiquitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                           Miller H.I., Henzel W.J., Ridgway J.B., Kuang W.-J., Chisholm V.,
                                                                                                                            YUH1 OR YJR099W OR J1941.
Saccharomyces crevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales;
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UBIQUITIN BINDING 2 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.1%; Score 6; DB 1; Length 236; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26385 MW; D239FEE25798B395 CRC64;
                                                           236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                             Biotechnology 7:698-704(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z49599; CAA89629.1; -.
                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                  RESULT 50
UBL1_YEAST
ID UBL1_YEAST
AC P35127;
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SEQUENCE
63
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Gaps

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0; Indels

2.1%; Score 6; DB 1; Length 235; 100.0%; Pred. No. 1.6e+02;

0; Mismatches

6; Conservative

Best Local Similarity

Query Match Matches

175 GGIFEL 180

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOI. Biochem. Parasitol. 32:113-119(1989).
-1- FUNCTION: FS800 is likely to have some function in the production or maintenance of the schistosome egg.
-1- DEVELOPMENTAL STAGE: Highest level only in mature worms, i.e.,
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Puerto Rican;
MEDLINE=89181810; PubMed=2927441;
Reis M.G., Kuhns J., Blanton R., Davis A.H.;
"Localization and pattern of expression of a female specific mENA in Schistosoma mansoni.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó:
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Pyridoxal phosphate biosynthetic protein pdxJ (PNP synthase).
PDXJ OR SO1351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           during egg production.
-!- MISCELLANEOUS: The two F800 proteins are read from two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 6; DB 1; Length 238; 100.0%; Pred. No. 1.7e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 AA; 27993 MW; FDFC8E9F4181B7F1 CRC64;
                                                                                                                       01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
16-OCT-8000 (Rel. 42, Last annotation update)
Schistosoma mansoni (Blood fluke).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-ASN.
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MEDLINE=22297686; PubMed=12368813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  overlapping reading frames.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J03999; AAA29883.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDXJ SHEON STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 TRGRSN 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 TRGRSN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6183;
                                                           F801 SCHMA
P16463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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SHEON
                                   F801_SCHMA
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RESULT 51
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MEDLINE=21016719; PubMed=11130712;

Minte O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Minte O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Munte O., Alonso J., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fulji C.Y.,

Andil J.E., Goldsmith A.D., Hansen N.F., Hughes B., Huizar L.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.W., Lenz C.A., Li J.H., Li Y.-P.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Militecher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
                                                                                                                                                                                                          Nat. Biotechnol. 20:1118-1123(2002).

Nat. Biotechnol. 20:1118-1123(2002).

-!- FUNCTION: Catalyzes the condensation of 1-deoxy-D-xylulose-5-phosphate (DXP) and 1-amino-3-(phosphohydroxy)propan-2-one to form pyridoxine 5-phosphate (PNP) (By similarity).

-!- PATHWAY: De novo synthesis of pyridoxine (vitamin B6) and pyridoxal phosphate.

-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).

-!- SIMILARITY: Belongs to the pdxJ family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A. Peldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.,
                                                                                                                                                       "Genome sequence of the dissimilatory metal ion-reducing bacterium
Shewanella oneidensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Unknown thylakoid lumen protein, chloroplast precursor.
ATIG76450 OR F1466.5 OR F15M4.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyridoxine biosynthesis; Complete proteome.
SEQUENCE 245 AA; 26559 MW; 9B66759082BA5AFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE015579; AAN54416.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGR00559; pdxJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGR; SO1351; -.
HAMAP; MP_00279; -; 1.
InterPro; IPR004569; PdxJ.
Pfam; PF03740; PdxJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 TSYPDP 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 TSYPDP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGREAMS;
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THL1_ARATH
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   SOW WE WANTED THE SOURCE CONTROL OF SOURCE CONTR
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                                                                                                                                                                                                                                                                                                                                                                                    important compartment.";
Submitted (AUG-2001) to Swiss-Prot.
-!- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
-!- CAUTION: Ref.! sequences differ from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.; "Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-Human, TISSUE-B-cell, and Fetal brain,
MEDLINE-95038831; PubMed=7951316;
Albertsen H.M., Smith S.A., Mazoyer S., Fujimoto E., Stevens J.,
                                                                                                                                                                                                                                                                                                                                                "The chloroplast lumen of Arabidopsis thaliana is a functionally
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                                                                                                                                                                                                                                                            Schubert M., Peterson U., Haas B., Funk C., Schroeder W.P., Kieselbach T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 6; DB 1; Length 247;
100.0%; Pred. No. 1.7e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                SEQUENCE OF 81-89; 118-145; 166-181; 185-200 AND 218-236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 AA; 27490 MW; FF2DB5627C7CEE67 CRC64;
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EMBL, AC012394; AAF16656.1; ALT_SEQ.
Chloroplast; Thylakoid; Transit periode.
1 26 TEANSIT 1 27 80 THYLAKOID.
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                                                                                                                                                    Nature 408:816-820(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nuclear autoantigen).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 KGFYYI 189
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                                                                                                                        chaliana.
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Matches
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SEQUENCE FROM N.A. (ISOPORM 1).

SPECIES=Human: TISSUE=Lung, Ovary, and Placenta;

MEDLINE=2338257; PubMed=12477932;

Altachal S.F., Zeeberg B. T., Grouse L.H., Derge J.G.,

Altachal S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K.,

Altachal S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K.,

Altachal S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Altachal S.F., Zeeberg B. Toshiyuki S., Carninci P., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Nilalon D.K., Muzny D.M., Schergren E.J., Lu X., Gibbs R.A.,

Nilalon D.K., Muzny D.M., Schergren E.J., Lu X., Gibbs R.A.,

Raheeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J. Myers R.M.,

Blakeeley R.W., Kraywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Human and mouse CDNA sequences.",

Proc. Maria M.A., Schein J.E., Jones S.J.M., Marra M.A.,

Proc. Maria M.A., Schein J.E., Sola E. M. Marra M.A.,

R. Human and mouse CDNA sequences.",

Proc. Maria M.A., Schein J. E., Schein J. E., Schein J. B. S., Stocker J. E., Schein J. B. S., Stocker J. S., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete organizations of the three member genes and a physical map of the approximately 150-kb region containing the alpha- and beta-subunit genes.";
                                                                                                   "A physical map and candidate genes in the BRCA1 region on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES-Human; TISSUE-Ovary; MEDLINE-5502586; PubMed-7545554; MAKi Y., Swensen J., Shattuck-Eidens D., Futreal P.A., Harshman K., Miki Y., Swensen J., Shattuck-Eidens D., Futreal P.A., Harshman K., Tavtigian S., Liu Q., Cochran C., Bennett L.M., Ding W.; "A strong candidate for the breast and ovarian cancer susceptibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Sequence and expression of mouse proteasome activator PA28 and the
Williams B., Rodriguez P., Cropp C.S., Slijepcevic P., Carlson M., Robertson M., Bradley P., Lawrence E., Harrington T., Sheng Z.M., Hoppes R., Sternberg N., Brothman A., Callahan R., Ponder B.A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=Mouse; STRAIN=C57BL/6; TISSUE=Spleen;
MEDLINE=97364691; PubMed=9218537;
Kandil E., Kohda K., Ishibashi T., Tanaka K., Kasahara M.;
"PA28 subunits of the mouse proteasome: primary structures and chromosomal localization of the genes.";
Immunogenetics 46:337-344(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kohda K., Ishibashi T., Shimbara N., Tanaka K., Matsuda Y.,
Kasahara M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=Mouse; STRAIN=129/SvJ;
MEDLINE=98250122; PubMed=9590240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=Mouse; STRAIN=B10.BR;
MEDLINE=97306277; PubMed=9162094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunol. 160:4923-4935(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       related autoantigen Ki.";
Immunogenetics 46:93-98(1997).
                                                                                                                                                    Nat. Genet. 7:472-479(1994).
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STRAIN=C-125 / JCM 9153;
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Q89AH7;
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TRANSMEM
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LIPID
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    à
                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                       Isoid=012920-2; Sequence=VSP_004516; NOCE=Has been shown to exist only in human so far; DISEASE: SERA FROW PATIENTS WITH SYSTEMIC LUPUS ERYTHEMATOSUS OFTEN CONTAIN ANTHEORIES THAT REACT WITH THE KI ANTIGEN. SIMILARITY: BELONGS TO THE PA28 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                           (in isoform 2)
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                                                                                                                                                                                                                                                                                                                                                                                                 erythematosus
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'Laa 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IS-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Membrane protein oxaA 1 precursor.
OXAA1 OR BH4064.
Bacillus halodurans.
Bacitlus halodurans.
Bacteria, Firmicutes; Bacillales; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116FAB47D60A26C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            A -> L (IN REF. 5)

Q -> L (IN REF. 5)

E -> K (IN REF. 5)

E -> K (IN REF. 7)

E -> K (IN REF. 7)

A -> G (IN REF. 5)

K -> G (IN REF. 5)
                                                                                                                                                                                                                                                                                                                                                                                            Proteasome; AlternaTive splicing; Systemic lupus VARSPLIC 135 135 T -> TPSGKGPHICFDLO /FTId=vSP_004516.
 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score v,
100.0%; Pred. No. 1.8e4
          Name=1;
IBoId=Q12920-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                               MGD; MGI:1096366; Psme3.
GO; GO:0005837; C:26S proteasome; TAS.
InterPro; IPR003185; PA28 alpha.
InterPro; IPR03186; PA28 beta.
Pfam; PF02251; PA28 alpha; 1.
Pfam; PF022521; PA28 beta; 1.
                                                                                                                                                                                                   BC008020; AAH08020.1; -. BC001423; AAH01423.1; -. BC002684; AAH02684.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 D
172 A
188 K
29506 MW;
                                                                                                                                                                                                                                 EMBL, D87911, BAA22041.1, -.
EMBL, U60330, AAC53297.1, -.
EMBL, AB007139, BAA28838.1, -
                                                                                                                                                                                         EMBL; U11292; AAB60335.1; -.
                                                                                                                                                                                                                                                                  EMBL; U25756; AAA93227.1; -. PIR, 138702; A60537. HSSP, Q06323; 1AVO. Genew; HGNC:9570; PSME3.
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 PDPILL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 PDPILL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                      MIM; 605129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 55
OXAL BACHD
ID OXAL BACHD
AC Q98CA5;
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CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                       EMBL;
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                                                                                                                                                                                                                                                 MEDLINE 99356711; PubMed=10427704;
Takami H., Masui N., Nakasone K., Horikoshi K.;
"Replication origin region of the chromosome of alkaliphilic Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB013492; BAA82682.1; -.
EMBL; AP001520; BAB07783.1; -.
EMBL; AP001520; BAB07783.1; -.
HAMAP; MF 01801; -; 1.
InterPro; IPR001708; 60kDa innermeb.
InterPro; IPR001708; 60kD IMP; I.
FRAM; PR00701; 60kDINNERMP.
PROSITE; PR00701; 60kDINNERMP.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Transmembrane; Lipoprotein; Signal; Palmitate; Complete proteome.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-palmitoyl cysteine (Potential).
S-diacylglycerol cysteine (Potential)
223AF5D688F161FD CRC64;
                                                                                                                        FTRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
Takami H., NakaBone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buchnera aphidicola (subsp. Baizongia pistaciae).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
NCBI_TaxID=135842;
[1]
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15-WAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Flagellar basal-body rod protein flgG (Distal rod protein).
FLGG OR BBP913.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 6; DB 1; Length 257;
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEMBRANE PROTEIN OXAA 1.
                                                                                    Biosci. Biotechnol. Biochem. 63:1134-1137(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. .v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 MI
79 PC
182 PC
214 PC
21 N-
21 S-
2923 MW;
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257 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 6; Conserv
                                                                  halodurans C-125.
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TNFS AOTTR
Q9BDM3;
                                                                                                                                                                                               SEQUENCE
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REPEAT
                                                                                            DOMAIN
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                                                                                Repeat
                                                                                                                                                                                REPEAT
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MEDLINE=22426901; PubMed=12522265;
MEDLINE=22426901; PubMed=12522265;
Van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F., Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J., Tamames J., Viguera E., Lactorre A., Valencia A., Moran F., Moya A.; Reductive genome evolution in Buchnera aphidicola."; Proc. Natl. Acad. Sci. U.S.A. 100:581-586 (2003).
Proc. Natl. Acad. Sci. U.S.A. 100:581-586 (2003).
FLAGELLAR ORGANELLE AND CONSISTS OF FOUR RINGS (L,P,S, AND M) MOUNTED ON A CENTRAL ROD. THE ROD CONSISTS OF ABOUT 26 SUBUNITS OF FLGG IN THE DISTAL PORTION, AND FLGB, FLGC AND FLGF ARE THOUGHT TO BUILD UP THE PROXIMAL PORTION OF THE ROD WITH ABOUT 6 SUBUNITS EACH (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McGeoch D.J., Cunningham C., McIntyre G., Dolan A.; "Comparative sequence analysis of the long repeat regions and adjoining parts of the long unique regions in the genomes of herpes simplex viruses types 1 and 2."; J. Gen. Virol. 72:3057-3075(1991).
                                                                                                                                                                               SIMILARITY: Belongs to the flagella basal body rod proteins family.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1%; Score 6; DB 1; Length 260; 100.0%; Pred. No. 1.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                  EMBL; AE014017; AA027035.1; -.
InterPro; IPR00144; Flag_bb_rod.
Pfam; PF00460; flg_bb_rod; 1.
PROSITE; PS00588; FlagELLA_BB_ROD; 1.
Flagellum; Complete protecome.
SEQUENCE 260 AA; 28215 MW; 0B9E1146CAD4690B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herpes simplex virus (type 2 / strain HG52).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92113549; PubMed=1662697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neurovirulence factor (ICP34.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 SEETIS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
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P28283;
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                                                                                                                                                                                                                                                     2 X 8 AA TANDEM REPEATS OF P-R-P-G-A-P-A-V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-L) (CD154 protein).
TNFSF5 OR CD40LG OR CD40L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ця
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps

Immunogenetics 53:315-328(2001).
Immunogenetics 53:315-328(2001).
PUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IgE production in the presence of IL-4. Involved in immunoglobulin class switching (By similarity).
SUBCELLUIAR LOCATION: Type II membrane protein. Also exists as extracellular soluble form (By similarity).
FM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
SIMILARITY: Belongs to the tumor necrosis factor family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aotus trivirgatus (Night monkey) (Douroucouli).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
                                                                                                                                                             2 X 5 AA TANDEM REPEATS OF R-R-G-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning, sequencing, and homology analysis of nonhuman primate Fas/Fas-ligand and co-stimulatory molecules."; Immunogenetics 53:315-328(2001).
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MEDLINE=21383618; PubMed=11491535;
Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Weiss W.R., Ansari A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.1%; Score 6; DB 1; Length 261; Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                 23
31
27908 MW; 4BBD13AF3D906D71 CRC64;
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GO; GO:0005174; F:CD40 receptor binding; ISS.
GO; GO:00042100; P:B-Cell proliferation; ISS.
GO; GO:0006954; P:inflammatory response; ISS.
GO; GO:000159; P:leukocyte cell adhesion; ISS.
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EMBL; D10471; BAA23428.1; -.
EMBL; 286609; CAB06759.1; -.
EMBL; 286609; CAB06706.1; -.
PIR; JQ1502; WMBEXE.
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12
31
31
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                                                                                                                                                                                                                                                                                                                                                                                        261 AA;
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                                                                                                                                                                             Prodom; Fuce.

PROSITE; PRO0251; TNF; 1.

PROSITE; PSS0049; TNF_2; 1.

Cytckine; Transmembrane; Glycoprotein; Signal-anchor.

Cytckine; Transmembrane; Glycoprotein; Signal-anchor.

Cytckine; Transmembrane; Glycoprotein; Signal-anchor.

CHAIN 1261 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBERA 5, MEMBERANE FORM.

TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 5, SOUTHELE FORM.

TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY NEWBER 5, SOUTHELE FORM.

TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY NEWBER 5, SOUTHELE FORM.

STOPPLASMIC (POTENTIAL).

A1 SIGNAL-ANCHOR (TYPE-II MEMBEANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Blood;
MEDLINE=96006582; PubMed=7590981;
Mertens B.E.L.C., Muriuki M., Gaidulis L.;
Mertens B.E.L.C., Muriuki M., Gaidulis L.;
"Cloning of two members of the TNF-superfamily in cattle: CD40 ligand and tumor necrosis factor alpha.";
Immunogenetics 42:430-431(1995).
Immunogenetics 42:430-431(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          class switching (By similarity).
SUBGELUIAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).
PTM: The soluble form derives from the membrane form by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TWES BOVIN STANDARD; PRT; 261 AA.
P51749;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (TNF-related activation protein) (TRAP) (T cell antigen GP39).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IgE production in the presence of IL-4. Involved in immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL)
85E1588B507901B5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 261;
5. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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100.0%; Pred. No. 1.8
:ive 0; Mismatches
  GO; GO:0030168; P:platelet activation; ISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                InterPro; IPR003265; TWF 5.
InterPro; IPR006052; TWF family.
InterPro; IPR0060502; TWF family.
InterPro; IPR0060565; TWF subf.
Pfam; PF00229; TWF; 1.
PRINTS; PR01702; CD4011GAND.
ProDom; PD008600; TWF 5; 1.
ProDom; PD002012; TWF 5; 1.
SWART; SM00207; TWF; 1.
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218
240
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TNF5_BOVIN
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(See http://www.isb-sib.ch/announce/
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-L) (CD154 protein).
TWRSF5 OR CD40LG OR CD40L.
Callithrix jacchus (Common marmoset).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaila; Eutheria; Primates; Platyrrhini; Callitrichidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SMULU, INF 1; 1.
PROSITE; PSS0049; TNF 1; 1.
PROSITE; PSS0049; TNF 2; 1.
Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
251 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEMBER 5, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEMBER 5, SOLUBLE FORM (BY SIMILARITY).
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 POTENTIAL.
240 N-LINKED (GLCNAC. . .) (POTENTIAL).
29242 MW; 8491FEFB30A787FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning, sequencing, and homology analysis of nonhuman primate Fas/Fas-ligand and co-stimulatory molecules."; Immunogenetics 53:315-328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IgE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Lymphocytes;
MEDLINE=211883618; PubMed=11491535;
Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Weiss W.R., Ansari A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 6; DB 1; Length 261;
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL). CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                           GO; GO:0016021; Cintegral to membrane; ISS.
GO; GO:000174; F:CD40 receptor binding; ISS.
GO; GO:0042100; P:B-cell proliferation; ISS.
GO; GO:0006954; P:inflammatory response; ISS.
GO; GO:0007159; P:leukocyte cell adhesion; ISS.
GO; GO:0030168; P:platelet activation; ISS.
InterPro; IPR003263; TNF 5mily.
InterPro; IPR008983; TNF family.
InterPro; IPR008983; TNF family.
InterPro; IPR008983; TNF family.
InterPro; IPR00365; TNF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.1%; Score 6; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.8¢
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                             entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD008600; TNF 5; 1.
ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
                                                                                                   EMBL; Z48469; CAA88363.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00229; TNF; 1.
PRINTS; PR01702; CD40LIGAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261
113
218
240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261
                                                                                                                                   S53090; S53090.
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261 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 GFYYIY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00229; TNF;
                                                                                                                                                        P29965; 1ALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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TNF5 C
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us-10-662-429-2.oligo.rsp

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CTE2 HUMAN
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ACT SITE
SEQUENCE
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CTE2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; F. PRO1702; F. PRO1702; PROD0600; TNF_5; 1.

R PRODOM; PD002012; TNF_subf; 1.

R SMART; SM00207; TNF_1 1.

R PROSTITE; PS00201; TNF_1; 1.

DR PROSTITE; PS50049; TNF_2; 1.

KM Cytokine; Transmembrane; Glycoprotein; Signal-anchor.

TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBRANE FORM.

TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY TWORN NECROSIS FACTOR LIGAND SUPERFAMILY TWO NECROSIS FACTOR
                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                     class switching (By similarity).
--- SUBUNIT: Homotriner (By similarity).
--- SUBUNIT: Homotriner (By similarity).
--- SUBCELLUIAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).
---- PIM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
---- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01.AUG-1990 (Rel. 15, Last sequence update)
28-REB-2003 (Rel. 41, Last annotation update)
Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-
xylan xylanohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
production in the presence of IL-4. Involved in immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 N-LINKED (GLCNAC. . .) (POTENTIAL). 29360 MW; 10CA588D923754EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.1%; Score 6; DB 1; Length 261; 100.0%; Pred. No. 1.8e+02; rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL). CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0016021, C:integral to membrane; ISS.
GO; GO:0005774; F:CD40 receptor binding; ISS.
GO; GO:0005774; F:CD40 receptor binding; ISS.
GO; GO:0005774; F:CD40 receptor binding; ISS.
GO; GO:000575; P:inflammatory response; ISS.
GO; GO:0007159; P:leukcyte cell adhesion; ISS.
GO; GO:0007159; P:leukcyte cell adhesion; ISS.
InterPro; IPRO06052; TNF 5.
InterPro; IPRO06052; TNF family.
InterPro; IPRO06053; TNF family.
InterPro; IPRO06053; TNF Tabf.
Pfam; PF00229; TNF; 1.
Prints; PRO0229; TNF; 1.
ProDom; PD008600; TNF 5; 1.
ProDom; PD008600; TNF 5; 1.
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                                                                                                                                                                                                                                                                                          entities requires a license agreement (Sons send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                  EMBL; AF344844; AAK37603.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1990 (Rel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clostridium saccharobutylicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 GGIFEL 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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NCBI_TaxID=169679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLOSA
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                                                                                                                                                                                                                                                                                                                                                                          HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                     linkages in xylans.
-!- PATHWAY: Xylan degradation.
-!- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
                                                                                  Zappe H., Jones W.A., Woods D.R.;
"Nucleotide sequence of a Clostridium acetobutylicum P262 xylanase
qene (xynB).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                    Nucleic Acids Res. 18:2179-2179(1990).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENDO-1,4-BETA-XYLANASE.
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1%; Score 6; DB 1; Length 261; 100.0%; Pred. No. 1.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339C3616F6FD14AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      -!- CAUTION: Was originally thought to originate from C.acetobutylicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xylan degradation; Hydrolase; Glycosidase; Signal. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8NGM3; Q9H3Y1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Proctein C20orf142 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00457; Glyco_hydro_li; 1.
PRANYS; PR00911; GLYCOSYL HYDROLES11.
PROSITE; PS00777; GLYCOSYL HYDROL_F11 1; 1.
PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR008985; Cond like lec gl.
InterPro; IPR001137; Glyco_hydro_ll.
                                                                    MEDLINE=90245673; PubMed=2336398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29032 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M31726; AAA23287.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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242
261 AA;
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SEQUENCE FROM N.A.
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Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle B., Hunt B.E., Jekosch K., Johnson C.M., Johnson D., Ray M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Lehvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A., Mille S.A., Mistry D., Moore M.J.F., Wullikin J.C., Nickerson T., A. Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Smith M.L., Scott C.E., Sehra H.K., Shownkeen R., Sims S., Swuce C.D., Smith M.L., Scott C.E., Sehra H.K., Shownkeen R., Sims S., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vauddin M., Wall M., Wallis J.M., Whitehead S.L., Whittaker P., Willey D.L., Williams S.A., Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Reck M., Thorpe M., Thorpe M., Thorpe M., Thorpe M., Thorpe M., Milliams S.A., Milming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Regers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                         "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 262; . 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Sco...
100.0%; Pred. No. ...
... 0; Mismatches
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EMBL; BC029662; AAH29662.1; -.
Genew; HGNC:16135; C20oxf142.
                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29855 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal, Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 AA;
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RA MUDINE-22346463; PubMed-1246681;
RA MIDINE-22346463; PubMed-1246681;
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yadaki I., Masegawa Y., Nogami A., Schonbach C., Gojobori T.,
Baldarelli R., Hill D.P. Bult C., Hume D.A., Quackenbush J.,
Baldarelli R., Endl D., Burdic C., Hume D.A., Quackenbush J.,
Baldarelli R., Fill D.P., Bult C., Hume D.A., Quackenbush J.,
Baldare J.A., Bradd D., Burdic V., Chothla C., Corbani L.E., Cousins S.,
RA Dalla E., Dragami T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Dalla E., Dragami T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,
RA Anai A., Kawaji H., Kawasawa N., Jackson I.J., Jarvis B.D.,
RA Ranai A., Kawaji H., Kawasawa N., Jackson I.J., Pertea G., Pecole G.,
RA Ranai A., Kawaji H., Kawasawa V., Rendad B., Lyons P.A.,
Magoltt D.R., Maltais L., Marchionni L., McKenzie L., Mikh H.,
RA Rayasi T., Numata K., Okido T., Para N., Setou M., Shimada K.,
Sultana R., Schneider C., Semple C.A., Setou M., Shimada K.,
Sultana R., Myrshaw-Boris A., Tanglawa N., Sarou M., Shimada K.,
Sultana R., Myrshaw-Boris A., Yanagisawa M., Yang I., Yang I.,
Yang I., Yang I.,
Wata K., Kawai J., Alawasura M., Sato K.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
Rahiari T., Waki K., Kawai J., Alawasura M., Xang I.,
Anai Yasunishi A., Soshino M., Waterston R., Lander E.S., Rogers J.,
Ratiney E., Hayahizahi Y.,
Ratiney E., Hayahizahi W.,
Ratine 40. Sato R.,
Ratiney E., Hayahizahi Y.,
Ratiney E., Sangaki K., Sasaki K., Sasaki K., Banasaki M., Waterston R., Lander E.S., Rogers J.,
Ratiney E., Sangashi Z., Ratine R.,
Ratine 40. Sato R.,
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Ratine 40. Sato R.,
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Ratine 40. 
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                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E -> Q (IN REF. 1; BAC29663).
G -> P (IN REF. 1; BAC29663).
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                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CS7BL/6J; TISSUE=Aorta, Cerebellum, and Vein; MEDLINE=22354683; PubMed=12466851;
                                              PSyzor, 2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
   262 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
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                                                                                                                                     10-OCT-2003 (Rel. 42, Last annotation
Protein C20orf142 homolog precursor.
PRT;
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39
262
78
114
166
211
240
169
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                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
CTE2 MOUSE
                                                                                                                                                                                                         C200RF142.
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TRANSMEM
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CONFLICT
CONFLICT
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SIGNAL
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Gaps

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0; Indels

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267 AA.

Page 36

Matches

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                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                               01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-CT-1994 (Rel. 30, Last amotation update)
Hypothetical 30.7 kDa protein in STE6-LOS1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Pohl T.M., Pohl F.M.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished observations (AUG-1994).
-!- SIMILARITY: SOME, TO MAMMALIAN DEOXYRIBONUCLEASE I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein. SEQUENCE 267 AA; 30739 MW; D635C3EBC2E37C11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.1%; Score 6;
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                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, Z28206, CAA82051.1; -. PIR, S38044, S38044. Germonline, 139960; -. SGD; SO001689; YKL206C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L) (CD154 protein).
INFSF5 OR CD40LG OR CD40L.
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nes 6; Conservative
                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4932;
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                                     YKU6 YEAST
P36040;
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ID TNF5_CHI
AC Q918D8;
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                                             SOW REPUBLICATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
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PROSITE; PS50893; ABC_TRANSPORTER 2; 1.
Hypothetical protein; ATP-binding; Transport; Complete proteome.
NP RIND 37 44 ATP (POTENTIAL).
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                                                                          Length 262;
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100.0%; Pred. No. 1.8e+02;
iive 0; Mismatches 0; Indels
                                                                      2.1%; Score 6; DB 1; Length 262;
100.0%; Pred. No. 1.8e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical ABC transporter ATP-binding protein MJ1023.
262 AA; 30016 MW; D28B971C521953BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 AA; 30316 MW; B195338E6ACED777 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methanococci; Methanococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 273:1058-1073(1996).
-1- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea, Euryarchaeota, Methanococci, Meth
Methanocaldococcaceae, Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC_transporter.
Pfam; PP000005; ABC_tran; I.
ProDom; PD000006; ABC_transporter; I.
SWART; SM00382; AAA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U67545; AAB99027.1; -.
                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanococcus jannaschii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=2190;
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Gaps

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DB 1; Length 267; 5. 1.8e+02; cches 0; Indels

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28-FEB-2003 (Rel. 41, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-L) (CD154 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: Homotrimer (By similarity).
-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tregaskes C.A., Young J.R., Burnside J.;
"Cloning of a putative chicken CD40 ligand.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Cytokine that binds to TWRRSF5. Mediates B-cell
proliferation in the absence of co-stimulus as well as IgE
production in the presence of LL-4. Involved in immunoglobulin
class switching (By similarity).
-!- SUBUNIT: Homotrimer (By similarity).
272 AA.
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Matches

δ g RESULT 65

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                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00207; INF 1: 1.

PROSITE; PS00251; TNF 1: 1.

PROSITE; PS50049; TNF 2: 1.

CYTOKINE; Transmembrane; Glycoprotein; Signal-anchor.

CYTOKINE; Transmembrane; Glycoprotein; Signal-anchor.

TOMOR NECROSIS FACTOR LIGAND SUPERFAMILY

TOMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEMBER 5, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEMBER 5, SOLUBLE FORM (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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28-FEB-2003 (Rel. 41, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Peptide deformylase, chloroplast precursor (EC 3.5.1.88) (PDF)
POlypeptide deformylase)
                               proteolytic processing (By similarity). SIMILARITY: Belongs to the tumor necrosis factor family.
extracellular soluble form (By similarity).

PTM: The soluble form derives from the membrane form by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; DB 1; Length 272;
No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                    GO; GO:0016021; C:integral to membrane; ISS.
GO; GO:005174; F:CD40 receptor binding; ISS.
GO; GO:0045174; F:CD40 receptor binding; ISS.
GO; GO:0045100; PsiB-cell proliferation; ISS.
GO; GO:000594; P:inflammatory response; ISS.
GO; GO:0007159; P:inflammatory response; ISS.
GO; GO:0007168; P:platelet activation; ISS.
InterPro; IPR008052; TNF 5.
InterPro; IPR008052; TNF 1ike.
InterPro; IPR008363; TNF like.
Fran; PF00229; TNF; 1.
PRINTS; PR01702; CD40LIGAND.
ProDom; PD002012; TNF 5; 1.
ProDom; PD002012; TNF 5; 1.
ProDom; PD002012; TNF 5; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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Local Similarity 100.0%; Pr
// Annervative 0;
                                                                                                                                                                                                         EMBL; AJ243435; CAB95748.2; -.
HSSP; P29965; 1ALY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30832 MW;
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251
272 AA;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lycopersicon esculentum (Tomato).
Bukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERBO J. 19:5916-5929(2000).

-1- FUNCTION: Removes the formyl group from the N-terminal Met of newly synthesized proteins (By similarity).

-1- CATALYTIC ACTIVITY: Formyl-L-methionyl peptide + H(2)0 = formate methionyl peptide.

-1- COPACTOR: Bindel i iron(II) ion (By similarity).

-1- COPACTOR: Bindel i iron(II) ion (By similarity).

-1- SIBGELMULAR LOCATION: Chloroplast (Potential).

-1- SIMILARITY: Belongs to the polypeptide deformylase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                     HSSP; P27251; IDEF.
InterPro; INFR000181; Pep deformylase.
Prem; PR01327; Pep deformylase; 1.
PR1NTS; PR01576; Pep deformylase; 1.
PR0001844; Pep deformylase; 1.
PR0001844; Pep deformylase; 1.
PR0001; PR00079; Pept deformyl; 1.
Protein blosynthesis; Hydrolase; Iron; Chloroplast; Transit peptide.
TRANS; T. 273 PEPTIDE DEPORMYLASE.
ACT_SITE 214 214 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Peptide deformylase, chloroplast precursor (EC 3.5.1.88) (PDF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20514156; PubMed=11060042; Giglione C., Serero A., Pierre M., Boisson B., Meinnel T., Giglione C., Serero A., Pierre M., Boisson B., Meinnel T., "Identification of eukaryotic peptide deformylases reveals universality of N-terminal protein processing mechanisms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 273;
                                                                                                                                                                                                                                                                                                                                                             214 BY SIMILARITY.
171 IRON (BY SIMILARITY).
217 IRON (BY SIMILARITY).
217 IRON (BY SIMILARITY).
48 T -> N (IN REF. 4).
505 R -> S (IN REF. 1).
730610 MW; 25CDA90EDED9603E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 6; I
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1.,
100.0%; Pre-
0, 1
                                                                                         EMBL, AF269165, AAG33980.1; -.. EMBL, AL163792; CAB87633.1; -. EMBL, AY050079; AAK92816.1; -.. EMBL, AY086673; AAM20307.1; -.. EMBL, AY085417; AAM62644.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Polypeptide deformylase), PDF1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 YPDPIL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 YPDPIL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Q9FV54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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REGULINE-99121113; PubMed=9461215;

REDINE-99121113; PubMed=9461215;

REDINE-99121113; PubMed=9461215;

RA Bevran M., Bancroft I., Bent E., Love K., Goodman H.M., Dean C.,

RA Bergkamp R., Dirkse W., van Staveren M., Stiekema W., Drost I.,

RA Haldey P., Hudson S.-A., Patel K., Murphy G., Piffanelli P.,

RA Medler H., Wedler E., Wambutt R., Weitzenegger T., Pohl T., Terryn N.,

RA Medler H., Wedler E., Wambutt R., Weitzenegger T., Pohl T., Terryn N.,

RA Moburg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S.,

ROtter P., Entian K.-D., Rieger M., Schaefer M., Funk B.,

Reller-Auer S., Silvey M., James R., Monfort A., Pons A.,

RA Meeller-Auer S., Silvey M., Jones R., Monfort A., Pons A.,

RA Piravandi E., Obermaier B., Hilbert H., Duesterhoeft A., Moores T.,

A Ones J.D.G., Eneva T., Palme K., Benes V., Rechman S., Ansorge W.,

Cooke R., Berger C., Delseny M., Voet M., Volckaert G., Mewes H.-W.,

RY Cooke R., Berger C., Chalwatzis N.;

RY Aralysis of I.9 Mb of contiguous sequence from chromosome 4 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                 Pfam; PF01327; Pep deformylase; 1.
PRINTS; PR01576; PDEFORMYLASE.
Probom; PR003844; Pep deformylase; 1.
TIGRPAMS; TIGRO079; Pept deformyl; 1.
Protein biosynthesis; Hydrolase; Iron; Chloroplast; Transit peptide.
TRANSIT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94339478; PubMed=8061317;
Collinge M.A., Walker J.C.;
"Isolation of an Arabidopsis thaliana casein kinase II beta subunit by complementation in Saccharomyces cerevisiae.";
Plant Mol. Biol. 25:649-658(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=CV. Columbia;
MEDLINE=20083488; PubMed=10617198;
MEDLINE=20083488; PubMed=trough g., Volckaert G.,
Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 6; DB 1; Length 279; 100.0%; Pred. No. 1.9e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  750F6406FDAC4233 CRC64;
                                                                                                                                                                                                                                                                                                                                                      IRON (BY SIMILARITY)
IRON (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2014 kinase II beta' chain (CK II).
CKB2 OR AT4617640 OR DL4855W.
Arabidopsis thaliana (Wouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY
                                                                                         InterPro; IPR000181; Pep_deformylase.
                             EMBL; AF250958; AAG33972.1; -.
HSSP; P27251; 2DEF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31197 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                 219
                                                                                                                                                                                                                                                                                                                                                   177
219
220
220
223
279 AA;
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P40229;
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METAL
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METAL
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Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,

Reicherlagartner M., de Simone V., Obermader B. Mache R., Mueller M.,

Kreis M., Delseny M., Puligdomenech P., Wateon M., Schmidtheini T.

Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,

Voe P., Hoheisel J., Zimmernam M., Wedler H., Ridley P.,

Langham S.-A., McCullagh B., Eilham L., Robben J.,

Ra Jangham S.-A., McCullagh B., Eilham L., Robben J.,

Ra Fraeken M., Weltiens I., Grymontyez B., Churang Y.-J., Vandenbussche F.,

Ra Braeken M., Weltiens I., Grymontyez B., Churang I., Aert R., Defoor E.,

Ra Meitzeneger T., Bothe G., Ramsperger I., Hilbert H., Braun M.,

Rolzer E., Brandt A., Peters S., Van Staveran M., Janche B.,

Ra Dereiser S., Hempel S., Feldpauch M., Lamberth S., Van den Dele H.,

Ra Dereiser S., Hempel S., Feldpauch M., Maltarcel R., De Glercq R.,

Ra Dereiser A., Buyshaart C., Gdelen J., Villarcel R., De Glercq R.,

Ra Dereiser B., Brandt A., Peters S., Conin A., Quail M., Brayalles S.,

Ra Clark L., Doggett J., Fall S., Kay M., Lennard N., McLay K.,

Ra Clark L., Doggett J., Fall S., Kay M., Lennard N., McLay K.,

Ra Borkova D., Bloecker H., Scharfen M., Grimm M., Lochnert T.-H.,

Ra Borkova D., Bloecker H., Scharfen M., Grimm M., Lochnert T.-H.,

Ra Gabel C., Puchs M., Parm B., Graefer M., Mueller-Auer S.,

Ra Gabel C., Puchs M., Parm B., Graefer M., Mueller-Auer S.,

Ra Gabel C., Puchs M., Parmen B., Graefer M., Mueller-Auer S.,

Rassenet O., Quilger F., Clabauld G., Muendelen M., Petber R.,

Rassenet O., Quilger F., Clabauld G., Muendelen M., Petber S.,

Ra Accaria P. Bever R., Berger C., Mondenbol M., Bergues M., Attend J., Torres A.,

Rhiller R., Schmidt W., Leeber S., France P., Belber R.,

Raccaria P., Bever M., Walcenbol M., Bargues M., Abrol J., Stock F.,

Raccaria P., Bever M., Walcenbol M., Bargues M., Abrol J., Stock J.,

Ratreille P., Couttney L., Cloud J., Abbott A., Scott K., Johnson D.,

Ram Minx P., Bentley D., Fulton B., Milane M., Hall J., Spiech J., Spiech J., Spiech J., Spiech J., Spiech J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMB outstation the burspean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 402:769-777(1999).

-!- FUNCTION: Plays a complex role in regulating the basal catalytic activity of the alpha subunit (By similarity).

-!- SUBUNIT: Tetramer composed of an alpha chain, an alpha', one beta chain and one beta' chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PTM: Phosphorylated by alpha chain (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U03984; AAA53234.1; -. EMBL; Z97343; CAB10544.1; -.
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Transferame, Serine/threonine-protein kinase, Phosphorylation. SEQUENCE 282 AA, 31978 MW, 507EABOA74ISDIE6 CRC64;

Pfam; PF01214; CK II beta; 1.
PRINTS; PR00472; CASNKINASEII.
ProDom; PD003829; CAS kinase II; 1.
PROSITE; PS01101; CK2_BETA; 1. InterPro; IPR000704; CAS_kinase_II.

EMBL; AL161546; CAB78767.1; -. PIR; S47968; S47968.

2.1%; Score 6; DB 1; Length 282; 100.0%; Pred. No. 1.9e+02;

Best Local Similarity

Query Match

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RACAMENTE-21849401; PubMed=11859360;

RA WEDLINE=21849401; PubMed=11859360;

RA WOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Squores U., Barown S., Chillingworth T., Churcher C.M.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gollins M., Connor R., Cronin N., Harris D., Hidalgo J., Hodgson G.,

RA Gonles L., Jones M., Leather S., McDonald S., McLean J.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA Holroyd S., Mongall K., Murphy I., Niblest D., Odell C.,

RA Holroyd S., Mongall K., Murphy I., Niblest D., Odell C.,

RA Nooney P., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch B.,

Rutherford K., Taylor R.G., Trivey A., Walsh S.V., Warren T., Whitchead S.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stewens K.,

RA Skelton J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Woodward J., Volckaert G., Aert R., Robben J., Hilbert H.,

RA Gabel C., Fuchs M., Fritzc C., Holzer B., Moestl D., Hilbert H.,

RA BOZZYM K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Goffeau A., Cadlel E., Dreano S., Gloux S., Lelaure V., Mortier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Bogar R.R., Chusde D., Jimenez J., Sanchez M., del Rey F., Benitco J.,

RA Bominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RA Shakovski G.V., Usbsery D., Barrell B.G., Nurse P.,

Nature 415:871-880(2002).

L'EDWILDIN: Required for the methylation step in diphthamide

L'EDWILDIN: Required for the methylation step in diphthamide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FWBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                0.77-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Probable diphthine synthase (EC 2.1.1.98) (Diphthamide biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biosynthesis.
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 2-(3-carboxy-3-aminopropyl)-L-histidine = S-adenosyl-L-homocysteine + 2-[3-carboxy-3-(methylammonio) propyl]-L-histidine.
-!- PATHWAY: Diphthamide biosynthesis; second step.
-!- SIMILARITY: Belongs to the diphthine synthase family.
                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GeneDB_SPombe, SPCC576.14; -.
InterPro, IPR000878; Cor/por Metransf.
InterPro, IPR004551; Dphthn_synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL031798; CAA21193.1; -. PIR; T41424; T41424.
                            STANDARD;
                                                                                                                                                                                                                                                                                                Schizosaccharomyces.
                                                                                                                                                                      methyltransferase).
SPCC576.14.
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4896;
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SCHPO
                            DPH5
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DOMAIN
TRANSMEM
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TRANSMEM
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIOUS SULFOXIDE AND N-OXIDE COMPOUNDS. THE C SUBUNIT ANCHORS THE OTHER TWO SUBUNITS TO THE MEMBRANE AND STABILIZE THE CATALYTIC SUBUNITS: (By similarity).
SUBUNIT: THE COMPLEX CONSIST OF THREE SUBUNITS: YNFF, THE REDUCTARSE; YNFG, AN ELECTRON TRANSFER PROTEIN, AND YNFH, A MEMBRANE ANCHOR PROTEIN (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAINE-K12;
MEDLINE-97251357; PubMed-9097039;
Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Baba T., Fujita K., Hayashi K., Mori H., Mori T., Motomura K., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Makino K., Miki T., Misobuchi K., Mori H., Mori T., Motomura K., Makino K., Makamura Y., Sampei G. Seki Y., Sivasundaram S., Tagami H., Takeda J., Takenoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Takenoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Takenoto G. The Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
DNA Res. 3:363-377(1996).
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Rilety M., Collado-Vides J., Glasner J.D., Rode C.K., Maybew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                       YNFH ECOLI STANDARD; PRT; 284 AA.
P76.73; P77142;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Anaerobic dimethyl sulfoxide reductase chain ynfH (DMSO reductase
                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                   2.1%; Score 6; DB 1; Length 283; 100.0%; Pred. No. 1.9e+02; iive 0; Mismatches 0; Indels
Pfam; PF00590; TP_methylase; 1.
TIGRFANs; TIGR00522; dphs; 1.
Transferase; Methyltransferase.
SEQUENCE 283 AA; 32044 MW; FF3300910CEC1AD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Strong, to E.coli dmsC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE000254; AAC74662.1; -.
EMBL; D90801; BAA15314.1; ALT INIT.
EMBL; D90802; BAA15324.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                   Enterobacteriaceae, Escherichia
                                                                               Local Similarity 100.
Les 6; Conservative
                                                                                                                                                                                                                                                                                                            anchor subunit ynfH).
                                                                                                                                                      213 SLCVAV 218
                                                                                                                          28 SLCVAV 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=562;
                                                                     Query Match
                                                                                                                                                                                                        YNFH ECOLI
                                                                                            Matches
                                                                                                                                                                                              RESULT 71
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PIR; H64914; H64914.
EccGene; EG13846; ynfH.
InterPro; IPR007059; DmsC.
Pfam; PF04976; DmsC; 1.
Hypothetical protein; Oxidoreductase; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 31:2134-2147(2003).

-!- FUNCTION: Involved in the biosynthesis of lipid A, a phosphorylated glycolipid that anchors the lippolysaccharide to the outer membrane of the cell (By similarity).

-!- CATALYTIC ACTIVITY: UDP-3-0-(3-hydroxytetradecanoyl)-N-acetylglucosamine + H(2)0 = UDP-3-0-(3-hydroxytetradecanoyl)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22569155; PubMed=12682364;
Weed T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A.,
Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of Chlamydophila caviae (Chlamydia psittaci GPIC): examining the role of niche-specific genes in the evolution of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydophila caviae.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last amnocation update)
10-DP-3-0-(3-hydroxymyristoyl] N-acetylglucosamine deacetylase
(EC 3.5.1.-) (UDP-3-0-acyl-GlcNAc deacetylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73F7D760FC4B1344 CRC64;
                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                          PERIPLASMIC (POTENTIAL).
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                                                                                                                                                                       PERIPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the lpxC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. No. 2e+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.1%; Score 6; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30523 MW;
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                                                                                                                                                                       9
30
45
66
66
107
115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
hes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 VIFTVL 25
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                                                                                                                                             Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=83557;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydiaceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPXC CHLCV
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=Rd (TWX20 / ATCC 51907;
MEDIJNB=5350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Sprigs T., Hedblom E., Cotton M.D.,
Witerback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Ruhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                          HAMAP; MF_00388; -; 1.
InterPro; IPR004463; LpxC.
Pfam; PF03331; LpxC; 1.
TIGRPAMB; TIGR00325; lpxC; 1.
Hydrolase; Lipid A biosynthesis; Lipid synthesis; Complete proteome.
SEQUENCE 285 AA; 31421 MW; 300EC1D08DB403D9 CRC64;
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=96186898; PubMed=8635745;
Chandler M.S., Smith R.A.;
"Characterization of the Haemophilus influenzae topA locus: DNA topoisomerase I is required for genetic competence.";
                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 269:496-512(1995).
--- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Putative HTH-type transcriptional regulator H11364 (ORF2)
                                                                                                                                                                                                                                        2.1%; Score 6; DB 1; Length 285; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               288 AA.
                                                                          EMBL; AE016994; AAP04840.1; -. TIGR; CCA00088; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, U20964; AAC43726.1; -. EMBL, U22816; AAC23011.1; -. PIR; D64171.
                                                                                                                                                                                                                                                           Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 169:25-31(1996).
                                                                                                                                                                                                                                                                                                                 146 ALGRKI 151
                                                                                                                                                                                                                                                                                                                                                   274 ALGRKI 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                       YHCS_HAEIN
P43011;
                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CLIP 11262 / Serovar 6a,

MEDLINE=21537279; PubMed=11679669;

Glaser P., Franqeul L., Buchrieser C., Rusniok C., Amend A.,

Glaser P., Franqeul L., Buchrieser C., Rusniok C., Amend A.,

Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

B. Moman E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Charbit A., Coefel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Andueno E., Maltournam A., Mata Vicente J., Ng E., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

Varquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

Comparative genomics of Listeria species.";

Science 294:849-852(2001).
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i - FUNCTION: Unusual circulary permuted GTPase that catalyzes rapid
hydrolysis of GTP with a slow catalytic turnover (By similarity)
-i - SUBUNIT: Monomer (Probable).
-i - SIMILARITY: Contains 1 engC GTPase domain.
                                                                                                                                                          H-T-H MOTIF (POTENTIAL).
VTGISLNF -> RAFIEFLSGLGLCSEIWENHEDNI
(IN REF. 1).
                                                                                                                                                                                                                                                                                                  ö
InterPro; IPR000847; HTH LyBR.
InterPro; IPR05119; LyBR_subst.
Pfam; PF00126; HTH 1; 1.
Pfam; PF03466; LyBR_substrate; 1.
PROSITE; PS50931; HTH LySR; 1.
Hypothetical protein; Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                         DB 1; Length 288; . 2e+02; ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                                                                                                                                                   EEF3C22374352980 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Probable GTPase engC protein 1 (EC 3.6.1.-).
ENGC1 OR LIN1933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 AA.
                                                                                                                                                                                                                                                       2.1%; Score 6; DB 1
100.0%; Pred. No. 2e+
tive 0; Mismatches
                                                                                                                                          HTH LYSR-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TICRFAMS; TICR00157; TICR00157; 1.
PROSITE; PSS0936; ENGC GTPASE; 1.
Hydrolase; GTP-binding; Complete proteome.
                                                                                                                                                                                                                   288 AA; 32422 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL596170; CAC97163.1; -. PIR; AC1674; AC1674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP; MF_01820; -; 1.
InterPro; IPR004881; DUF258.
                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF03193; DUF258; 1
                                                                                                                                      59
38
288
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                                                                                                                                                                                                                                                                                                                                     106 KQQNIS 111
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                     Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                       24 KOONIS 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Listeria innocua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LISIN
                                                                                                                                                        DNA BIND
CONFLICT
                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q92AI9;
                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 74
EGC1_LISIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carraine Exches, A. Serovar 1/2a;

MEDLINE=21537279; PubMed=11679669;

MEDLINE=21537279; PubMed=11679669;

MEDLINE=21537279; PubMed=11679669;

Maguero F., Frangeul L., Buchriseer C., Rusniok C., Amend A.,

Baquero F., Barche P., Bloecker H., Brandt P., Chakraborty T.,

Maguero F., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Dentian K.-D., Fshih H., Garcia-del Portillo F., Garrido P.,

Machier L., Goebel M., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

Macquez-Boland J.-A., Voss H., Wehland J., Cossart P.,

"Comparative genomics of Listeria species";

Science 294:849-852(2001).

"FUNCTION: Unusual circulary permuted GTPase that catalyzes rapid hydrolysis of GTP with a slow catalytic turnover (By similarity).

"Subunit: Monomer (Probable).
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                         ·,
ENGC GTPASE.

GTP (PROBABLE).

GTP (PROBABLE).

GTP (PROBABLE).

KNUCKLE-LIKE CYSTEINE CLUSTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNUCKLE-LIKE CYSTEINE CLUSTER.
                                                                                                                                                                                        DB 1; Lenz
Mo. 2e+02;
O; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
NCBI_TaxID=1639,
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218 GTP (PROBABLE).
258 KNUCKLE-LIKE CYSTEINE CLUS
32744 MW; 4C44B33EE7159B56 CRC64;
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PIK, AC1302;
Listilat; IMO01819;
A HAMAR, WE 01820; -; 1.
R InterPro; IPR004881; DUF258.
B FREEM; PR03193; DUF258; 1.
DR PROSITE; PS50936; ENGC_GTPASE; 1.
FROSITE; PS50936; ENGC_GTPASE; 1.
FROSITE; PS50936; ENGC_GTPASE; 1.
TO AT 12 115 GTP (PROBABLE).
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15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Probable GTPase engC protein 1 (EC 3.6.1.-).
ENGC1 OR LW01819.
Listeria monocytogenes.
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100.0%; Pred. No. 2e+
tive 0; Mismatches
72 219 ENG
112 115 GTE
164 171 GTE
214 218 GTE
245 258 KMN
291 AA; 32741 MW; 2
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QY 109 NISPLV 114

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Search completed: March 23, 2004, 09:22:44
Job time: 23 secs
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26, Appl 50, Appl 268, App 6548, Ap 5502, Ap 5440, Ap 5745, Ap

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Result

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                                                                                                                                                                                                                                                                                      ADDRESSEE: Kathryn A. Anderson, Immunex Corporation STREET: 51 University Street CITY: Seattle STATE: WA
                                                                                                                         Sequence 2, Application US/08670354
Patent No. 5763233
GENERAL INFORMATION:
APPLICANT: Steven R. Wiley and
APPLICANT: Steven R. Wiley and
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF ERQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: REALBLE FORDY disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
SOFTWARE: Microsoft Word, Version 6.0.1
SOFTWARE: Microsoft Word, Version 6.0.1
GURERNT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-UN-1996
CLASSIFICATION NUMBER: US 08/496,632
FILING DATE: 29-UN-1995
CLASSIFICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION NUMBER: US 08/548,368
FILING DATE: 10-NOV-1995
CLASSIFICATION NUMBER: 32,172
REGISTRATION NUMBER: 32,172
REGISTRATION NUMBER: 32,172
REGISTRATION NUMBER: 32,172
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELECHOMENICATION INFORMATION:
TELEPRAN: (206) 587-0430
TELEFAX: (206) 233-0644
                          ALIGNMENTS
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TELEK: 756822
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.0
Matches 281; Conservative
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MOLECULE TYPE: protein
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                                                                                                                  US-08-670-354-2
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61 DDSYWDPNDEESRMSPCWQVKWQLRQLVRKKMILRTSEETISTVQEKQQNISPLVREKGPO 120
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Sequence 1, Application US/08780496

Patent No. 6046048

GENERAL INFORMATION:

APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim ITLE OF INVENTION:

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 281;
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                           241 SIYQGGIFELKENDRIFVSVINEHLIDMDHEASFFGAFLVG 281
241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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100.0%; Pred. No. 5.6e-279;
tive 0; Mismatches 0;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBW PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/780,496
FILING DATE: 08-Jan-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                         APPLICANT: Ashkenazi, Avi J.
TITLB OF INVENTION: APO-2 LIGAND
FILLE REFERENCE: 11669.22US03
CURRENT APPLICATION NUMBER: US/08/584,031A
CURRENT FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                 US-08-584-031-1; Sequence 1, Application US/08584031A; Patent No. 6030945; GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-08-584-031-1
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Best Local Similarity
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847-937-0378
    TELEPHONE: 847-937-03'
TELEFAX: 847-938-2623
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                                               TELEX:
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US-08-83-086-10
Sequence 10, Application US/08883086
Sequence 10, Application US/08883086
Patent No. 6171787
Fatent No. 6171787
TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
NUMBER OF SEQUENCES: 13
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NAME: Porembaki, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6134.US.01
TELECOMMUNICATION INFORMATION:
           NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REPERENCE/DOCKET VIMBER: 20,600
TELEPHONE: 415/225-981
TELEPHONE: 415/92-981
TELEX: 415/92-981
TELEX: 415/92-981
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ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.'
Matches 281; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                   100.0%; Score 281; DB 3; Length 281; 100.0%; Pred. No. 5.6e-279; tive 0; Mismatches 0; Indels
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100.0%; Score 281; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 5.6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels
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; Sequence 2, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
    APPLICANT: Wiley, Steven R.
    APPLICANT: Geodwin, Raymond G.
    TITLE OF INVENTION: Cytokine that Induces Apoptosis
    FILE REFERENCE: 2835-E
    EARLIER PELICATION NUMBER: US/09/320,424
    CURRENT FILING DATE: 1998-11-10
    EARLIER FILING DATE: 1998-03-26
    EARLIER PELICATION NUMBER: 08/670,354
    EARLIER PELICATION NUMBER: 08/670,354
    EARLIER PELICATION NUMBER: 08/648,368
    EARLIER PELICATION NUMBER: 08/548,368
    EARLIER PELICATION NUMBER: 08/548,368
    EARLIER PELING DATE: 1995-11-01
    EARLIER PELING DATE: 1995-10-25
    EARLIER PELING DATE: 1995-06-29
    NUMBER OF SEQ ID NOS: 25
    NUMBER OF SEQ ID NOS: 25
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6171787e
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SEQ ID NO 2
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Matches 281; Conservative
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                                                                                                          FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLIMKSARNSCWSKDAEYGLY 240
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                           61 DDSYWDPNDEESMASPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                               121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSCHSFLSNIHLRNGELVIHEKG 180
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DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRISEETISTVQEKQQNISPLVRERGPQ 120
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APPLICANT: RASHALL, LISA A.
APPLICANT: ROSHAK, AMY K.
APPLICANT: TAN, KONG B.
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR, TITLE OF INVENTION: TWE
FILE REPERANCE: GH-50008-2
CURRENT APPLICATION NUMBER: US/09/333,593A
CURRENT APPLICATION NUMBER: 08/916,625
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR FILING DATE: 1997-08-09
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASELSQ for Windows Version 3.0
SEQ ID NO 6
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100.0%; Score 281; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 5.6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels
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YOUNG, PETER R.
MARSHALL, LISA A.
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ORGANISM: HOMO SAPIENS
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61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEFIISTVQEKQQNISPLVRERGPQ 120
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                                                         APPLICANT: Bienkowski, Michael J
APPLICANT: Mills, Cynthia J
APPLICANT: Jones, David A
APLICANT: JONES, David A
TITLE OF INVENTION: TNP-Related Death Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDER ADDRESS: A
ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
ADDRESSEE: Legal Services
STREFT: 301 Henrietta Street
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100.0%; Pred. No. 5.6e-279;
ive 0; Mismatches 0;
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; Sequence 11, Application US/09157864; Patent No. 6440694; GENERAL INFORMATION:
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NAME: Kerber, Lori L.
REGISTRATION NUMBER: 41,113
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INPORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amin
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616/833-8897
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Best Local Similarity
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ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Acceptors
FITLE OF INVENTION: Receptors
FILE REFERENCE: PF5.0
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT APPLICATION NUMBER: 60/369,860
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR PILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR PILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
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            APPLICANT: Goodwin, Raymond G.
APPLICANT: Goodwin, Raymond G.
TILLE OF INVENTION: CYTCKINE that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/825,563
CURRENT APPLICATION NUMBER: US/09/825,563
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 09/190,046
PRIOR APPLICATION NUMBER: 09/190,046
PRIOR APPLICATION NUMBER: 09/190,046
PRIOR APPLICATION NUMBER: 09/190,046
PRIOR APPLICATION NUMBER: 09/640,641
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1996-06-25
PRIOR FILING DATE: 1996-06-25
PRIOR FILING DATE: 1995-11-01
PRIOR FILING DATE: 1995-10-01
PRIOR FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOSTWARE: PATCHIN VOWER: 22
SOSTWARE: PATCHIN VOWE: 2.0
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Best Local Similarity 100.0%; Pred. No. 5.6e-279;
Matches 281; Conservative 0; Mismatches 0;
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Patent No. 6538938
GENERAL INFORMATION:
GENERAL INFORMATION:
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US-10-039-785-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 281; DB 4; Length 281; Best Local Similarity 100.0%; Pred. No. 5.6e-279; Matches 281; Conservative 0; Mismatches 0; Indel8 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application PC/TUS9610895
GENERAL INFORMATION:
APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STRRET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 SIYQGGIFBLKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-06-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR APPLICATION NUMBER: 60/294,473
PRIOR APPLICATION NUMBER: 60/293,473
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APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/1
FILING DATE: 25-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
FILING DATE: 01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2.
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ZIP: 98101
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PCT-US96-10895-2
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SYWDPNDEESMNSPCWQVKWQLRQLVRKMILRISEETISTVQEKQQNISPLVRERGPQRV 122
                                                                         61 SYWDPNDEESMNSPCWQVKWQLRQLVRKMILRISEETISTVQEKQQNISPLVRERGPQRV 120
                                                                                                                                                                                                                                            181 YIYSQTYFRFQEEIKENTKUDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLYSI 240
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                                                                                                                       AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY
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Patent No. 6204236

GENERAL INFORMATION:
APPLICANT: Wiley, Seven R.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: CYtokine that Induces Apoptosis
FILE REPRENCE: 2835-E
CURRENT FILING DATE: 1999-05-26
CURRENT APPLICATION NUMBER: US/09/320,424

CURRENT PILING DATE: 1999-10-10

EARLIER APPLICATION NUMBER: 09/190,046

EARLIER PELING DATE: 1998-11-10

EARLIER APPLICATION NUMBER: 09/048,641

EARLIER PELING DATE: 1998-11-0

EARLIER PELING DATE: 1998-11-0

EARLIER PILING DATE: 1996-06-25

EARLIER PILING DATE: 1995-06-06-29

EARLIER PILING DATE: 1995-06-29

EARLIER APPLICATION NUMBER: 08/548,368

EARLIER PELING DATE: 1995-06-29

NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                      241 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 279
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100.0%; Pred. No. 5.5e-183;
tive 0; Mismatches 0;
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; Patent No. 6521228
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-320-424-11
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Matches 187; Conservative
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Best Local Similarity
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US-09-825-563-11
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Patent No. 6346388

GENERAL INFORMATION:

APPLICANT: Michael R. Brigham-Burke
APPLICANT: Peter R. Young

TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TRI AND TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TRI AND TRILE REFERENCE: GH-50030

CURRENT APPLICATION NUMBER: 60/055,513

PRIOR APPLICATION NUMBER: 60/055,513

PRIOR APPLICATION NUMBER: 60/055,980

PRIOR PILING DATE: 1997-08-26

PRIOR PILING DATE: 1997-08-26

PRIOR FILING DATE: 1997-08-26

PRIOR FILING DATE: 1997-08-26

MUMBER OF SEQ ID NOS: 9

SOFTWARE PASESEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 279;
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Pred. No. 6.2e-277;
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NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                             TELEFAX: (206) 233-0644
TELEK: 756822
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                     LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.(
Matches 279; Conservative
                                                                                                                                                                                                                                                   ropology: linear
MOLECULE TYPE: protein
PCT-US96-10895-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 3
LENGTH: 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
APPLICANT: TITLE OF INVENTION: Cytokine that Induces Apoptosis TITLE OF INVENTION: Cytokine that Induces Apoptosis FILE REFERENCE: 2835-E CURRENT APPLICATION NUMBER: US/09/825,563 CURRENT FILING DATE: 2001-04-02 PRIOR APPLICATION NUMBER: 09/320,424 PRIOR FILING DATE: 1999-05-26 PRIOR APPLICATION NUMBER: 09/190,046 PRIOR FILING DATE: 1998-11-10 PRIOR FILING DATE: 1998-03-26 PRIOR PILING DATE: 1998-03-26 PRIOR FILING DATE: 1998-03-26 PRIOR FILING DATE: 1998-03-26 PRIOR FILING DATE: 1998-11-01 PRIOR FILING DATE: 1995-11-01 PRIOR FILING DATE: 1995-11-01 PRIOR FILING DATE: 1995-11-01 PRIOR FILING DATE: 1995-06-29 NUMBER OF SEQ ID NOS: 25 SECRETARIES PARCHETING VARIABRE: 08/548,568 PRIOR FILING DATE: 1995-06-29 NUMBER OF SEQ ID NOS: 25 SECRETARIES PARCHETIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wiley, Steven R.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT FILING DATE: 1999-05-26
EARLIER APPLICATION NUMBER: 09/190,046
EARLIER FILING DATE: 1998-11-10
EARLIER FILING DATE: 1998-11-10
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 09/648,641
EARLIER APPLICATION NUMBER: 08/670,354
EARLIER FILING DATE: 1996-06-25
EARLIER PILING DATE: 1995-06-25
EARLIER PILING DATE: 1995-06-29
EARLIER PILING DATE: 1995-06-29
EARLIER PILING DATE: 1995-06-29
EARLIER PILING DATE: 1995-06-29
EARLIER PILING DATE: 1995-06-29
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100.0%; Pred. No. 5.5e-183;
tive 0; Mismatches 0;
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; ORGANISM: synthetic fusion
US-09-825-563-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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LENGTH: 253
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LENGTH: 256
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 SYPDPILLIMKSARNSCWSKDABYGLYSTYQGGIFBLKENDRIFVSVTNEHLIDMDHEASF
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                                                                                              Length 256;
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                                                                                        Query Match 66.5%; Score 187; DB 3; Length 25 Best Local Similarity 100.0%; Pred. No. 5.6e-183; Matches 187; Conservative 0; Mismatches 0; Indels
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APPLICANT: Wiley, Steven R.
APPLICANT: Wiley, Steven R.
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REPERBUCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/825,563
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 09/320,424
PRIOR FILING DATE: 1999-05-26
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 09/190,046
PRIOR APPLICATION NUMBER: 08/670,354
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1995-06-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 13
LENGTH. 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 13, Application US/09825563
; Patent No. 6521228
; ORGANISM: synthetic fusion US-09-320-424-13
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CURRENT APPLICATION NUMBER: US/09/565,423
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: UNKNOWN
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
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Patent No. 5763223
GENERAL INFORMATION:
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Matches 161; Conservative
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MEDIUM TYPE: Floppy
    FILE REFERENCE: 2879-72
                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                 LENGTH: 161
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Patent No. 6475987
GENERAL INPOMATION:
APPLICAMT: Shu, Hong-Bing
ITILE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
ITILE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLIMK 120
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APPLICANT: WILEY, S.R.
TITLE OF INVENTION: POR TREATMENT AND DIAGNOSIS OF DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Laboratories
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 61.9%; Score 174; DB 3; Length 177; Best Local Similarity 100.0%; Pred. No. 7.7e-170; Matches 174; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60064-6050
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,343A
FILING DATE: 12-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6048.US.P2
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APPLICATION NUMBER:
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                     ; Sequence 7, Application US/09105343A; Patent No. 6207642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: BECKER, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 604
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6207642e
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  250 FGAFLVG 256
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                                                             RESULT 16
US-09-105-343A-7
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US-09-565-423-7
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61 FYYIYSQIYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLIMKSARNSCWSKDAEYGLY 120
                                                                                                                                            121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                        181 FYYIYSQTYFREQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                     57.3%; Score 161; DB 4; Length 161; 100.0%; Pred. No. 1.3e-156; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161
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TITLE OF INVENTION: Cytokine That Induces Apoptosis NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: RIPOPPY disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION: A35
PRIOR APPLICATION: A35
ATTONNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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RESULT 21
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                                                                                                                                                                                                    Query Match 32.0%; Score 90; DB 1; Length 101; Best Local Similarity 100.0%; Pred. No. 3.1e-84; Matches 90; Conservative 0; Mismatches 0; Indels
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APPLICANT: Wiley, Steven R.
APPLICANT: Goodwain, Raymond G.
TITLE OF INVENTION:
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/320, 424
CURRENT APPLICATION NUMBER: US/09/320, 424
CURRENT APPLICATION NUMBER: 09/190, 046
EARLIER APPLICATION NUMBER: 09/190, 046
EARLIER FILING DATE: 1998-11-10
EARLIER FILING DATE: 1998-11-00
EARLIER FILING DATE: 1998-11-01
EARLIER FILING DATE: 1998-05-25
EARLIER FILING DATE: 1995-11-01
EARLIER FILING DATE: 1995-11-01
EARLIER FILING DATE: 1995-11-01
EARLIER FILING DATE: 1995-11-01
EARLIER FILING DATE: 1995-11-01
EARLIER FILING DATE: 1995-11-01
EARLIER FILING DATE: 1995-10-02
NUMBER OF SEQ ID NOS: 25
COFTWARE: PATENTING DATE: 1995-06-29
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Patent No. 652128
GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis FILE REPERRACE: 2835-E
CURRENT APPLICATION NUMBER: US/09/825,563
                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-320-424-4; Sequence 4, Application US/09320424; Patent No. 6284236
; INFORMATION FOR SEQ ID NO: 4:
; SRQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; TYPE: amino acid
; WOLECULE TYPE: protein
US-08-670-354-4
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1 MAMMEVQGGBSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 32.0%; Score 90; DB 4; Length 101; Best Local Similarity 100.0%; Pred. No. 3.1e-84; Matches 90; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US96-10895-4
; Sequence 4, Application PC/TUS9610895
; GENERAL INFORMATION:
    APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/496,632
FLING APPLICATION:
PRIOR APPLICATION NUMBER: US 08/548,368
FLING DATE: 01-NOV-1995
CLASSIFICATION:
CLASSIFICATION:
CLASSIFICATION:
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NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 09/320,424
PRIOR FILING DATE: 1999-05-65
PRIOR FILING DATE: 1999-05-66
PRIOR FILING DATE: 1998-11-10
PRIOR PELING DATE: 1998-11-10
PRIOR PELING DATE: 1998-03-26
PRIOR PELING DATE: 1998-03-26
PRIOR PELING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1995-06-25
PRIOR FILING DATE: 1995-10-01
PRIOR FILING DATE: 1995-11-01
PRIOR FILING DATE: 1995-11-01
PRIOR FILING DATE: 1995-11-01
PRIOR FILING DATE: 1995-11-01
SRIOR FILING DATE: 1995-11-01
SRIOR FILING DATE: 1995-11-01
SRIOR FILING DATE: 1995-11-01
SRIOR FILING DATE: 1995-10-01
SRIOR FILING DATE: 1995-10-01
SRIOR FILING DATE: 1995-10-01
SRIOR FILING DATE: 1995-10-01
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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ORGANISM: Homo sapiens
                          FEATURE:
NAME/KEY: UNSURE
                                                                                                                NAME/KEY: UNSURE LOCATION: 34
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LENGTH: 15
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Sequence 12, Application US/09632287A
Sequence 12, Application US/09632287A
Sequence 12, Application
APPLICANT: Hsu, Hailing
APPLICANT: Boyle, William J
TITLE OF INVENTION: Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family
FILE REFERENCE: 0.017/35550A
CURRENT APPLICATION NUMBER: US/09/632,287A
CURRENT FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/147,294
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                                                                                                                                                                                                                                                                                                          1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
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                                                                                                                                                                                     Length 101;
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                                                                                                                                                                                                                                   0; Indels
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APPLICANT: Jobert, S.
APPLICANT: diordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
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32.0%; Score 90; DB 5; Le
Best Local Similarity 100.0%; Pred. No. 3.1e-84;
Matches 90; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1999-08-04
VWHEER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
                   SEQUENCE CHARACTERISTICS:
LENGTH: 101 amino acids
TYPE: amino acid
  INFORMATION FOR SEQ ID NO:
                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US96-10895-4
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LENGTH: 59
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OTHER INFORMATION: Description of Artificial Sequence: No. 6673771el Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/09628665
Patent No. 667371
GENERAL INFORMATION:
APPLICANT: Greene, Mark I.
APPLICANT: Murali, Ramachandran
APPLICANT: Kinosaki, Masahiko
TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity
FILE REFERENCE: UPN3831
CURRENT APPLICATION WUMBER: US/09/628,665
                                                                                                                                                                                                                                                                                                                       8.5%; Score 24; DB 4; Length 59; 100.0%; Pred. No. 5.1e-17; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.3%; Score 15; DB 4; Length 15;
100.0%; Pred. No. 2.3e-08;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAMMEVQGGPSLGQTCVLIVIFTV 24
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                                                                                           CTHER INFORMATION: Xaa = Glu, Val

NAME/KEY: UNSURE

LOCATION: 33,57

COTHER INFORMATION: Xaa = Leu, Pro

NAME/KEY: UNSURE

LOCATION: 25,32

COTHER INFORMATION: Xaa = Leu, Val

US-09-621-976-6479
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EBEREAL INFORMATION:
APPLICANT: Greene, Mark I.
LOCATION: 27
OTHER INFORMATION: Xaa = Glu, Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                        24; Conservative
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Best Local Similarity
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US-08-670-354-6
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                                                                                                          FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6673771el Sequence
US-09-628-665-32
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Patent No. 6207642
GENERAL INFORMATION:
APPLICANT: WILEY, S.R.
TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
TITLE OF INVENTION: POR TREATMENT AND DIAGNOSIS OF DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDOLT Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.0%; Score 14; DB 3; Length 183; 100.0%; Pred. No. 2.3e-06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                           Query Match 5.3%; Score 15; DB 4; Length 19; Best Local Similarity 100.0%; Pred. No. 2.9e-08; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,343A
FILING DATE: 12-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/02859
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INPORMATION:
NAME: BECKER, Cheryl L.
REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 6048.US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-935-1729
                                                                                                                                                                                                                                                                                 191 RPQEEIKENTKNDKQ 205
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SEQUENCE CHARACTERISTICS:
LENGTH: 183 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                   ORGANISM: Artificial Sequence
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; MOLECULE TYPE: No. 6207642e
US-09-105-343A-8
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 32
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Matches 14; Conservative
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TELEFAX: 847-938-2623
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 60064-6050
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                                                                                                                                                                                                  ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
                                               GENERAL INFORMATION:
APPLICANT: Steven R. Wiley and
APPLICANT: Raymond G. Goodwin.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wiley, Steven R.
APPLICANT: Wiley, Steven R.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT FILING DATE: 1999-05-26
REALLER APPLICATION NUMBER: 09/190,046
BARLIER PILING DATE: 1998-11-10
BARLIER APPLICATION NUMBER: 09/048,641
RAKLIER FILING DATE: 1998-03-26
BARLIER PELING DATE: 1998-03-36
BARLIER APPLICATION NUMBER: 08/670,354
                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-JUN-1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION ATA:
APPLICATION NUMBER: US/08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION NUMBER: US/08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION 1435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
Sequence 6, Application US/08670354; Patent No. 5763223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-320-424-6
; Sequence 6, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: TENGTH: 291 ami-
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TOPOLOGY: lim
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                                                                                                                                                                                                                                                                                                                           ZIP: 98101
COMPUTER READABLE FORM:
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RESULT 27

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Halling
APPLICANT: How, Hailing
APPLICANT: Wooden, Scott K
APPLICANT: Wooden, Scott K
TITLE OF INVENTION: Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family
TITLE REFERENCE: 01017/35550A
CURRENT FILING DATE: 2000-008-03
PRIOR PRILING DATE: 1999-08-04
NUMBER: OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 87
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                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Bloppy disk
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
CLASSIFICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION NUMBER: 2835-WO
TELECOMMUNICATION NUMBER: 2835-WO
TELECOMMUNICATION NUMBER: 2835-WO
TELECOMMUNICATION NUMBER: 2835-WO
TELECOMMUNICATION NUMBER: 2835-WO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
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amino acid
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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// MOLECULE TYPE: protein

PCT-US96-10895-6
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Best Local Similarity
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ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-632-287A-13
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TELEX: 73
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        STATE:
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STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: CYCOKine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION: CYCOKine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/825,563
CURRENT APPLICATION NUMBER: 09/320,424
PRIOR RILING DATE: 1999-06-26
PRIOR PLING DATE: 1999-06-26
PRIOR FILING DATE: 1999-01-26
PRIOR FILING DATE: 1996-06-26
PRIOR RILING DATE: 1996-03-26
PRIOR APPLICATION NUMBER: 08/570,354
PRIOR RILING DATE: 1996-06-25
PRIOR APPLICATION NUMBER: 08/540,368
PRIOR APPLICATION NUMBER: 08/540,368
PRIOR PLING DATE: 1996-06-25
PRIOR PLING DATE: 1995-11-01
PRIOR PLING DATE: 1995-10-01
PRIOR FILING DATE: 1995-06-29
NUMBER OF SEC 1D NOS: 25
COUNTY NOT APPLICATION NUMBER: 08/496,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application PC/TUS9610895
GENERAL INFORMATION:
APPLICANT: Immunex Corporation.
TITLE OF INVEXTON: Cytckine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
EARLIER FILING DATE: 1996-06-25
EARLIER PELING DATE: 1996-06-25
EARLIER FILING DATE: 1995-11-01
EARLIER APPLICATION NUMBER: 08/496,632
EARLIER APLICATION NUMBER: 08/496,632
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver. 2.0
ENGTWARE: PATENTIN Ver. 2.0
ELENGTH: 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 6, Application US/09825563
; Patent No. 6521228
                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 VQYIYKYTSYPDPI 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6521228
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 ; ORGANISM: murine
US-09-320-424-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 30
PCT-US96-10895-6
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US-09-825-563-6
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LENGTH: 291
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                                                                                                                                                                                   Length 172;
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100.0%; Pred. No. 36;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MCGATTY, Thomas J.
APPLICANT: Kroll, Kristen
APPLICANT: Krell, Kristen
TITLE OF INVENTION: Geminin Gene and Protein
FILE REFERENCE: 0725.1055-001
CURRENT PAPLICATION NUMBER: 0509/096,724B
CURRENT FILING DATE: 1998-06-11
PRIOR PILING DATE: 1998-06-13
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FASLERQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 209
TYPE: PRI
CREATH: 209
TYPE: PRI
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Sequence 24, Application US/09096724B
Sequence 24, Application US/09096724B
Setent No. 6548290
SERERAL INFORMATION:
APPLICANT: MCGAILY, Thomas J.
APPLICANT: Kirschner, Marc W.
TITLE OF INVENTION: Geminin Gene and Protein
FILE REPERENCE: 0725.1055-001
CURRENT APPLICATION NUMBER: US/09/096,724B
CURRENT APPLICATION NUMBER: US/09/096,724B
CURRENT APPLICATION NUMBER: US/09/096,724B
PRIOR APPLICATION NUMBER: 05/085,371
PRIOR FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 209
                                                                                                                                                                                2.5%; Score 7; DB 4;
100.0%; Pred. No. 31;
tive 0; Mismatches
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2.5%; Score 7; DB 4;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches
                                           ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence B, Application US/09096724B
; Patent No. 6548290
; GENERAL INFORMATION:
                                                                                                                                                                                                            Best Local Similarity 100.0
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                        272 ASFFGAF 278
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; ORGANISM: human
US-09-096-724B-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 34
US-09-096-724B-8
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                                                                                                                                                                                Query Match
          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 35
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Batent No. 6380370

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION NUMBER: US/09/134,001C

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 5649
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                                                                                                                                                                                                                                                           APPLICANT: MCDONALD, PETER J
APPLICANT: MCDONALD, ALAN M
TITLE OF INVENTION: CLONING AND EXPRESSION OF TOXOPLASMA ANTIGENS AND
TITLE OF INVENTION: USE OF RECOMBINANT ANTIGENS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 GATEHOUSE ROAD
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,481
FILING DATE: 12-APR-1993
CLASSIFICATION DATA:
RPILICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 109-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: SYENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 446-102PCT
TELECOMMUNICATION: NUMBER: 446-102PCT
                                                                                                                                                          ; Sequence 2, Application US/07972481; Patent No. 5578453; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (703) 205-8000
TELEPAX: (703) 205 8050
INFORMATION POR SEQ ID NO: 2:
SEQUENCE CHARACTERISTIGS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 amino acids
65 YIYSQTYFRFQE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-07-972-481-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 FQEEIKE 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                 US-07-972-481-2
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Sequence 34, Application US/09831642
| Patent No. 663571
| Patent No. 6635751
| GENERAL INFORMATION:
| APPLICANT: HAZE, Kyosuke et al. |
| TITLE OF INVENTION: ENDOPLASMIC RETICULUM STRESS TRANSCRIPTION FACTORS ATF6 AND CREB FILE REPERRNCE: 1422-0474P
| CURRENT APPLICATION NUMBER: US/09/831,642
| CURRENT FILING DATE: 2001-05-11
| NUMBER OF SEQ ID NOS: 83
| SOFTWARE: PatentIn version 3.1
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2.5%; Score 7; DB 4; Length 700;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FASTESCO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,125
CLASSIFICATION BOTO
CLASSIFICATION BATA:
APPLICATION BATA:
APPLICATION NUMBER: 60/024,033
FILING DATE: 12-AUG-1996
ATTORNEY AGENT INFORMATION
NAME: JANET E. REED, PH.D.
REGISTRATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: 36,252
REFERENCE/DOCKET NUMBER: RUEGES 97-0009
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 115-563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.5%; Score 7; DB 4 Best Local Similarity 100.0%; Pred. No. 87; Matches 7; Conservative 0; Mismatches
                                                   ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 554 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 215-563-4044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
       Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 KALGRKI 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             477 KALGRKI 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO FRAGMENT TYPE: N ORIGINAL SOURCE: US-08-909-125-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS
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LENGTH: 700
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Parent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 189
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Sequence 6, Application US/08909125

Patent No. 6495737

Patent No. 6495737

APPLICANT: KLESSIG, DANIEL

APPLICANT: KLESSIG, DANIEL

APPLICANT: KLESSIG, DANIEL

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IMPROVING

TITLE OF INVENTION: SALICYLIC ACID-INDEPENDENT SYSTEMIC ACQUIRED DISEASE RESISTANG

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dann, Dorfman, Herrell and Skillman
                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: PREDMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7595
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STREET: 1601 Market Street Suite 720
                                                                                                                  ; Sequence 7595, Application US/09489039A; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Chlamydia pneumoniae
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Best Local Similarity
7, Conserve
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9 QEEIKEN 15
                                                                                                US-09-489-039A-7595
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APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Taylor, Robert
APPLICANT: Eriel, Douglas
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: Most, Michael H.P.
APPLICANT: Most, Michael H.P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: MITH ANTIBIOTICS
TITLE OF INVENTION: WITH ANTIBIOTICS
                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: No. 6673771el Sequence US-09-628-665-31
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Patent No. 6642023

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bace, John
ITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof
Patent No. 6642023

FILE REFERENCE: 7969-086-999

CURRENT APPLICATION NUMBER: US/09/612,402B

CURRENT PILING DATE: 2000-07-06

PRIOR PILING DATE: 1997-10-02

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn version 3.0

LENGTH: 24
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                                                                                                                                                                                                                                                                                                                                                   Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 24;
                                                                                                                                                                                                                                                                                                                                              Query Match 2.1%; Score 6; DB 4;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.1%; Score 6; DB 4;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/09/628,665
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/146,094
PRIOR PILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTLY VEY: 2.1
LENGTH; 10
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CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 50, Application US/09030619B ; Patent No. 6503881
                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Chlamydia sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                           157 SRSGHS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 LSNLHL 169
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APPLICANT: Krieger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 43
US-09-612-402B-26
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US-09-030-619-50
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                                                                                  GENERAL INFORMATION:
APPLICANT: Gaffney, Thomas
APPLICANT: Gaffney, Thomas
APPLICANT: Wendland, Juergen
APPLICANT: Wendland, Juergen
APPLICANT: Wendland, Juergen
APPLICANT: Wendland, Juergen
APPLICANT: Philippsen, Peter
TITLE OF INVENTION: No. 6291660el Fungal Genes Required For No. 6291660mal Growth And
TITLE OF INVENTION: Development
FILE REFERENCE: CGC2046
CURRENT APPLICATION NUMBER: US/09/415,522A
CURRENT FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 2071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: No. 6673771el Sequence
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APPLICANT: Greene, Mark I.
APPLICANT: Murali, Ramachandran
APPLICANT: Minosaki, Masahiko
TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity
FILE REFERENCE: URN3831
CURRENT APPLICATION UNBER: US/09/628,665
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/146,094
PRIOR FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31, Application US/09628665
Fatent No. 6673771
GENERAL INFORMATION:
APPLICANT: Greene, Mark I.
APPLICANT: Murali, Ramachandran
APPLICANT: Minosaki, Masahiko
TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity
FILE REFERENCE: UPN3831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.5%; Score 7; DB 3; Length 2071; 100.0%; Pred. No. 2.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.1%; Score 6; DB 4; Length 6; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 6; Conservative 0; Mismatches 0; Indels
                 US-09-415-522-6
; Sequence 6, Application US/09415522A
; Patent No. 6291660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-628-665-13
; Sequence 13, Application US/09628665
; Patent No. 6673771
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Ashbya gossypii
US-09-415-522-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 SSPNSKN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 SSPNSKN 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRSGHS 6
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                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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Faquence 6648, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICATION OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLOOM OF A BLO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
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CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
2.1%; Score 6; DB 4
Best Local Similarity 100.0%; Pred. No. 1.3
Matches 6; Conservative 0; Mismatches
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REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: <Unknown>
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TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Acinetobacter baumannii
US-09-328-352-6548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 5502:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 78 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: antino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: PC
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                                                                      US-09-328-352-6548
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                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                        DB 4; Length 28;
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Sequence 2bc, 6348328

Fatent No. 6348328

GENERAL INFORMATION:

APPLICANT: Black, Michael

APPLICANT: Hodgson, John

APPLICANT: Knowles, David

APPLICANT: Nicholas, Richard

APPLICANT: Stodola, Robert

TAVENTION:

TAVENTION:

No. 6348328el Compounds

Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: F8815EQ for Windows Version 2.0
CUREBNY APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia
                                                                                                                                                                                                                                                                Query Match 2.1%; Score 6; DB 4. Best Local Similarity 100.0%; Pred. No. 64; Matches 6; Conservative 0; Mismatches
                                                                                                                                                              ; OTHER INFORMATION: Indolicidin Analogue US-09-030-619-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P50475
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COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
TYPE: IBM Compatible
TYPE: IBM Compatible
TYPE: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 268:
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MOLECULE TYPE: No. 6348328e
                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 610-270-5090
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                      89 RKMILR 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 RKMILR 16
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US-08-858-207A-268
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; SEQ ID NO 50
                                                                                                                                     FEATURE:
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Sequence 8267, Application US/09543681A

Sequence 8267, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:
APPLICANT: GARY BRETON

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709-1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

SNUMBER OF SEQ ID NOS: 8344

SEQ ID NO 8267

LENGTH: 105

TYPE: PRI

TYPE: PRI

TYPE: PRI

TYPE: PRI

TYPE: PRI

TYPE: PRI

TYPE: PRI

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Sequence 99, Application US/08946329A
Patent No. 6057091
GENERAL INFORMATION:
APPLICANT: Beachy, Philip A.
APPLICANT: Porter, Jeffrey A.
ITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
NUMBER OF SEQUENCES: 109
CORRESPONDENCE Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FRETENG for Windows Version 2.0b
CURRENT APPLICATION DATA:
FILING DATE: 07-00T-1997
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APPLICATION NUMBER: 60/061,323
FILING DATE: 07-0CT-1996
APPLICATION NUMBER: 08/729,743
FILING DATE: 10-JUL-1996
APPLICATION NUMBER: 08/567,357
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/349,498
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Liea A.
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 38,347
REJEPHONE: 619/678-5099
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Proteus mirabilis
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 RNGELV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 RNGELV 49
                                                                                                                                                                                                                                                                                                                                      La Jolla
                                                                                                                                                                                                                                                                                                                                                                                            USA
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US-09-543-681A-8267
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                                                                                                                                                                                                                                                                                                                                                                 STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Sequence 5440, Application US/09543681A
Patent No. 6605709

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: UNDERST. US/09/543,681A

FILE REFERENCE: 2709-1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR APPLICATION NUMBER: US 60/128,706

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 5440
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Patent No. 6562958
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                            Ouery Match 2.1%; Score 6; DB 4; Length 78; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 6; Conservative 0; Mismatches 0; Indels
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          ;
i NAME/KEY: misc_feature
;
LOCATION: (B) LOCATION 1...78
;
SEQUENCE DESCRIPTION: SEQ ID NO: 5502:
US-09-107-532A-5502
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CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5745
LENGTH: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Acinetobacter baumannii
US-09-328-352-5745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Proteus mirabilis
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Best Local Similarity 100.0
Perion 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            21 NDEESM 26
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US-09-328-352-5745
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US-08-946-329A-99
      FEATURE:
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Patent No. 5871734
GENERAL INFORMATION:
APPLICANT: Lobb, Roy R.; Burkly, Linda C.
TITLE OF INVENTION: Treatment for Asthma with VLA-4 Blocking
TITLE OF INVENTION: Agents
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADINESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                2.1%; Score 6; DB 4; Length 105;
100.0%; Pred. No. 2.1e+02;
tive 0; Mismatches 0; Indels
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MEDIUM TIPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
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COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/456,193
FILING DATE: 31-MAY-1995
FILING DATE: 18-MAY-1995
FILING DATE: 18-MAY-1995
FILING DATE: 18-MAY-1995
FILING DATE: 12-MAY-1995
FILING DATE: 12-MAY-1995
FILING DATE: 12-MAY-1993
FILING DATE: 12-MAY-1993
FILING DATE: 12-MAY-1993
FILING DATE: 12-MAY-1993
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FILING DATE: 12-MAY-1993
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FILING DATE: 13-MAY-1993
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amino acid
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                                                             Query Match
Best Local Similarity 100.
Matches 6; Conservative
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COUNTRY: USA
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Best Local Similarity
                                                                                                                                                                                                     162 SFLSNL 167
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                                                                                                                                                                                                                                                                      3 SFLSNL 8
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CITY: Boston
US-09-543-681A-8267
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                                                                                                                                                                                                                                                                                                                                                                          RESULT 52
US-08-822-830B-4
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APPLICANT: Lobb, Roy R.; Burkly, Linda C.
TITLE OF INVENTION: Treatment For Inflammatory Bowel Disease
CORRESPONDENCE 11
CORRESPONDENCE ADDRESS:
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APPLICANT: Burkly, Linda C.
TITLE OF INVENTION: TREATMENT FOR INFLAMMATORY BOWEL DISEASE FILE REFERENCE: 10274-004003
CURRENT APPLICATION NUMBER: US/09/157,452B
CURRENT FILING DATE: 1998-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 6; DB 2; Length 106; 100.0%; Pred. No. 2.1e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Myers, Louis (PLM)
REGISTRATION VNDRER: 35,965
REFERENCE/DOCKET NUMBER: BGP-031USCP2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRICK APPLICATION DATA: 05 06/7/3/83/PRICK APPLICATION DATA: 05 06/7/3/83/PRICK APPLICATION NUMBER: US 08/284,603 FRILNG DATE: 11-4UG-1994
PRIOR APPLICATION NUMBER: PCT/US93/00924
FILING DATE: 02-FEB-1993
PRIOR APPLICATION DATA: 02-FEB-1993
PRIOR APPLICATION DATA: 05 07/835,139
                                                                                                                                                                           ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: APPLICATION NUMBER: US 08/373,857
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/456,124
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TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 12-FEB-1992
ATTORNEY/AGENT INFORMATION:
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amino acid
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                                                                                                                                                                                                                                          Massachusetts
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Best Local Similarity
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PCT-US93-00924-4
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Patent No. 6602503
Fatent Reference: Painlip R.
FILE REFERENCE: 10274-007001
CURRENT APPLICATION NUMBER: US/08/454,899G
CURRENT PAPLICATION NUMBER: US 08/004,798
PRIOR PILING DATE: 1993-01-12
FRIOR PILING DATE: 1994-01-07
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FatentSEQ for Windows Version 4.0
SEQ ID NO. 10
FATENT FATENT FATENT NUMBER: PATENT NOR PATENT NUMBER OF SEQ ID NO. 10
FATENT NUMBER OF SEQ ID NOS: 109
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FATENT NUMBER OF SEQ I
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STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
PRIOR APPLICATION NUMBER: US 08/950,660
PRIOR FILING DATE: 1997-10-15
PRIOR PRIOR DATE: 1995-01-18
PRIOR FILING DATE: 1995-01-18
PRIOR FILING DATE: 1994-08-11
PRIOR APPLICATION NUMBER: US 08/284,603
PRIOR FILING DATE: 1994-08-11
PRIOR PILING DATE: 1993-02-02
PRIOR PILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-12
PRIOR FILING DATE: 1992-02-12
PRIOR FILING DATE: 1992-02-12
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASELSEQ for Windows Version 3.0
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GENERAL INFORMATION:
APPLICANT: Lobb, Roy R.
TITLE OF INVENTION: Treatment for Asthma
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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Matches 6; Conservative
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ORGANISM: Mus musculus
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; Sequence 4, Application PC/TUS9300924
; GENERAL INPORMATION:
    APPLICANT: Lobb, Roy R.
; TITLE OF INVENTION: Treatment for Inflammatory Bowel Disease
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
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                                                                                               COMPUTER: ISM PC compatible
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COMPUTER: ISM PC compatible
APPLICATION NUMBER: PCT/US93/00030
CLASSIFICATION:
NAME: McNicholas, Janet M.
REFERENCE/DOCKET NUMBER: 92,307-A; D002 CIP PCT
TELECOMMUNICATION INFORMATION:
TELEFAX: 312-715-1000
TELEFAX: 312-715-1000
TELEFAX: 312-715-1000
TELEFAX: 312-715-1000
TELEFAX: SEQUENCE CHARACTERISTICS:
COMPUTER: ACCOUNTY COMPATION COMPUTER: CHARACTERISTICS:
COMPUTER: ACCOUNTY COMPUTER: CHARACTERISTICS:
COMPUTER: ACCOUNTY COMPUTER: CHARACTERISTICS:
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NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERCE/DOCKET NUMBER: 92,308-A; D003 CIP PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
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COMPUTER READABLE FORM:
MEDIUM TYER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: PCT/US93/00924
FILING DATE: 19930202
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STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
                                                                                 Floppy disk
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AMINO ACID
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Matches 6; Conservative
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INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE: protein
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MOLECULE TYPE: protein
                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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COUNTRY: US
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APPLICANT: Lynn Dougette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 CURRENT FILING DATE: 1998-08-13 PRIOR PLILING DATE: 1997-11-08 PRIOR PLILING DATE: 1997-08-14 NUMBER: US 60/055,779 PRIOR PLILING DATE: 1997-08-14 NUMBER: OF SEQ ID NOS: 5674 SEQ ID NOS: 5674 SEQ ID NOS: 5674
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APPLICANT: Gary Breton et. al

APPLICANT: Gary Breton et. al

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

LENGTH: 117
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APPLICANT: DELEYS, Robert
APPLICANT: MAERTENS, Geert
TITLE OF INVENTION: LIMMONDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VIRUS
FILE REFERENCE: 2752-18
CURRENT APPLICATION NUMBER: US/08/635,886C
CURRENT FILING DATE: 1996-04-25
PRIOR APPLICATION NUMBER: PCT/EP94/03555
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Best Local Similarity 100.0%; Pred. No. 2.3
Matches 6; Conservative 0; Mismatches
                   ; Sequence 5132, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5132
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CRGANISM: Klebsiella pneumoniae
US-09-489-039A-9835
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US-09-134-001C-5132
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                   Query Match 2.1%; Score 6; DB 5; Length 106; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 6; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENEET: 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                    sequence 5264, Application US/09621976; Patent No. 6639063; Patent No. FORMATION: APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 47
OTHER INFORMATION: Xaa = Ala, Ser, Thr
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COCATION: 2,40
OTHER INFORMATION: Xaa = Ala,Thr
NAME/KEY: UNSURE
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OTHER INFORMATION: Xaa = Arg, Ser
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LOCATION: 80
OTHER INFORMATION: Xaa = Cys, Tyr
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INFORMATION: Xaa = Gly,Ser
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OTHER INFORMATION: Xaa = Pro,Gln
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; OTHER INFORMATION: Xaa = Pro,Thr
US-09-621-976-5264
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INFORMATION: Xaa = Asp,Gly
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OTHER INFORMATION: Xaa = His,Gln
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Best Local Similarity 100.
Matches 6; Conservative
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ORGANISM: Homo sapiens
                                                                                                               99 TISTVQ 104
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74 TISTVQ 79
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NAME/KEY: UNSURE
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LENGTH: 114
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37 QRVAAH 42

RESULT 59

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; SEQ ID NO 240
; LENGTH: 128
; TYPE: PT
; ORGANISM: hepatitis C virus
US-08-635-886C-240
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APPLICANT: DELEXS, Robert
APPLICANT: DELEXS, Robert
APPLICANT: MARRIENS, Geert
APPLICANT: MARRIENS, Geert
TITLE OF INVENTION: URUS
TITLE OF INVENTION: VIRUS
FILE REPERENCE: 255:94
CURRENT APPLICATION NUMBER: US/08/974,690C
CURRENT PILING DATE: 1997-11-19
PRIOR APPLICATION NUMBER: PCT/PE94/03555
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR APPLICATION NUMBER: EP 93402718.6
NUMBER OF SEQ ID NOS: 286
SOFTWARE: Patentin version 3.1
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Patent No. 6555114

GEBERAL INPORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: WERSTENS, Robert

APPLICANT: WERSTENS, Geert
TITLE OF INVENTION: URUS
TITLE OF INVENTION: VIRUS
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100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/08/635,886C
CURRENT FILING DATE: 1994-04-25
PRIOR APPLICATION NUMBER: PCT/EP94/03555
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR APPLICATION NUMBER: EP 93402718.6
NUMBER OF SEQ ID NOS: 286
SOFTWARE: Patentin version 3.1
PRIOR FILING DATE: 1994-10-28
PRIOR PEDLICATION NUMBER: EP 93402718.6
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SEQ TWARE: Patentin version 3.1
SEQ ID NO 248
LENGTH: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 248, Application US/08974690C; Patent No. 6613333; GENERAL INFORMATION:
                                                                                                                                                     ; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-248
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LENGTH: 119
TYPE: PRI
ORGANISM: hepatitis C virus
                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 6; Conservative
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Matches 6; Conservative
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US-08-635-886C-240
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US-0914-690C-240

Sequence 240, Application US/08974690C

Sequence 240, Application US/08974690C

Sequence 240, Application US/08974690C

Sequence 240, Application US/08974690C

GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEYS, Robert

APPLICANT: DELEYS, Robert

TITLE OF INVENTION: IMMUNOOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: VIRUS

FILE REPRENCE: 2551-94

CURRENT APPLICATION NUMBER: US/08/974,690C

CURRENT FILING DATE: 1997-11-19

PRIOR APPLICATION NUMBER: EP 934402718.6

PRIOR FILING DATE: 1993-11-04

NUMBER OF SEQ ID NOS: 286

SOFTWARE: PatentIn version 3.1

SEQ ID NO 240

LENGCTH: 128
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Patent No. 6617156
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BNTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: UNMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
FRIOR PELLOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENT NOS: 6812
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 3666
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Query Match 2.1%; Score 6; DB 4; Length 128; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 6; Conservative 0; Mismatches 0; Indels
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2.1%; Score 6; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0
Matches 6; Conservative
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Gaps

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Sequence 3775, Application US/09134001C

Patent No. 6380370

Patent No. 6380370

Patent No. 6380370

Patent No. 6380370

TITLE OF INVENTION: DELIBERATION: DELIBERATIOR TO STAPHYLOCOCCUS

TITLE OF INVENTION: DATE: 1996/134,001C

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR PILING DATE: 1997-11-08

PRIOR PILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 3776

LENGTH: 138

TYPE: PRT

TYPE: PRT

CRGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4265
APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27904
LENGTH: 135
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-4265
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US-09-252-991A-27904
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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Squence 1855, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
AFFILICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: ALEUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 18565
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Patent No. 655195

Ratent No. 655195

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196-136

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
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2.1%; Score 6; DB 4; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
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US-09-252-991A-27904
; Sequence 27904, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
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US-09-252-991A-22722
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                                116 ERGPOR 121
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US-09-252-991A-18565
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259 SVTNEH 264
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        US-09-134-001C-3901
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APPLICANT: LYND BOUCEtte-Stamm et al

APPLICANT: LYND DOUCEtte-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTENCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PALENTIN VERSION 3.1

SEQ ID NO 6375

LENGTH: 140
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APPLICANT: Belyavsky, Anna
APPLICANT: Duchinskaya, Natalia
APPLICANT: Luchinskaya, Natalia
TITLE OF INVENTION: CAMELLO GENE FAMILY AND USES THEREOF
FILE REFERENCE: 63475/258
CURRENT APPLICATION NUMBER: US/09/593,887
CURRENT APPLICATION NUMBER: US/09/593,887
FRIOR APPLICATION NUMBER: US/09/593,887
NUMBER OF SEQ ID NOS: 26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
LENDIH: 144
                                      2.1%; Score 6; DB 4; Length 138; 100.0%; Pred. No. 2.6e+02; tive 0; Mismatches 0; Indels
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US-09-134-000C-6375
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; ORGANISM: Homo sapiens
US-09-593-887-8
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Best Local Similarity
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US-09-134-001C-3776
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US-10-012-542-458

RESULT 75

RESULT 73

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Sequence 458, Application US/10012542

Patent No. 6627741

GENERAL INPORMATION:

PAPLICANT' Ruben et al.

TITLE OF INVENTION: 94 Human Secreted Proteins

FILE REFERENCE: P2029P1

CURRENT APPLICATION NUMBER: US/10/012,542

CURRENT FILING DATE: EARLIER APPLICATION NUMBER: 09/461,325

PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14

PRIOR PRILING DATE: EARLIER FILING DATE: 1999-66-16

PRIOR PRILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-12

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Search completed: March 23, 2004, 09:24:47 Job time : 25 secs

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Query Match 2.1%; Score 6; DB 4; Length 147; Best Local Similarity 100.0%; Pred. No. 2.8e+02; Matches 6; Conservative 0; Mismatches 0; Indels

128 GTRGRS 133 ||||||| 43 GTRGRS 48

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Sequence 6, Appli
Sequence 17, Appli
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Sequence 118, Appli
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Sequence 11, Appl
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Sequence 76, Appl

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61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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        DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0;
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COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION DATE: US/08/971,317A
FILING DATE: 17-NOV-1997
CLASSIFICATION 1 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: THE PELTA LIGAND AND USES
TITLE OF INVENTION: THERBOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: No. US20010010925Ale
                                                                                                                                                                                                                                                                                                                                                     US-08-971-317A-8; Sequence 8, Application US/08971317A; Publication No. US20010010925A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Goller, Mimi C
REGISTRATION NUMBER: 39,046
REFERENCE/DOCKET NUMBER: 62:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 935-7550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 281 amino acids
amino acid
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TELEX:
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MEDIUM TYPE: Diskett
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ZIP: 60064-3500
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                                                           Sequence 10/5, Ap
Sequence 38, Appl
Sequence 65/72, A
Sequence 1, Appli
Sequence 26, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 34476, A
      Sequence 86, Appl
Sequence 71, Appl
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                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08916625B
Publication No. US20010010924A1
GENERAL INFORMATION:
APPLICANT: DEEN, KEITH C.
APPLICANT: YOUNG, PETER R.
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED
TITLE OF INVENTION: RECEPTOR, TR6
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
ATHER F. P.O. BOX 980
CTIT: VALLEY FORGE
4 US-10-154-419-86

4 US-10-146-733-71

4 US-10-146-733-81

5 US-10-369-493-1075

US-09-928-457-38

2 US-10-282-122A-65772

4 US-10-066-551-1

4 US-10-272-411-26
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ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

OPERATING SYSTEM: OF Windows Version 2.0

OPERATION DATA:
                                                                                                                                                                           US-09-900-530A-19
US-09-864-761-34476
US-09-776-724A-187
                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEG for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,625B FILING DATE: 22-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION NUMBER: 08/853,684
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 60/041,230
FILING DATE: 14-MARCH-1997
ATPONEY,AGENT INFORMATION:
NAME: PRESTIA, PAULE
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: 23,031
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
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R: GH-50008-1
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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Matches 281; Conservative
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STRANDEDNESS: sin
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181 FYYIYSQIYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 240
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                                                                                                                                            Query Match
100.0%; Score 281; DB 9; Length 2
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels
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100.0%; Score 281; DB 9; Length 2.
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels
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TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22USO3
CURRENT APPLICATION NUMBER: US/09/934,465
CURRENT FILING DATE: 2001-08-21
PRIOR FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver: 2.0
SOFTWARE: Patentin Ver: 2.0
LENGTH: 281
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 8 LENGTH: 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1, Application US/09934465
; Patent No. US20020102233A1
                                                                                ; ORGANISM: Homo sapiens
US-09-193-663-8
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                              TYPE: PRT
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Patent No. US20020012968A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: No. US20020012568A1e1 Drosophila Tumor Necrosis Factor Class Mole TITLE OF INVENTION: Variants Thereof
FILE REFERENCE: D0016.np
CURRENT APPLICATION NUMBER: US/09/813,329
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEC ID NOS: 65
                                                                                                                         240
                                      FYYIYSQTYFRFQEEIKENTKUDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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100.0%; Score 281; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                          SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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TITLE OF INVENTION: THR-DELTA LIGAND AND USES THEREOF
FILE REFERENCE: 6255.US.02
CURRENT APPLICATION NUMBER: US/09/193,663
CURRENT FILING DATE: 1998-11-17
BARLIER APPLICATION WHEER: 60/065,916
BARLIER PILLING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09193663; Patent No. US20020055624A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.0
SEQ ID NO 17
LENGTH: 281
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US-09-193-663-8
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COUNTRY: US
    Best Local Similarity
Matches 281; Conserv
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TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
SUPPRIOR FILING DATE: PROGRAM
SOFTWARE: PERL Program
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TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
FILE REPERENCE: PPS59
CURRENT APPLICATION NUMBER: US/10/202,062
CURRENT FILING DATE: 2002-07-25
PRIOR PRILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.0
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030108871A1 059509CD1
SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                 Sequence 118, Application US/09919039
Publication No. US20030108871A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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ORGANISM: human
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US-10-202-062-20
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                                                                       1 MANMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
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                            Gaps
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                         0; Indels
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APPLICATION NUMBER: US/10/662,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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STREET: 9410 Key West Avenue
CITY: Rockville
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FILING DATE: 13-MAR-1997
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION WUMBER: 34,610
REFERENCE/DOCKET NUMBER: PF261
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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SEQUENCE CHARACTERISTICS
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COMPUTER READABLE FORM:
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                         281; Conservative
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APPLICATION NUMBER: US/08/816,981
FILING DATE: 13-MAR-1997
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APPLICATION NUMBER: US/10/662,431
FILING DATE: 16-8ep-2003
CLASSIFICATION: 530
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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NAME: Kimball, Paul, C.
REGISTRATION NUMBER: 34,610
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SEQUENCE CHARACTERISTICS
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COMPUTER READABLE FORM:
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Matches 281: Conserment
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                                   DDSYWDPNDEBSWNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                           121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                        61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRISEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                   1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                               241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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TITLE OF INVENTION: Apoptosis Inducing Molecule I
NUMBER OF SEQUENCES: 10
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APPLICATION NUMBER: US/10/662,430
FILING DATE: 16-Sep-2003
CLASSIFICATION: 530
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FILING DATE: 13-MAR-1997
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 34,610
REFERENCE/DOCKET NUMBER: PF261
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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Publication No. US20040048340A1
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SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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Best Local Similarity 100.0
Matches 281, Conservative
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US-10-662-430-2
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RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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                                                                                                                            1 MAMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                              241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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IITLE OF INVENTION: Apoptosis Inducing Molecule I
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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US-10-001-054-54
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APPLICANT:
APPLICANT:
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           181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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100.0%; Score 281, DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0
                                        241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                     241 SIYQGGIFELKENDRIFVSVINEHLIDMDHEASFFGAFLVG 281
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                                                                                                                  Sequence 66, Application US/10039785
Publication No. US20020067646A1
GENERAL INFORMATION:
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JS-10-039-785-66
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US-10-011-125-4

RESULT 12

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121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0
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Sequence 4, Application US/10011125
Publication No. US20020142388A1
GENERAL INFORMATION:
TITLE OF INVENTION: BACTERIAL HOST STRAINS
FILE REFERENCE: P1804R1
CURRENT APPLICATION NUMBER: US/10/011,125
CURRENT PILING DATE: 2001-12-07
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 10
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CURRENT FILING DATE: 2001-11-30
PRIOR PAPLICATION NUMBER: 60/059114
PRIOR PILING DATE: 1997-09-17
PRIOR PAPLICATION NUMBER: 60/079689
PRIOR APPLICATION NUMBER: 60/079920
PRIOR PAPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/08299
PRIOR PILING DATE: 1998-04-24
PRIOR PILING DATE: 1998-04-24
PRIOR PILING DATE: 1998-04-24
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Publication No. US20020192209A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gurney, Austin
Hebert, Carolyn
Henzel, William
Kabakoff, Rhona
Shelton, David
Smith, Victoria
Watanabe, Colin
Wood, William
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Goddard, Audrey
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US-10-011-125-4
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Page

A PELLICATION NUMBER: 09/929404

DR FILING DATE: 2001-08-13

DR APPLICATION NUMBER: 09/941992

DR APPLICATION NUMBER: 09/946374

DR APPLICATION NUMBER: 09/946374

DR FILING DATE: 2001-09-04

DR FILING DATE: 1998-09-10

R PILING DATE: 1998-09-10

DR APPLICATION NUMBER: PCT/US99/00106

DR PILING DATE: 1999-01-05

DR APPLICATION NUMBER: PCT/US99/05028 PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PELING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-06
PRIOR FILING DATE: 2000-01-06
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11 PRIOR APPLICATION NUMBER: PC1/USOU/USE11
PRIOR APPLICATION NUMBER: PC7/USOU/05684
PRIOR PILING DATE: 2000-03-15
PRIOR PLING DATE: 2000-03-15
PRIOR PLING DATE: 2000-03-30
PRIOR PILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: PC7/USOU/14042
PRIOR PILING DATE: 2000-05-17
PRIOR PLING DATE: 2000-05-17
PRIOR PLING DATE: 2000-05-17
PRIOR PLING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: PC7/USOU/14941
PRIOR PLING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PC7/USOU/15264
PRIOR PLING DATE: 2000-06-21
PRIOR PLING DATE: 2000-06-21
PRIOR PLING DATE: 2000-06-11
PRIOR APPLICATION NUMBER: PC7/USOU/23522
PRIOR APPLICATION NUMBER: PC7/USOU/23523
PRIOR PLING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: PC7/USOU/3352
PRIOR PLING DATE: 2000-08-11
PRIOR PLING DATE: 2000-08-11
PRIOR PLING DATE: 2000-11-10
PRIOR PLING DATE: 2000-11-10
PRIOR PLING DATE: 2000-11-10 FILING DATE: 1999-03-08
APPLICATION NUMBER: PCT/US99/08615
FILING DATE: 1999-04-20
APPLICATION NUMBER: PCT/US99/12252
FILING DATE: 1999-06-02
APPLICATION NUMBER: PCT/US99/20111 FILING DATE: 1999-09-01 PAPLICATION NUMBER: PCT/US99/20594 FILING DATE: 1999-09-08 APPLICATION NUMBER: PCT/US99/28313 APPLICATION NUMBER: PCT/US99/28634 FILING DATE: 1999-12-01 APPLICATION NUMBER: PCT/US99/30095 FILING DATE: 1999-11-30 APPLICATION NUMBER: PCT/US99/28551 FILING DATE: 1999-12-02 FILING DATE: 2000-02-18
APPLICATION NUMBER: PCT/US00/05841 R APPLICATION NUMBER: 09/872035 FFILING DATE: 2001-06-01 R APPLICATION NUMBER: 09/88236 R FILING DATE: 2001-06-14 R FILING DATE: 2001-06-14 R FILING DATE: 2001-07-30 R APPLICATION NUMBER: 09/924419 FILING DATE: 2001-03-09 APPLICATION NUMBER: 09/866034 FILING DATE: 2001-05-25 FILING DATE: 2001-08-06 APPLICATION NUMBER: 09/927796 FILING DATE: 2001-08-06 PRIOR

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COUNTRY: USA
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Publication No. US20030013099A1

GRNERAL INFORMATION:
APPLICANT: Lasek, Amy W.
APPLICANT: Karpf, Adam R.
APPLICANT: Karpf, Adam R.
APPLICANT: RAPPI, Adam R.
APPLICANT: PA-0047 US
CURRENT APPLICATION NUMBER: 105/10/093,766
CURRENT FILING DATE: 2002-03-07

SOFTMADED: PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PROF. PR
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US-10-093-766-54
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PRIOR APPLICATION NUMBER: PCT/USO1/06520
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR PLILING DATE: 2001-03-01
PRIOR FILING DATE: 2001-03-01
PRIOR FILING DATE: 2001-05-25
PRIOR PLILORION NUMBER: PCT/USO1/17092
PRIOR PLILORION NUMBER: PCT/USO1/17000
PRIOR PLILING DATE: 2001-06-01
PRIOR PLILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/USO1/21066
PRIOR PLILING DATE: 2001-06-20
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ORGANISM: Homo sapiens
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SEQ ID NO 54
LENGTH: 281
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Best Local Similarity
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                                                                                                         1 MANMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
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                                                       1 MAMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKOMODKYSKSGIACFLKE
Gaps
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     0; Indels
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MEDIUM TYPE: 3.5 Diskette
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/174,654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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Mills, Cynthia J
Jones, David A
TITLE OF INVENTION: THF-Related Death Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kerber, Lori L.
REGISTRATION NUMBER: 41,113
REFERENCE/DOCKET NUMBER: 6111.N CN1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616/833-0974
  0; Mismatches
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; SEQUENICE DESCRIPTION: SEQ ID NO: 11:
$5.10-174-654-11
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STREET: 301 Henrietta Street
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-174-654-11
; Sequence 11, Application US/10174654
; Publication No. US20030044937A1
; GENERAL INFORMATION:
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STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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  Matches 281; Conservative
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| OS-10-222-6/5/-/2 |
| Publication No. US20030180296A1 |
| GENERAL INFORMATION: |
| APPLICANT: Salcedo et al. |
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL |
| TITLE OF INVENTION: Receptors |
| TITLE OF INVENTION: Receptors |
| TITLE OF INVENTION: Receptors |
| TITLE OF INVENTION: Receptors |
| TITLE OF INVENTION: Receptors |
| TITLE OF INVENTION: Receptors |
| FILE REFERENCE: PFS85 |
| CURRENT APPLICATION NUMBER: 60/341,237 |
| PRIOR APPLICATION NUMBER: 60/369,877 |
| PRIOR APPLICATION NUMBER: 60/364,828 |
| PRIOR PELLING DATE: 2002-04-05 |
| PRIOR FILING DATE: 2002-06-04 |
| PRIOR PELLORITON NUMBER: 60/396,591 |
| PRIOR PELLORITON NUMBER: 60/396,591 |
| PRIOR FILING DATE: 2002-08-15 |
| PRIOR FILING DATE: 2002-08-15 |
| PRIOR FILING DATE: 2002-11-13 |
| NUMBER OF SEQ ID NOS: 72 |
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100.0%; Score 281; DB 14;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0;
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100.0%; Score 281; DB 14;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0;
                                    CURRENT APPLICATION NUMBER: US/10/218,547

CURRENT FILING DATE: 2002-08-15

PRIOR APPLICATION NUMBER: 60/312,542

PRIOR PILING DATE: 2001-08-16

PRIOR PILING DATE: 2001-10-30

NUMBER OF SEQ ID NOS: 57

SOFTWARE: Patentin version 3.1

SEOFTWARE: Patentin version 3.1

SEOFTWARE: Patentin version 3.1
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                    FILE REFERENCE: PF561
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Publication No. US20030100074A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
                                                                                                                                                                                                                                                                                                                                                                                                   181 FYYIYSQIYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 240
                                                                                                DDSYMDPNDEESMNSPCWQVKWQLRQLVRKWILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                         61 DDSYMDPNDEBESMINSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGFQ 120
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APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
FILE REFERENCE: PFS54
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin version 3.0
SEQ ID NO 41
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; Publication No. US20030059862A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-10-151-882-41
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APPLICANT: Ni, Olan
APPLICANT: Rosen, Craig A
APPLICANT: Rosen, Craig A
APPLICANT: Relating Jun
APPLICANT: Relating Jun
APPLICANT: Relating Jun
APPLICANT: Relating To Human Tumor Necrosis Factor-Gamma Beta
TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta
FILE REPRENCE: PF573
CURRENT APPLICATION NUMBER: US/10/316,793
CURRENT FILING DATE: 2001-206-23
FRICH APPLICATION NUMBER: 60/326,294
FRICH FILING DATE: 2002-08-23
FRICH APPLICATION NUMBER: 00/899,059
FRICH FILING DATE: 2001-08-24
FRICH FILING DATE: 2001-03-26
FRICH APPLICATION NUMBER: 60/216,879
FRICH FILING DATE: 2001-07-06
FRICH APPLICATION NUMBER: 60/13-66
FRICH APPLICATION NUMBER: 60/13-66
FRICH FILING DATE: 2001-04-27
FRICH FILING DATE: 2001-04-27
FRICH FILING DATE: 2000-07-07
FRICH FILING DATE: 2000-04-27
FRICH FILING DATE: 2000-04-27
FRICH FILING DATE: 2000-04-27
FRICH FILING DATE: 2000-04-27
FRICH FILING DATE: 2000-04-27
FRICH FILING DATE: 1999-05-03
FRICH APPLICATION NUMBER: 60/134,067
FRICH FILING DATE: 1999-05-03
FRICH APPLICATION NUMBER: 60/132,227
FRICH APPLICATION NUMBER: 60/132,227
FRICH FILING DATE: 1999-05-03
FRICH FILING DATE: 1999-05-03
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FRICH FILING DATE: 1999-05-03
                                                          181 FYYIYSQIYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLIMKSARNSCWSKDAEYGLY 240
121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                              181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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                                                                                                                                                                                                   241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                        241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                        Sequence 26, Application US/10310793; Publication No. US20030198640A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 100.
Matches 281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yu, Guo-Liang APPLICANT: Ni, Jian
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                                                       1 MAMMENQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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100.0%; Score 281; DB 14;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0;
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CURRENT PEPLICATION NUMBER: US/10/139,785

CURRENT FILING DATE: 2002-05-07

PRIOR PELING DATE: 2002-06-07

PRIOR FILING DATE: 2002-04-05

PRIOR FILING DATE: 2001-04-05

PRIOR PILING DATE: 2001-12-20

PRIOR APPLICATION NUMBER: 60/331,310

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-10-09

PRIOR FILING DATE: 2001-10-09

PRIOR FILING DATE: 2001-09

PRIOR FILING DATE: 2001-09

PRIOR FILING DATE: 2001-09

PRIOR FILING DATE: 2001-09

PRIOR FILING DATE: 2001-09

PRIOR FILING DATE: 2001-09

PRIOR FILING DATE: 2001-05-21

PRIOR FILING DATE: 2001-05-21

PRIOR FILING DATE: 2001-05-21

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 66

SEQ ID NOS: 66

SEQ ID NOS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 66, Application US/10139785
Publication No. US20030190685A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-10-139-785-66
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APPLICANT: Brightam-Burke, Michael R.
APPLICANT: Voung, Peter R.
TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TRI AND TR2
FILE REPERENCE: GH-50030-D1
CURRENT PILING DATE: 2011-10-25
PRIOR PILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/055,513
PRIOR FILING DATE: 1997-08-13
PRIOR FILING DATE: 1997-08-26
PRIOR PRILING DATE: 1997-08-26
PRIOR PILING DATE: 1997-08-29
PRIOR FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 279
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APPLICANT: FOX, Judith A.

APPLICANT: Kelley, Sean K.

APPLICANT: Xiang, Hong

TITLE OF INVENTION: APO-2L RECEPTOR AGONIST AND CPT-11 SYNERGISM
FILE REFERENCE: P1838H: 105/10/333,712

CURRENT APPLICATION NUMBER: US/10/333,712

PRIOR APPLICATION NUMBER: PCT/US01/23691

PRIOR PILING DATE: 2001-07-27

PRIOR PILING DATE: 2001-07-27

PRIOR PILING DATE: 2001-07-27

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 1

LENGTH: 281

TYPE: PP"
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; Publication No. US20020115110A1
; GENERAL INFORMATION:
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Best Local Similarity
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100.0%; Pred. No. 2.2e-273;
tive 0; Mismatches 0;
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; Publication No. US20040005314A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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APPLICANT: Pfizenmaier, Klaus
APPLICANT: Walatt, Harald
APPLICANT: Wuest, Thomas
APPLICANT: Wuest, Thomas
APPLICANT: Moosmayer, Dieter
TITLE OF INVENTION: Site-specific Antibody-mediated Activation of Proapoptotic Cytok
TITLE OF INVENTION: AMAIZE (Antibody-mediated Apoptosis Inducing Cytokines)
FILE REFERENCE: 1708.002051
                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: Description of sequence 6: synthetic amino acid sequence of an
OTHER INFORMATION: anti-body-cytokine AMAIZe fusion protein of the invention exempl
OTHER INFORMATION: TRAIL-AMAIZE (40)
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                 CURRENT APPLICATION NUMBER: US/10/389,223A
CURRENT FILING DATE: 2003-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
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CURRENT FILING DATE: 2003-03-14
NUMBER OF SEQ ID NOS: 12
SSCTWARE: Patentin Ver. 2.1
SSQ ID NO 4
LENGTH: 480
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                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
FILE REFERENCE: 1708.002US1
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Best Local Similarity
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                                                                                                                                          LENGTH: 461
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APPLICANT: Wajant, Harald
APPLICANT: Wajant, Harald
APPLICANT: Wase, Thomas
APPLICANT: Mosenayer, Dieter
TITLE OF INVENTION: Site-specific Antibody-mediated Activation of Proapoptotic Cytoki
TITLE OF INVENTION: AMAIZE (Antibody-mediated Apoptosis Inducing Cytokines)
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                                                                                                                                                                                                                                                                   121 AAHITGIRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY 180
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                                                                                                                                          63 SYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRV 122
                                                                                                                                                                                      61 SYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRV 120
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                                              3 MMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDD
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  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 279
                                                                                                                                                                                                                                                                                                                                                                                                                               243 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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Patent No. US20020061525A1

GENERAL INFORMATION:
APPLICANT: ROGATION YELIN et al.
TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS

CURRENT APPLICATION NUMBER: US/09/855,544A

CURRENT FILING DATE: 2001-05-19

NUMBER OF SEQ. ID NOS: 16

SOFTWARE: Patentin Ver. 2.1
  0; Mismatches
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  Conservative
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US-09-855-544A-16
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61 IHEKGFYYIYSQTYFRFQEBIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                     114 VRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE 173
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     Combination and Use in Gene Therapy
                                                                                                                                                                                                                                                                                                                                        Query Match 59.8%; Score 168; DB 9; Le Best Local Similarity 100.0%; Pred. No. 3.4e-160; Matches 168; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 3.4e-158;
Matches 166; Conservative 0; Mismatches 0;
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GENERAL INPORMATION:
APPLICANT: BOYLE, WILLIAM
TITLE OF INVENTION:
FILE REFERENCE: A-570B
CURRENT APPLICATION NUMBER: US/09/779,050A
CURRENT APPLICATION NUMBER: US/09/779,050A
WINNER APPLICATION NUMBER: 00/181,800
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATCHIN VERSION 3.0
SEQ ID NO 16
TITLE OF INVENTION: Combination and Use in Gerlie Bries Reference: 5006-1-002
CURRENT APPLICATION NUMBER: US/09/900,530A
CURRENT FILING DATE: 2002-03-19
PRIOR PELING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 168
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ORGANISM: homo sapiens
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US-09-779-050A-16
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US-10-216-074-7
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Sequence 2. Application US/10389223A
Publication No. US20040033511A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wajant, Harald
APPLICANT: West, Thomas
TITLE OF INVENTION: Site-specific Antibody-mediated Activation of Proapoptotic Cytoki
TITLE OF INVENTION: Sate-specific Antibody-mediated Apoptosis Inducing Cytokines)
TITLE OF INVENTION: UNABER: US/10/389,223A
TITLE OF INVENTION NUMBER: US/10/389,223A
CURRENT APPLICATION NUMBER: US/10/389,223A
CURRENT FILING DATE: 2003-03-14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2.
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Patent No. US20020128438A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Seal, Dae-Wu
APPLICANT: Billiar, Timothy R.
TITLE OF INVENTION: DNA CASSECTE for the Production of
TITLE OF INVENTION: Secretable Recombinant Trimeric Trail Proteins, Tetracycline
TITLE OF INVENTION: Aboxycycline-Inducible Adeno-Associated Virus Vector, Their
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                                                                                                                                                    414 SYPDPILLMKSARNSCWSKDARYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 473
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                           ESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEIKENTXNDKQMVQYIYKYT 214
                                                                      354 ESSRSGHSFLSNIHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT 413
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100.0%; Pred. No. 9.1e-179;
tive 0; Mismatches 0;
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OTHER INFORMATION: Stop codon: NT 1843-1845
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ORGANISM: Artificial Sequence
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Matches 187; Conservative
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US-09-900-530A-10
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US-10-389-223A-2
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Sequence 5, Application US/10185425; Publication No. US20030053984A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: Linker
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OTHER INFORMATION: Flag
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NAME/KEY: DOMAIN
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US-09-855-544A-13
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GENERAL INFORMATION:

APPLICANT: Shu, Hong-Bing

TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 2879-72

CURRENT APPLICATION NUMBER: US/10/216,074

CURRENT APPLICATION NUMBER: US/09/565,423

PRIOR FILING DATE: 2000-05-05

PRIOR PELING DATE: 2000-05-05

PRIOR FILING DATE: 2000-05-06

PRIOR FILING DATE: 2000-05-06

PRIOR FILING DATE: 1999-05-06

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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| Sequence 11, Application US/10338083
| Publication No. US20030166559A1
| GENERAL INFORMATION:
| APPLICANT: Dealarlans, John K
| APPLICANT: Dealarlans, John K
| APPLICANT: Dahiyat, Bassil I.
| APPLICANT: Dahiyat, Bassil I.
| APPLICANT: Dahiyat, Bassil I.
| APPLICANT: Dahiyat, Bassil I.
| APPLICANT: Dahiyat, Bassil I.
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| APPLICANT: Dahiyat, Bassil I.
| APPLICANT: Dahiyat, Bassil I.
| APPLICANT: Dahiyat, Bassil I.
| APPLICANT: Dahiyat, Bassil I.
| APPLICANT: Dahiyat, Bassil I.
| FILER REFERENCE: A-11273-2
| CURRENT APPLICATION NUMBER: US, 10/336, 803
| PRIOR APPLICATION NUMBER: US, 60/3445, 805
| PRIOR APPLICATION NUMBER: US, 60/3445, 805
| PRIOR APPLICATION NUMBER: US, 60/373, 453
| PRIOR PRILING DATE: 2002-04-17
| NUMBER OF SEQ ID NOS: 23
| SEQ ID NO 11
| LENGTH: 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.3%; Score 161; DB 14; Length 161; 100.0%; Pred. No. 3.5e-153; ive 0; Mismatches 0; Indels (
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Matches 161; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       161
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APPLICANT: TECHORP, Jurg
APPLICANT: Techorp, Jurg
APPLICANT: Techorp, Jurg
APPLICANT: Schedder, Pascal
APPLICANT: Schedder, Pascal
APPLICANT: Schedder, Pascal
APPLICANT: Chief and Development Ltd.
APPLICANT: Schedder, Pascal
APPLICANT: Chief and Schedder, Pascal
APPLICANT: Holler, Nils
TITLE OF INVENTION: Recombinant Fusion Proteins
FILE OF INVENTION: Recombinant Fusion Proteins
FILE REFERENCE: 1708.001091
CURRENT APPLICATION NUMBER: US/10/185,425
CURRENT APPLICATION NUMBER: US/10/185,425
FRIOR PILING DATE: 2002-06-28
FRIOR PILING DATE: 2000-12-20
FRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 5
SEQ ID NO 5
LENGTH: 296
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240 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
                                             121 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 161
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OTHER INFORMATION: mouseACRF30 aa 18-111
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COATION: (111)...(296)
CHER INFORMATION: humanTRAIL aa 95-281
US-10-185-425-5
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238 GLYSIYQ 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: AGREGATI, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Scot A.
APPLICANT: Warster, Scot A.
APPLICANT: Wood, William
APPLICANT: Wood, William
TITLE OF INVENTION: NUCLEIC
TITLE OF INVENTION: NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERBENCE: P1206R1
CURRENT APPLICATION NUMBER: EXALIER APPLICATION NUMBER: 09/247,225
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
FRIOR PILING DATE: EARLIER FILING DATE: 1999-02-09
FRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
FRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                            50.2%; Score 141; DB 9; Length 246; 100.0%; Pred. No. 5.9e-133; ive 0; Mismatches 0; Indels
; Sequence 13, Application US/09855544A
; Patent No. US2020061525A1.
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS;
; FILE REPRENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PATENTIN Ver. 2.1
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US-10-116-378-29
                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                  SEQ ID NO 13
LENGTH: 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.1%; Score 107; DB 9; Length 113; 100.0%; Pred. No. 3.9e-99; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.4%; Score 105; DB 9; Length 188; 100.0%; Pred. No. 6.2e-97; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/09855544A

Patent No. US20020061525A1

GENERAL INFORMATION:
APPLICANT: Rodrigo YELIN et al.
TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
FILE REFERENCE: 2786-0173P
CURRENT APPLICATION NUMBER: US/09/855,544A

CURRENT FILING DATE: 2001-05-19
NUMBER OF SEQ ID NOS: 16

SEQ ID NO 14

SEQ ID NO 14

LENGTH: 188
                                                                                                                                                                                                                 APPLICANT: Rodrigo YELIN et al.
TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
FILE REPERBENCE: 2786-0173P
CURRENT APPLICATION NUMBER: US/09/855,544A
CURRENT FILING DATE: 2001-05-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 113
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; GENERAL INFORMATION:
; APPLICANT: ROdrigo YELIN et al.
                                                                                                                                          ; Sequence 15, Application US/09855544A ; Patent No. US20020061525A1
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Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
121 GLYSIYQ 127
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Sequence 33427, Application US/09864761
; Sequence 33427, Application US/09864761
; Parent No. US2020048763A1
; Parent No. US2020048763A1
; PAPLICANT: Rank, David R.
; APPLICANT: Rank, David R.
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILL REPERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-06-08-03
; PRIOR FILING DATE: 2000-06-03
; PRIOR FILING DATE: 2000-10-04
; PRIOR FILING DATE: 2000-10-04
; PRIOR FILING DATE: 2000-10-04
; PRIOR FILING DATE: 2000-10-04
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CURRENT APPLICATION NUMBER: US/110/399,018
PRIOR PELING DATE: 2003-04-10
PRIOR FILING DATE: 2001-0-11
PRIOR FILING DATE: 2001-0-11
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                      116 ERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV 175
                                                                                                                                                                                                                                                                             1 ERGEORVAAHITGTRGRSNTLSSFNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RISEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGR 56
                                                                                                                                                                                   0; Gaps
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                                                                                                                           30.2%; Score 85; DB 14; Length 85; 100.0%; Pred. No. 3.6e-77; tive 0; Mismatches 0; Indels
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19.9%; Score 56; DB 15; I
Best Local Similarity 100.0%; Pred. No. 3.2e-48;
Matches 56; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                   176 IHEKGFYYIYSQTYFRFQEBIKENT 200
                                                                                                                                                                                                                                                                                                                                                                               61 IHEKGFYYIYSQTYFRFQEEIKENT 85
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                                                                                                                                                                                         85; Conservative
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ORGANISM: Homo sapiens
                              TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                             Best Local Similarity
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US-10-399-018-20
                                                                ; ORGANISM: HOT
US-10-286-696-12
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                                                                                                                                         Query Match
LENGTH:
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Publication No. US20030129706A1
GRNERAL INFORMATION:
APPLICANT: Heu, Hailing
APPLICANT: Heu, Hailing
APPLICANT: Boyle, William J
TITLE OF INVENTION: Fhm, A No. US20030129706Alel Member of the TNF Ligand Supergene CURRENT APLICATION NUMBER: US/10/286,696
CURRENT APPLICATION NUMBER: US/10/286,696
CURRENT FILING DATE: 2002-11-01
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31.0%; Score 87; DB 9; Length 88;
Best Local Similarity 100.0%; Pred. No. 3.7e-79;
Matches 87; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                             Query Match 32.0%; Score 90; DB 9; Length 98; Best Local Similarity 100.0%; Pred. No. 4e-82; Matches 90; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/09855544A

Patent No. US20020061525A1

GENERAL INFORMATION:
ATITE OF INVENTION: SEQUENCES OF TRAIL VARIANTS

TITE OF INVENTION: SEQUENCES OF TRAIL VARIANTS

TITE OF INVENTION: SEQUENCES 186-0173P

CURRENT APPLICATION NUMBER: US/09/855,544A

CURRENT PILING DATE: 2001-05-19

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 9

LENGTH: 88
TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS FILE REFERENCE: 2786-0173P CURRENT APPLICATION NUMBER: US/09/855,544A CURRENT FILING DATE: 2001-05-19 NUMBER OF SEQ ID NOS: 16 SOFTWARE: PATENTIN Ver. 2.1 SEQ ID NO 10 LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
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PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
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US-09-855-544A-9
                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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US-10-286-696-12
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 3.4e-36;
Matches 44; Conservative 0; Mismatches 0; Indels
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                           Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQ 44
                                                                           0; Indels
                                                                                                                            1 MAMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQ 44
                                                                                                                                                       1 MARMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTXVYFTNELKQ 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Barnes Jewish Hospital
APPLICANT: Lam, Jonathan
APPLICANT: Lam, Jonathan
APPLICANT: Teltelbaum, Steven
TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
FILE REFERENCE: 60019620-0202
CURRENT APPLICATION NUMBER: 10/272,411
CURRENT FILING DATE: 2002-10-15
PRIOR FILING DATE: 2001-10-15
                        15.7%; Score 44; DB 9; L¢
100.0%; Pred. No. 3.3e-36;
tive 0; Mismatches 0;
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TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
TILE REFERENCE: 2786-0173P
CURRENT APPLICATION NUMBER: 05/09/855,544A
CURRENT FILING DATE: 2001-05-19
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 12
LENGTH: 55
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                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/0985544A Patent No. US20020061525A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-272-411-24
; Sequence 24, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
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                                                                                 44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                             Query Match
Best Local Similarity
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Matches 34; Conserv
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US-09-855-544A-12
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                                                                                 Matches
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN BIA74, SIGNAL = 0.9

OTHER INFORMATION: EXPRESSED IN BIA74, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN MARKOW, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.97

OTHER INFORMATION: EXPRESSED IN HEAT', SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HEAT', SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HEAT', SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HEAT', SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HEAT', SIGNAL = 1.00e-19

OTHER INFORMATION: EXPRESSED IN HEAT', EVALUE 3.00e-19

OTHER INFORMATION: EST_HUMAN HIT: H54628.1, EVALUE 3.00e-18
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PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR PLING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
PROPER FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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Patent No. US2002006152541

GENERAL INFORMATION:
APPLICANT: Redrigo YELIN et al.
TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
FILE REFERENCE: 2786-0173P
CURRENT APPLICATION NUMBER: US/09/855,544A
CURRENT FILING DATE: 2001-05-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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SEQ ID NO 33427
LENGTH: 50
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LENGTH: 52
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INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING SAMETHODS OF USE THEREOF
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Steinman, Ralph
TITLE OF INVENTION: A PROTEIN BELONGING TO THE TWF SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/210,115
APPLICATION NUMBER: 09/210,115
ATTORNEY/AGBNT INFORMATION:
NAME: Jackson Esg., David A.
RESTSRENCE/COCKET NUMBER: 66,742
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
         STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/873,829
FILING DATE: 04-Jun-2001
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mus musculus
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/10017910; Publication No. US20020159970A1; GENERAL INFORMATION:
APPLICANT: Choi, Yongwon; Mong, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 291 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 133521
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 VQYIYKYTSYPDPI 220
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                    STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Hackensack
                               CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 48
US-10-017-910-6
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Wong, Brian
Josien, Regis
Steinman, Ralph
TITLE OF INVENTION: A PROTEIN BELONGING TO THE TWF SUPERFAMILY
METHODS OF USE THEREOF
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100.0%; Pred. No. 1.2e-05;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
GENERAL INFORMATION:
APPLICANT: Barnes Jewish Hospital
APPLICANT: Barnes Jewish Hospital
APPLICANT: Ram, Jonathan
APPLICANT: Ross, F. Patrick
APPLICANT: Teitelbaum, Steven
TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
FILE REFERENCE: 60019620-0206
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 60/329,393
PRIOR APPLICATION NUMBER: 60/329,393
PRIOR FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                           12.1%; Score 34; DB 14; L
100.0%; Pred. No. 2.4e-26;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TRGRSNTLSSPNSKNEKALGRKINSWESSRSGHS 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/09779050A
Patent No. US20020160416A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BOYLE, WILLIAM
APPLICANT: HSU, HAILING
ITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
FILE REFERENCE: A-570B
CURRENT APPLICATION NUMBER: US/09/779,050A
CURRENT FILING DATE: 2001-02-12
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATENTIN VETSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 6, Application US/09873829
; Publication No. US20030185820A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Choi, Yongwon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 VQYIYKYTSYPDPI 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.0*
Best Local Similarity 100.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 34, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CRGANISM: Mus musculus
US-09-779-050A-17
                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: BOWN
US-10-272-328A-24
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US-09-779-050A-17
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LENGTH: 172
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                                                                                                                                                                                                                                                                                                     SEQ ID NO 24
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TITLE OF INVENTION: METHOD FOR DETERMINING MASS ALTERING MOIETY IN PEPTIDES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lam, Jonathan
APPLICANT: Ross, F. Patrick
APPLICANT: Ross, F. Patrick
TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
FILE REFERENCE: 60019620-0202
CURRENT APPLICATION NUMBER: US/10/272,411
PRIOR PILING DATE: 2002-10-15
PRIOR PILING DATE: 2001-10-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Barnes Jewish Hospital
APPLICANT: Lam, Jonathan
APPLICANT: Ross, F. Parrick
APPLICANT: Teitelbaum, Steven
TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
FILE REFERENCE: 60019620-0206
                 FILE REFERENCE: 9124.137USNO
CURRENT APPLICATION NUMBER: US/10/399,018
CURRENT APPLICATION NUMBER: US/10/399,018
CURRENT FILING DATE: 2003-04-10
PRIOR FILING DATE: 2001-10-11
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 21
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; Sequence 25, Application US/10272328A;
; Publication No. US2003010944A1;
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25, Application US/10272411
Publication No. US20030100068A1
GENERAL INFORMATION:
APPLICANT: Barnes Jewish Hospital
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin version 3.1

SEQ ID NO 25

LENGTH: 10

TYPE: PRT

OCGANLEM: Homo sapiens

US-10-272-411-25
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                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
US-10-399-018-21
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                                                                                                                                                                                                                                                                                          TYPE: PRT
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Sequence 13, Application US/10286696

Sequence 13, Application US/10286696

GENERAL INFORMATION:
APPLICANT: Wooden, Scott K
APPLICANT: Boyle, William J
ITILE OF INVENTION: Fhm, A No. US20030129706A1e1 Member of the TNF Ligand Supergene J
FILE REFERENCE: 01017/355506

CURRENT APPLICATION NUMBER: US/10/286,696

CURRENT FILING DATE: 2002-11-01

PRIOR FILING DATE: 1999-08-04

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PATENCE 1200-11 Ver. 2.0

SEQ ID NO 13

LENGTH: 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.3%; Score 12; DB 14; Length 87;
100.0%; Pred. No. 0.00066;
tive 0; Mismatches 0; Indels
                                                                                    ATTOR MAPPLICATION NUMBER: US 09/447,035
RILING DATE: 1999-11-22
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-200
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEFAX: 201-343-1684
INFORMATION POR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/10/017,910
FILING DATE: 14-Dec-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mus musculus
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 50
US-10-399-018-21
Sequence 21, Application US/10399018
; Publication No. US20040002118A1
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 291 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 VQYIYKYTSYPDPI 220
                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 VQYIYKYTSYPDPI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULB TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 12, Conservative
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APPLICANT: Smilansky, Zeev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-286-696-13
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Best Local Similarity 100...
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ORGANISM: Plasmodium
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Matches
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US-10-272-328A-27

Sequence 27, Application US/10272328A

Publication No. US2003010944A1

GENERAL INFORMATION:
APPLICANT: Barnes Jewish Hospital

APPLICANT: Lam, Jonathan
APPLICANT: Lam, Jonathan
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: WOSS, F. Patrick

APPLICANT: APPLICANT: WOSS, WOSS THEREOF

TITLE OF INVENTY APPLICATION WUMBER: US/10/272,328A

CURRENT APPLICATION WUMBER: 60/329,393

PRIOR FILING DATE: 2001-10-15

WUMBER OF SEQ ID NOS: 51

SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                Sequence 27, Application US/10272411
Publication No. US20030100068A1
GENERAL INPORMATION:
APPLICANT: Barnes Jewish Hospital
APPLICANT: Lam. Jonathan
APPLICANT: Taitelbaum, Steven
ITILE OF INVENTION: RANKL MIMICS AND USES THEREOF
FILE REFERENCE: 60019620 -020.
CURRENT APPLICATION NUMBER: US/10/272,411
CURRENT FILING DATE: 2002-10-15
PRIOR FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 52
SOFTARE: Patentin version 3.1
SEQ ID NO. 27
LENGTH: 9
SOFTWARE: PatentIn version 3.1
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Matches 9, Conservative
                                                                                                                                                 Best Local Similarity 100.
Matches 10; Conservative
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ORGANISM: Homo sapiens
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                                                                       ; ORGANISM: Homo sapiens
US-10-272-328A-25
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US-10-272-411-27
                 SEQ ID NO 25
LENGIH: 10
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cavalic David K
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No. 36; Matches 7; Conservative 0; Mismatches 0; Indels
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US-10-424-599-255595
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Squence 186624, Application US/10424599
Squence 186624, Application US/10424599
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
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TITLE OF INVENTION: Soy Nucleic Acid Molecules
TITLE OF INVENTION
                                         APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 112
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Publication No. US20030082758A1
GENERAL INFORMATION:
APPLICAWT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PAZOCI.
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
FILOS APPLICATION NUMBER: US/2002-03-12
NUMBER OF SEQ ID NOS: 653
FILOS APPLICATION NUMBER: PATORIAL REMOVED - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 112;
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US-10-424-599-186624
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US-10-424-599-143535
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                    APPLICANT: Zhou Yihua
                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Glycine max
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US-10-103-313-421
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LENGTH: 125
TYPE: PRT
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Sequence 263624, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Vinua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 263624
LENGTH: 42
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LOCATION: (1)..(60)
OTHER INFORMATION: unsure at all Xaa locations
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100.0%; Pred. No. 50;
ive 0; Mismatches
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 258329
LENGTH: 60
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Sequence 143535, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K
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Best Local Similarity 100.C
Matches 7; Conservative
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Sequence 4, Application US/10178055

Publication No. US20030105008A1

GENERAL INFORMATION:

APPLICANT: Dhar, Suman

TITLE OF INVENTION: AND POLYCOMAVIRUSES

TITLE OF INVENTION: AND POLYCOMAVIRUSES

TITLE OF INVENTION: AND POLYCOMAVIRUSES

TITLE OF INVENTION: AND POLYCOMAVIRUSES

CURRENT PELING DATE: 2002-06-21

CURRENT PELING DATE: 2001-06-21

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.1

SEQ ID NO
                                                                               Sequence 64832, Application US/10425114

Sequence 64832, Application US/10425114

Publication No. US20040034888A1

GENERAL INPORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cavaic, David K.

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT PILLING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NOS 4832

TENDATH: 10-6

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US-10-425-114-64832
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Matches 7; Conservative
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ORGANISM: Homo sapiens
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118 PNSKNEK 124
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ORGANISM: Zea mays
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US-10-178-055-2
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US-10-178-055-4
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GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: 1916323) B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

LENGTH: 170

LENGTH: 170
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La ROSa Thomas J
APPLICANT: Kovalic David K
APPLICANT: APONDWEN:
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATF: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
EENGTH: 184
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Best Local Similarity 100.0%; Pred. No. 1.38+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                         Query Match 2.5%; Score 7; DB 14; Length 125; Best Local Similarity 100.0%; Pred. No. 94; Matches 7; Conservative 0; Mismatches 0; Indels
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US-10-424-599-164595
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US-10-424-599-235009
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2.5%; Score 7; DB 12; Le
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0;
; ORGANISM: Homo sapiens
US-10-103-313-421
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US-10-424-599-164595
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Establicant: Avail R
APPLICANT: About K
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Sequence 4, Application US/10145602

Sequence 4, Application No. US20030171563A1

GENERAL INFORMATION:

TITLE OF INVENTION: REGULATORS OF BACTERIAL VIRULENCE FACTOR EXPRESSION

FILE REFERENCE: KCC 4766

CURRENT APPLICATION NUMBER: US/10/145,602

CURRENT FILING DATE: 2002-05-13

FRICAR APPLICATION NUMBER: US 60/291,917

PRIOR FILING DATE: 2001-05-18

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PATENTIN Version 3.1
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2.5%; Score 7; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                               Length 241;
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                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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US-10-424-599-276617
                                                                                                                                                                                                                                                                                                               Query Match
2.5%; Score 7; DB 9; Les
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0;
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; Publication No. US20040031072A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Staphylococcus aureus
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1105
LENGTH: 241
                                                                                                                              TYPE: PRT GRGANISM: Homo sapiens US-09-925-301-1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 QEEIKEN 199
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              APPLICANT: Dhar, Suman
TITLE OF INVENTION: GEMININ AND ORC3N INHIBIT REPLICATION OF HERPESVIRUSES, PAPILLOMN
TITLE OF INVENTION: GEMININ AND ORC3N INHIBIT REPLICATION OF HERPESVIRUSES,
TITLE OF INVENTION: GAND POLYCMAVIRUSES
FILE REFERENCE: BOO801/70253 (JAV/MXA)
CURRENT APPLICATION NUMBER: US/10/178, 055
PRIOR APPLICATION NUMBER: US 60/299, 963
PRIOR PAPLICATION NUMBER: US 60/299, 963
PRIOR FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PALENTIN Version 3.1
SEQ ID NO 2
LENGTH: 209
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Sequence 2. Application US/09997165

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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PA.106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT PILING DATE: 2001-08-10
PRIOR PLIING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: PCT/USO0/05882
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
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Patent No. US20020052308A1
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 7; Conservative
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Best Local Similarity 100.(
Matches 7; Conservative
APPLICANT: Dutta, Anindya
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ORGANISM: Homo sapiens
US-09-997-165-2
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ORGANISM: Homo sapiens
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US-09-997-165-2
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APPLICANT:
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Sequence 1984, Application US/10369493

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Glodiman, Barry S.
APPLICANT: Glodiman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: DLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (5205.) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 1984

LENGTH: 420
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; Sequence 18, Application US/09808483
; Patent No. US20020001824A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Ligand-gated anion channels of insects
; FILE REFERENCE: Le A 34 397
; CURRENT APPLICATION NUMBER: US/09/808,483
; CURRENT FILING DATE: 2001-03-14
; PRIOR FILING DATE: 2001-03-14
; PRIOR FILING DATE: 2000-03-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.1
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Sequence 54850, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT; ORGANISM: Drosophila melanogaster US-09-808-483-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 PILLMKS 225
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US-10-369-493-1984
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LENGTH: 418
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APPLICANT: Ohlsen, Kari,
APPLICANT: Ohlsen, Kari,
APPLICANT: Ohlsen, Kari,
APPLICANT: Passick, John
APPLICANT: Passick, John
APPLICANT: Passick, John
APPLICANT: Wall, Daniel
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RESULT 75

US-10-289-762-189

US-10-289-762-189

Sequence 189, Application US/10289762

Publication No. US20040006218A1

GENERAL INFORMATION:

APPLICANT: GETIffais,

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve

TITLE OF INVENTION: and treatment of infection

TITLE REFERENCE: 97.003-999

CURRENT APPLICATION NUMBER: US/10/289,762

NUMBER OF SEQ ID NOS: 6849

SEQ ID NOS: 6849
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                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                          Query Match 2.5%; Score 7; DB 15; Length 429; Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.5%; Score 7; DB 15; Length 429; Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 7; Conservative 0; Mismatches 0; Indels
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| PRIOR FILING DATE: 2000-09-14 |
| PRIOR APPLICATION NUMBER: 0027549.5 |
| PRIOR FILING DATE: 2000-11-10 |
| PRIOR APPLICATION NUMBER: 0031706.5 |
| PRIOR FILING DATE: 2000-12-22 |
| NUMBER OF SEQ ID NOS: 664 |
| SEQ ID NO 227 |
| LENGTH: 429
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; ORGANISM: Chlamydia pneumoniae
US-10-289-762-189
                                                                                                                                                                                                                                   TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-227
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Abu71443 Human neo

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ABG71905
ABP60546
AAE36258
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ADD14080
ADD19010
ADB76953
AAW76332
AAW95032
AAW95032
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AAW95032
AAW961495
ADB61495
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AAY01516
AAY72935
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ADC03335
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AA029543
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AAY27019
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ABG72257
AAU99301
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AAE11038
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AAO17496
AAO17495
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AABE1476
ADB61480
ADB61482
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AAU79598
Aaw19777 Novel Cyt
Aaw27134 Human Apo
Aaw76829 Human TEA
Aaw41354 Human AGP
Aay4136 Human AGP
Aay27012 Human Ago
Aay81956 Human Apo
Aay81956 Human Apo
Aab28691 Human Apo
Aab28691 Human Agp
Aab28691 Human AGP
Aab50977 Human AGP
Aab51954 Human TEA
Aab613691 Human TEA
Abb8131630 Human TEA
Abb8131630 Human TEA
Aab1662 Human Apo
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                                    March 23, 2004, 09:15:55 ; Search time 60 Seconds (without alignments) 1323.264 Million cell updates/sec
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                                                                  281
1 MAMMEVQGGPSLGQTCVLIV......NEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                          Description
                                                                                                                       1586107
      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                 1586107 segs, 282547505 residues
                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                  Post-processing: Listing first 100 summaries
                           protein search, using sw model
                                                                                                                                                                                                                                                                          AAW27134

AAW168787

AAW56760

AAW4354

AAX01517

AAX21012

AAX81956

AAX81956

AAB28691

AAB28691

AAB5674

AAB67343
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ABB08133
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11: geneseqp1990s:*
2: geneseqp1990s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003as:*
6: geneseqp2003bs:*
8: geneseqp2003bs:*
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Match Length D
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AAU79600 AAU79599 AAG03752 ABG72258 AAU79595 AAW19790

AAU79593 ABG73861 ABU10205

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TRA
                                                                                                                                                                                          Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy.
Aael1032 Human
Abu08559 Human
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                                                                                                                                                                                                                                                                                                                                                                                               /label= Glycosylation
/note= "putative N-linked glycosylation site"
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/note="Claim 2"
41. .281
/label= Extracellular_region
                                                                                                                                                                                                                                                                                                                              'label= Transmembrane_region
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/label= Cytoplasmic_region
                                           ALIGNMENTS
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AAE11032
ABU08559
                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                  AAW19777 standard; protein; 281 AA.
                                                                                                                                                                                                                                                           'note= "Claim 4"
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'note= "Claim 3"
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/note= "Claim 1"
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                                                                                                                                                                    Novel cytokine Apo-2 ligand
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32.0
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                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
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                                                                                                                                               22-SEP-1997
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Peptide
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the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft
versus host disease or inflammation.
                                                                                                                                                                                                      61 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                           RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                            181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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                                                                                                                                                                          61 DDSYNDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                             1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
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                                                                                                                                  1 MAMMEVOGGPSLGOTCVLIVIFTVLLOSLCVAVTYVYFTNELKOMODKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apoptosis inducing molecule-I; AIM-I; autoimmune disorder; tumour necrosis factor ligand superfamily; AIM-I altered expression; neoplasia inhibition; anti-inflammatory agent.
                                                         Gaps
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                 Length 281;
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                 Score 281; DB 2; I
Pred. No. 1.8e-266;
100.0%; Scc...
100.0%; Pred. No. 1...
0; Mismatches
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                                                         Conservative
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                                    Similarity
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                                                       281;
              Query Match
Best Local S:
Matches 281
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(IMMV) IMMUNEX CORP

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tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be used for treating cachexia, cerebral malaria, rheumatoid arthritis or osteoporosis, for preventing graft-host rejection, and as anti-inflammatory agents, for treating endotoxic shock or to prevent activation of HIV
                                                                                                                                                                                                  1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTVELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "potential KEX2 protease processing site"
                                                                                                                                                 ;
0
                                                                                                                     Length 281;

    281
    1abel= Extracelular domain
    note= "contains a receptor-binding region"

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                                                                                                                  100.0%; Score 281; DB 2; Length 2
100.0%; Pred. No. 1.8e-266;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="potential N-glycosylation site"
149. .150
/note= "potential KEX2 protease process
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/label= Cytoplasmic_domain
19..38
/label= Transmembrane_domain
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                                                                                         Sequence 281 AA;
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01-NOV-1995;
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                                                                                                                                                                                                                         Human tumour necrosis factor related apoptosis inducing ligand (TRAIL) (AAW19787) is a novel cytckine that induces apoptosis of certain target cells, including cancer cells and virally infected cells. Its amino acid sequence was deduced from cDNA clone HuAIC (AAT72848), deposited in vector pDC409 as ATCC 69849. Recombinant TRAIL polypeptides (esp. soluble polypeptides) can be expressed in host cells and used in the treatment of cancer (e.g. leukaemia, lymphoma and melanoma) and viral infections, or to raise antibodies that may be useful for treating thrombotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammation, arthritis, septicaemia, autoimmune disease, restenosis, transplant rejection; infection; ischaemia; brain injury; bone disease; acute respiratory disease syndrome, acquired autoimmune disease syndrome; AIDS; cancer; atherosclerosis; Alzheimers disease; TRAIL; TNF; TL2. tumour necrosis factor-related apoptosis-inducing ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                     TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected cells - useful for treating thrombotic microangiopathy, cancer and viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumour necrosis factor related receptor; human; treatment; stroke;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 281; DB 2; Length 281; 100.0%; Pred. No. 1.8e-266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0, Mismatches
                                                                                                                                                                                           Claim 10; Page 43-44; 62pp; English
                                                                                                                                                        infection and for use in assays.
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                               Goodwin RG;
                                                                  WPI; 1997-118715/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                     microangiopathies
                                                                                      N-PSDB; AAT72847
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 281 AA;
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                             Wiley SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW76829;
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25-JUN-1996;
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                                                                                US5763223-A.
                                                                                                       09-JUN-1998.
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Domain
                      Region
                                              Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLIMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FYYIYSQTYFRFQEEIKENTKNDKQWVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                         receptor, TL2 (also known as tumour necrosis factor-related apoptosis-inducing ligand, TRAIL). This protein is used in a method resulting in the isolation of the novel human TNR related receptor. TR6 TR6 polypeptides and polynucleotides can be used in the treatment of chronic and acute inflammation, arthritis, septicaemia, autoimnume diseases (e.g. inflammatory bowel disease, isolated), transplant rejection, graft vs. host disease, infection, stroke, ischaemia, acute respiratory disease syndrome, restenoisis, brain injury, (acquired autoimnume disease syndrome) hubs, bone diseases, cancer (e.g. lympho-proliferative disorders), atherosclerosis and Alzheimers disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour necrosis factor related apoptosis ligand; TRAIL; research; human; cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.
                                                                                                                                                                                                                This sequence represents the human tumour necrosis factor (TNF)-related
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAMMEVQGGPSLGQICVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                    DNA encoding tumour necrosis factor receptor TR6 - and corresponding polypeptide, antibody, agonist, antagonist, etc.
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                                                                                                                                                                                                                                                                                                                                                                                    Length 281;
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                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 281; DB 2; L
100.0%; Pred. No. 1.8e-266;
iive 0; Mismatches 0;
                                                                                                                                                                                         Disclosure, Page 32-33; 34pp; English.
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                                                                    SMIK ) SMITHKLINE BEECHAM CORP.
                     97US-0041230P.
97US-00853684.
97EP-00310562.
                                             97US-00916625
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Matches 281; Conservative
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                                                                                                                WPI; 1998-523156/45.
N-PSDB; AAV63096.
                                                                                          Young PR;
                                                                                                                                                                                                                                                                                                                                                            Sequence 281 AA;
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23-DEC-1997;
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                      14-MAR-1997;
                                              22-AUG-1997;
                                   09-MAY-1997;
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                                                                                          Deen KC,
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This represents a human tumour necrosis factor related apoptosis ligand (TRAIL) polypeptide. The human and murine TRAIL polypeptides can induce apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful for producing the recombinant TRAIL polypeptides, which may be useful in studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells feg. to isolate antigens for vaccine development). The polypeptides can be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal treatment of blood or bone-marrow), or to treat viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding cytokine TNF-related apoptosis ligand polypeptides - useful for producing recombinant polypeptides for research and therapy of leukaemia, lymphoma, melanoma and viral infections.
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100.0%; Pred. No. 1.8e-266;
iive 0; Mismatches 0; Indels
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                                      "N-terminal cytoplasmic domain"
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                                                                                                    "transmembrane region"
                                                                                                                                                                                  /note= "extracellular domain"
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95US-00548368.
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Best Local Similarity 100.
Matches 281; Conservative
                                                                     19. .38 /note= "
1. .18
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goodwin RG, Wiley SR,
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N-PSDB; AAV29518.
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Neurodegenerative disease; autoimmune disease; inflammatory disease; lupus erythematosus; rhuematoid arthritis; SEP; apoptotic; Protein associated with neurodegenerative and autoimmune diseases.

lupus erythematosus; rhuematoid surface receptor; TRAIL protein.

Homo sapiens FR2766713-A1

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AAY01517 standard; peptide; 281 AA.

AAY01517

(first entry)

27-MAY-1999

AAY01517;

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The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis factor (TNP)-related protein, involved in inflammation, myelopoiesis and bone resorption. It has the same nucleic acid and antho acid (aa) sequences as the TNF-related apoptosis-induced ligand (TRAIL) described in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay reagents for detecting AGP-1 expression and antagonistic compounds are used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus cused to treat inflammation (e.g. rheumatoid arthritis, systemic lupus erythematosus, psoriasis, scleroderma, infection-related inflammation) or bone resorption diseases (e.g. osteoporoais, osteomyalitis, hypercalcaemia, Paget's disease). AGP-1 can be used to treat hypercalcaemia, paget's disease). AGP-1 can be used to treat marrow cells, particularly neutrophils and lymphocytes, e.g. where caused marrow cells, particularly neutrophils and lymphocytes, e.g. where caused transformed with expression vectors containing AGP-1 DNA, are used to produce recombinant AGP-1
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                                                     Human; AGP-1; tumour necrosis factor-related protein; TNF; inflammation; bone resorption; haematopoietic disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein useful for treating inflammation, bone resorption and haematopoietic
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                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-00660562
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                                                                                                                                                                                                                                  WO9746686-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1996;
                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                      06-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnson MJ,
Human AGP-1.
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Use of polypeptide derived from TRAIL protein for diagnosis of degenerative disease - autoimmunity and inflammation, also useful in prevention or treatment, and similar use of corresponding ligand and

Claim 2; Page 13; 21pp; French.

nucleic acid

Perron

Rieger F, Belliveau JF,

(INMR) BIO MERIEUX

WPI; 1999-156177/14.

97FR-00010176.

04-AUG-1997;

05-FEB-1999.

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The specification describes the use a polypeptide corresponding to at disast the primary sequence of part of the present sequence to produce a diagnostic, prophylactic or therapeutic composition useful in cases of degenerative, autoimmune and inflammatory diseases. The polypeptides can be used in treatment of neurodegenerative disease, lupus erythematosus, nhuematoid arthritis, and SEP. The polypeptides are apoptotic in central nervous system cells, antigenic and specifically recognise the surface receptor of the TRAIL protein. The polypeptide is a marker of disease and anti-TRAIL antibody or a TRAIL equivalent that binds to specific alth an receptors, inhibiting formation of natural complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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100.0%; Pred. No. 1.8e-266;
ive 0; Mismatches 0;
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                             cytokine, designated Apo-2 ligand, useful for inducing apoptosis
                                                                                                                     autoimmune disorder;
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                                                                                                                                                                                                                                                                                                                                                                    Schwall RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 281; DB 2; Length 281; 100.0%; Pred. No. 1.8e-266; ive 0; Mismatches 0; Indels (
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                                                                                                                     Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; lupus; immune-mediated glomerular nephritis; human.
                                                                                                                                                                                                                                                                                                                                                                    RM,
                                                                                                                                                                                                                                                                                                                                                                    Pitti
                                                                                                                                                                                                                                                                                                                                                                    O'connel MT,
                                                                                        Human Apo-2 ligand (Apo-2L) polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                associated with increased apoptosis
AAY27012 standard; protein; 281 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 1A; 86pp; English.
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98US-00060533.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               mammalian cancer cells.
                                                           (first entry)
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Best Local Similarity 100.
Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 281 AA;
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                                                                                                                                                                                                 WO9936535-A1.
                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                             15-JAN-1999;
                                                                                                                                                                                                                                                                                          15-JAN-1998;
                                                                                                                                                                                                                                                                                                          15-APR-1998;
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This sequence is the human Apo-2 ligand protein, which is recognised by monoclonal antibodies produced by the hybridoma cell lines of the invention. The hybridoma cell lines are deposited under the American Type Culture Collection Accession Numbers ATCC HB-1225, HB-1225, and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic assays for Apo-2 ligand, e.g. detecting its expression in specific cells, tissues, or serum. The antibodies may also be employed as therapeutics. For instance, anti-Apo-2 ligand antibodies which holock Apo-2 ligand activity, like Apo-2 ligand antibodies which holock Apo-2 ligand activity, like Apo-2 ligand-induced apoptosis, may be employed to treat pathological conditions or diseases associated with increased apoptosis. They are also useful for the affinity purification of Apo-2 ligand from recombinant cell culture or natural sources. The Apo-2 ligand itself may be used to treat diseases e.g. cancer, by inducing apoptosis in cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated monoclonal antibodies having antigen specificity for Apo-2 ligand, e.g. 2G6, 2E11 or 5C2, useful for detecting the expression of Apo-2 ligand serum, and for treating diseases associated with increased
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                                                                                                                                                                                                                                                       Apo-2 ligand; human; monoclonal antibody; hybridoma cell line; diagnosis;
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241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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100.0%; Pred. No. 1.8e-266;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                    Human Apo-2 ligand protein sequence
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                                                                                                 AAY81956 standard; protein; 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-00780496.
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                                                                                                                                                                                                                                                                              therapy; apoptosis; cancer.
                                                                                                                                                                               (first entry)
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Best Local Similarity 100.
Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
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N-PSDB; AAA07425.
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                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apoptosis.
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                                                                                                                                        AAY81956;
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                                                             RESULT 9
                                                                              AAY8195
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The present invention describes an antibody that binds to a human protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434; PRO4075; PRO3657; PRO1295; PRO1293; PRO1263; PRO4344; PRO4354; PRO4075; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer activity and can be used to diagnose tumours in mammals, by detecting complex formation when the antibody is contacted with test cells. Increased expression of genes encoding (I) can also be detected to diagnose tumours. Agents which inhibit the activity of (I), especially the antibodies, or an antisense oligonucleotide which hybridises to genes encoding (I), can be used to inhibit tumour growth, preferably by inducing cell death. Methods from the present invention can be used to identify compounds which inhibit the biological activity of (I). AAC58019 to AAC58102 represent PCR primers and hybridisation probes used in examples from the present invention for human PRO sequences. AAC58103 to AAC5812 and AAB24031 to AAB24040 represent human PRO sequences. AAC58103 to protein sequences given in the exemplification of the present invention
Antibodies specific for PRO polypeptides, used to diagnose and inhibit the growth of tumors in mammals, and to identify inhibitors of PRO
                                                                                                                                                                                                                                                                                                                    Human, tumour, diagnosis, neoplastic disease, proliferation, cancer, identification, tumourigenesis, anticancer, detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gurney AL, Roy MA, Watanabe CK,
                                                     241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                        241 SIYQGGIFELKENDRIFVSVINEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                      Human PRO1096 protein sequence SEQ ID NO:51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide activity or expression.
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                                                                                                                                                                               AAB24038 standard; protein; 281
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99WO-US020111.
99US-0162506P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
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N-PSDB; AAC58120.
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                                                                                                                                                                                                                                                                                                                                                                                                              WO200053750-A1.
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01-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-OCT-1999;
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                                                                                                                                                                                                                    AAB24038;
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ID AAB2
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The present sequence represents a human TRAIL (tumour necrosis factor (TNF) related apoptosis-inducing ligand) polypeptide. The specification describes a method for enhanced killing of tumour cells. The method comprises contacting a susceptible tumour cell with a synergistic mixture of a TRAIL receptor ligand and a diterpencid triepoxide in a combined dosage to kill at least 50 % of the cells. This mixture is synergistic, and so is active at lower doses and against otherwise resistant cell lines. The method is used for killing tumour cells, especially solid tumours or carcinomas (especially mammary carcinoma or non-small cell
                                                                                                                                                                                     FYXIYSQTYFRFQERIKENTKNDKQMVQYIXKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                 61 DDSYWDPNDEBSKMSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                     MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Killing of tumor cells, e.g. solid tumors or carcinoma, comprises administration of synergistic combination of diterpenoid diepoxide and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, TRAIL, tumour necrosis factor; TNP; diterpenoid triepoxide; TNF related apoptosis-inducing ligand; tumour cell; TRAIL receptor ligand; solid tumour; carcinoma; mammary carcinoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumor necrosis factor related apoptosis-inducing ligand.
                                                                                                                                                                                                                                      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                          241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of a human TRAIL polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 23-24; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                           AAB08545 standard; protein; 281 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-small cell lung carcinoma.
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100.0%; Score 281; DB 3; Length 281; 100.0%; Pred. No. 1.8e-266; tive 0; Mismatches 0; Indels (

Query Match
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Matches 281; Conservative

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1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE

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Sequence 281 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is human AGP-1, a type II transmembrane protein. Fusion proteins comprising an FC immunoglobulin region fused to the Netarninal portion of the AGP-1 protein have been produced. The fusion proteins can be used to induce apoptosis in a tissue, and to treat proliferative disorders, immune disorders, or virally-induced disorders. The proliferative disorders include cancers, such as breast, prostate, lung or colon cancer. The viral infections include hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune disorders may be autoimmune disorders or transplant rejection. Cardiovascular diseases such as arterioscales may also be treated. The AGP-1 containing fusion proteins have increased biological activity compared to the soluble AGP-1 proteins used in prior art therapies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; AGP-1; type II transmembrane protein; cytostatic; antiviral; antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV; human immunodeficiency virus; apoptosis; proliferative disorder; cancer; hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder; transplant rejection; cardiovascular disease; arteriosclerosis.
                                                                                                                                                                                                                                                  FYYIXSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusion protein of AGP-1 protein and an Fc region, used to treat proliferative disorders, immune disorders, and virally-induced disorders.
                                                                                                                                                                                                                              FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 240
                                                                                  DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                        DDSYMDPNDEESMNSPCWQVKWQLRQLVRXMILRTSEETISTVQEKQQNISPLVREKGPQ 120
                                                                                                                                                          RVAAHITGTRGRSNTLSSPNSKNBKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                         RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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                    MAMMEVOGGPSLGOTCVLIVIFTVLLQSLCVAVTYVYFINELKQMQDKYSKSGIACFLKE
                                      MAMMEVQGGPSLGQTCVLLVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                  SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                              121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSCHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                             Human, PRO, cytostatic, nootropic, neuroprotective, respiratory general,
antiinflammatory; antiangiogenic; immunosuppressive, immunostimulant;
PRO agonist; cancer, inflammatory disorder; immunological disorder.
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                                                                                                              MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                   121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                               DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                                             181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLIMKSARNSCWSKDAEYGLY
                         Gaps
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 Length 281;
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100.0%; Pred. No. 1.8e-266;
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99US-0170262P.
99WO-US030095.
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99US-0140650P.
99US-0141037P.
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                          Matches 281; Conservative
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               Similarity
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06-JAN-2000;
11-FEB-2000;
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Best Local
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                                                                                     Twenty eight nucleic acids encoding PRO polypeptides which are useful for treating various tumors, e.g. breast cancer, and other inflammatory, angiogenic and immunological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                        The present sequence is one of twenty eight novel PRO polypeptides. The PRO polypeptides and their agonists, including antibodies, peptides, and small molecule agonists, may be used to treat various tumours, e.g., cancers such as breast cancer, ovarian cancer, renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer, central nervous system cancer, melanoma or leukaemia. They are also useful for treating other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandlar, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunological
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                      Kabakoff RC;
                                                                                                                                                                                                                                                                                                                                   Gaps
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                      Henzel W,
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                     Hebert C,
Wood WI;
                      Gurney AL, He
Watanabe CK,
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                                                                                                                                     Claim 31; Fig 54; 188pp; English.
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                     Goddard A,
Smith V,
(GETH ) GENENTECH INC
                                                         2001-016509/02
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Apo2 ligand.
                                                                   N-PSDB; AAC91579
                                                                                                                                                                                                                                                                                       Sequence 281 AA;
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                    Baker KP, G
Shelton DL,
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                                                                                                                                                                                                                                                                                                                                       The present invention relates to a formulation comprising Apo-2 ligand and divalent metal ions. Apo-2 ligand and the formulation are useful for tracting cancers and viral infections. Addition of divalent metal ions for making Apo-2 ligand and formulations containing Apo-2 ligand results in increased yield and stability of Apo-2 ligand trimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                          Use of divalent metal ions for making Apo-2 ligand and in formulations containing Apo-2 ligand for increasing yield and stability of ligand trimers, useful for therapeutic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, tumour necrosis factor, TNF, cytokine, cytostatic, virucide, TNF related apoptosis inducing ligand, TRAIL; cancer, viral infection; human immunodeficiency virus; HIV, leukaemia; gene therapy; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKOMQDKYSKSGIACFLKE
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                                                    Leung
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/label= N_terminal_cytoplasmic_domain
                                                 H,
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100.0%; Pred. No. 1.8e-266;
ive 0; Mismatches 0;
                                                    Koumenis
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/label= Extracellular_domain
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                                            Kelley RF, Kou
okh Z, Simmons
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                                                                          Shahrokh Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE11031 standard; protein; 281
                                                                                                                                                                                                                                                                                        Claim 6; Fig 1; 60pp; English.
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Best Local Similarity 100.0
Matches 281, Conservative
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/label= T
                                                    Hymowitz
Pai R, Sh
(GETH ) GENENTECH INC
                                                                                                                              WPI; 2001-123012/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 281 AA;
                                                 Ashkenazi AJ,
O'connell M,
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The invention relates to a cytokine designated as tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis of certain target cells, including cancer cells and virally infected cells. The TRAIL polypeptides are useful in killing cancer cells, in treating viral infections (e.g. bovine viral diarrhoea or human melanoma), as a research reagent useful in studying apoptosis including the regulation of programmed cell death. TRAIL DNA sequences may be employed in developing a gene therapy approach to treating disorders mediated by defective or insufficient amounts of TRAIL, in the production of TRAIL polypeptides and as probes or primers in polymerase chain reactions (PCR). The present sequence is human TRAIL protein
                                                                                                                                                                                                                                                                                                                  New tumor necrosis factor related apoptosis inducing ligand polypeptides for treating viral infections (e.g. bovine viral diarrhea or human immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Col 45-48; 41pp; English
                                                                                                     95US-00548368.
96US-00670354.
98US-00048641.
                                                   99US-00320424
                                                                                                                                                         98US-00190046
                                                                                    95US-00496632
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                                                                                                                                                                                          (IMMV ) IMMUNEX CORP.
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                                                   26-MAY-1999;
                                                                                                                                     26-MAR-1998;
                                                                                   29-JUN-1995
                                                                                                                      25-JUN-1996
                04-SEP-2001
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                                                                                                   1 MAMMEVQGGPSLGGTCVLIVIFTVLLQSLCVAVTYVFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                            DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                        DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                                                                                                                                      PYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                       1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                     121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNIHLRNGELVIHEKG
                                     Gaps
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100.0%; Score 281; DB 4; Length 281; 100.0%; Pred. No. 1.8e-266; ive 0; Mismatches 0; Indels
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                                     Matches 281; Conservative
                  Local Similarity
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 Query Match
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AAB48350 standard; protein; 281 AA
                                               (first entry)
                                                             Human TL2 polypeptide.
                                              20-APR-2001
                               AAB48350;
RESULT 16
                BXXXXX
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DDSYWDPNDEESKNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240

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241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

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The invention relates to a human tumour necrosis factor (TNF) related
receptor, TR6. TR6 can be expressed by standard recombinant methodology.
The TR6 polypeptides are useful for treating chronic and acute
inflammation, rheumatoid arthritis, septicemia, autoimmune diseases (e.g.
inflammation, rheumatoid arthritis, septicemia, autoimmune diseases (e.g.
inflammation, rheumatoid arthritis, septicemia, autoimmune diseases (e.g.
to inflammation, restenosis, brain injury, AIDS, bone diseases cancer,
atherosclerosis, and Alaheimer's disease. These may also be used to
inhibit production of TNF-alpha and eicosanoids, as research reagents and
materials for discovering treatments and diagnostics to animal and human
diseases. The polypeptides may further be used as immunogens to produce
antibodies immunospecific for the TR6 polypeptides. The polynucleotides
may also be used as hybridization probes for CDNA and genomic DNA, for
solating full-length cDNAs and genomic clones encoding TR6 and of other
genes having high sequence similarity to TR6 gene, and for chromosome
contains also known as TRALI (MFF-related apoptosis-inducing ligand) and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New tumor necrosis factor related receptor TR6 polynucleotides and polypeptides useful for e.g. for treating chronic and acute inflammation, arthritis, septicemia, autoimmune diseases, infection, cancer, bone
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                                      antiinflammatory; immunosuppressive; cerebroprotective; vasotropic; antiathatic; anti-HIV; osteopathic; cytostatic; antiatherosclerotic; nootropic; neuroprotective, antiathritic; antirheumatic; antiischemic; gene therapy; vaccine; TNP-alpha; bone disease; cancer; TRAIL.
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                       necrosis factor; TNF; TNF related receptor; TR6; human; TL2;
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100.0%; Pred. No. 1.8e-266;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Page 26; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            Marshall LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a ligand for the TL2 polypeptide
                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                   12-JUN-2000; 2000WO-US016134.
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                                                                                                                                                                                                                                                                                                                                                                                            Young PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-112223/12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 281 AA;
                                                                                                                                                                                   WO200077191-A1
                                                                                                                                            Homo sapiens.
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The invention relates to treating an individual at risk for or suffering from infection with a pathogenic or opportunistic organism. The method involves administering a combination of two to five agents comprising:

(a) dendritic cell mobilisation factor; (b) dendritic cell maturation agent; (c) dendritic cell activation agent; (d) T cell enhancing factor; or (e) activated, antigen-specific T cells. The methods are useful for treating an individual at risk for or suffering from infection with a pathogenic or opportunistic organism, e.g. viruess (e.g. HIV), bacteria (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g. T. cruzi, which causes Chaga's disease). The methods are sepecially useful for treating an individual suffering from immunosuppression by method is useful for treating inflammations, chickenpox, oral or genital herpes, mononucleosis, multifocal leukoencephalogathy, hepatitis, AIDS, T cell leukemia or I cell lymphoma. The activated antigen-presenting dendritic cells are useful as a vaccine adjuvant. The present sequence
                                                                                                                                                                                                                                                                      Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial; fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV; tuberculostatic; cytostatic; human; TRAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating an individual suffering from infection, e.g. inflammation, chickenpox or AIDS, by administering a combination of dendritic cell mobilization factor or maturation agent, T cell enhancing factor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maliszewski CR, Butz EA, Miller RE;
241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represents a human TRAIL polypeptide fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 40-42; 43pp; English.
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                                                                                                              ABB08133 standard; protein; 281
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                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen-specific T cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  De Smedt IN,
                                                                                                                                                                                                                                 Human TRAIL polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMMV ) IMMUNEX CORP.
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                                                                                                                                                                                                                                                                                                                                                                                       WO200236141-A2.
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120

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1 MANMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE

1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE

100.0%; Score 281; DB 5; Length 281;

100.0%; Pred. No. 1.8e-266; ive 0; Mismatches 0;

281; Conservative

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Query Match Best Local Similarity

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                        121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                              240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating an individual with tumors or cancers, e.g. liver cancer or brain tumor, by administering a combination of dendritic cell populations, \mathtt{T} cell enhancing factors and activated, antigen-specific \mathtt{T} cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bearing subject. The method involves administering a combination of 2 to 5 agents comprising dendritic cell mobilisation factor, dendritic cell maturation agent, tumours filling agent, Tell enhancing factor or activated, antigen-specific Tells. The method is useful for treating tumours or cancers in a subject e.g. skin cancer, prostate cancer, liver cancer, tumours of the bone, brain or spinal cord, actinic keractosis, or cervical intraepithelia neoplasia. The present amino acid sequence represents the human TRAIL protein that was used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
                                                                                                            181 FYYIYSQTYFRPQEBIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
    RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                            PYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maliszewski
                                                                                                                                                    SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                                                                                                                                                      ABG31630 standard; protein; 281 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                    Human TRAIL protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200266044-A2.
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This invention relates to a novel method for enhanced killing of tumour cells comprising contacting a tumour cell with a synergistic combination of a death domain receptor ligand and a diterpenoid triepoxide. This method has cytostatic activity and works by blocking TNF-alpha mediated induction of c-IAP2 and c-IAP1. The method of the invention may be used for treating tumours, particularly solid tumours, e.g. carcinoma, mammary adenocarcinoma and non-small cell lung carcinoma also neurological malignancies, e.g. non-Hodgkin's lymphoma, malignancies, non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, malignant cutaneous T-cells, mycosis fungoides, non-MF cutaneous T-cell lymphoma, lymphomatoid papulosis, T-cell rich cutaneous lymphoid hyperplasia, bullous pemphigoid, discoid lupus erythematosus, lichen planus. The combination may be administered
DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                  61 DDSYWDPNDEBSWNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                              RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                           121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                          FYYIYSQTYFRFQEEIKENTKNDKQMVQXIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDABYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRAIL; TNF; apoptosis; tumour; death domain receptor ligand; diterpenoid triepoxide; cytostatic activity; c-IAP2; c-IAP1; carcinoma; mammary adenocarcinoma; non-small cell lung carcinoma; neurological malignancy; lichen planus; non-Hodgkin's lymphoma; chronic lymphocytic leukaemia; anti-angiogenic; malignant cutaneous T-cell; lymphomatoid papulosis; anti-metastatic; non-MF cutaneous T-cell lymphoma; mycosis fungoides; anti-tumour; T-cell rich cutaneous lymphoid hyperplasia; bullous pemphigoid; discoid lupus erythematosus; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of a synergistic combination of death domain receptor ligands and diterpenoid triepoxides for killing of tumor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human TNF related apoptosis inducing ligand (TRAIL) protein.
                                                                                                                                                                                                                                        241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABK13192.
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                                                                                                                                                                                                                                                                                                                                                                    DDSYWDPNDEESMNSPCWQVKWQLRQLVRXMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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with other active agents, e.g. anti-metastatic, anti-tumour or anti-angiogenic agents. The potent synersy between the diterpenoids and the death domain ligands allows increased killing at equivalent or lower doses, and can sensitise otherwise resistant cells. This sequence represents the human TNF related apoptosis inducing ligand (TRAIL) protein sequence. TRAIL is a death domain receptor used in the used method of the invention in combination with diterpenoid triepoxides to kill tumours by induction of apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of CPT-11 which is a chemotherapeutic agent of the topoisomerase I inhibitor class, and Apo-2 ligand receptor agonist for enhancing apoptosis in mammalian cells, or for treating cancer in a mammal.
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                                                                                                                                                                                                                                                               1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                         100.0%; Score 281; DB 5; Length 281; 100.0%; Pred. No. 1.8e-266; tive 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                              Matches 281; Conservative
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                                                                                                                                                                                                            Local Similarity
                                                                                                                                                          Sequence 281 AA;
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14-DEC-2000; 2000US-0256162P.

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The present sequence is that of human Apo-2 ligand (Apo-2L or TRAIL). The invention relates to methods of inducing apoptosis in mammalian cells, and especially to the topoisomerase I inhibitor class) to chemotherapeutic agent of the topoisomerase I inhibitor class) to synergistically induce apoptosis in mammalian cells, in particular mammalian cancer cells (claimed). The cells may be in cell culture or in a mammal, e.g. a mammal suffering from cancer or a condition in which induction of apoptosis in the cells is desirable. A claimed method of treating cancer in a mammal comprises administering CPT-11 and Apo-2L receptor agonist, where the CPT-11 is caministered about 6-72 hours prior to administration of the Apo-2L receptor agonist sequence) and anti-DRS coeptor agonist. Exposure of the cancer cells to CPT-11 and Apo-2L receptor agonist sequence) and anti-DRS of anti-DRS receptor attribodies. Exposure of the cancer cells to CPT-11 and Apo-2L receptor agonist leads to upregulation of DR4 and DR5 receptors, canti-DR5 receptor agonist leads to upregulation of DR4 and DR5 receptors.

Cativity, An example illustrates the synergistic inhibition of tumour controls and approach and activity and anti-DR5 corrections.
Claim 18; Page 79-80; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COLO205 colon carcinoma cells
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Sequence 281 AA;

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DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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                                                                                                                                                                                                                                    61 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                      1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
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                100.0%; Score 281; DB 5; Length 281; 100.0%; Pred. No. 1.8e-266; cive 0; Mismatches 0; Indels (
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Query Match
Best Local Similarity 100.
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Human Apo-2 ligand protein sequence SEQ ID NO:4. ABP51954 standard; protein; 281 AA (first entry) 09-OCT-2002

Bacterial host, protease, degP, prc, spr, anti-VEGF antibody, antibody, humanised, Apo2 ligand, anti-CD18, anti-tissue factor, 2C4, anti-CD20, anti-vascular endothelial growth factor; anti-Her-2, anti-CD40, Fab, anti-CD11a; Fab'2, Fab'2-leucine zipper fusion; anti-VEGF Fab.

Homo sapiens.

WO200248376-A2

20-JUN-2002

07-DEC-2001; 2001WO-US047581.

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in present interior describes an escipiant coil strain () described in chromosomal degp and precesse Degp and Prc, respectively, and harbouring a mutant spr gene, the product of mutant spr gene suppresses grawth phenotypes exhibited by strains harbouring prc mutants.

(1) is useful for producing a polypeptide, by culturing (1) comprising nucleic acid encoding the polypeptide, which is heterologous to the strain, such that the uncleic acid is expressed, and recovering the heterologous polypeptide from the strain. The heterologous polypeptide from the strain. The heterologous polypeptide is proteolytically sensitive. Culturing of (1) is performed in a fermentor of proteolytically sensitive. Culturing of (1) is performed in a fermentor of proteolytically sensitive. Culturing of (1) is performed in a fermentor of proteolytically sensitive. Culturing of (1) is performed in a fermentor of proteolytically sensitive. Culturing of (1) is performed in a fermentor of polypeptide is an antibody (numanised or full-length estrain. The polypeptide is an antibody (numanised or full-length estrain. The polypeptide is an antibody is an anti-dody is an antibody. The antibody is also an antibody fragment having a light chain (kappa light chain). The antibody fragment having a light chain (kappa light chain). The antibody fragment having a light chain (kappa light chain). The antibody fragment staper fusion, anti-cissue factor Fab'2-leucine zipper fusion, anti-cissue factor Fab'2-leucine zipper fusion with a 6-histidine tag, anti-citsue capted fragment anti-vEGF Fab, with or without a histidine tag, and anti-citsue capper fusion with a 6-histidine tag, and anti-citsue inversents a human Apo-2 ligand amino acid sequence from the present
                                                                                                                                                                                                                              Novel Escherichia coli strain useful for producing polypeptide, deficient in degP and prc encoding protease, and harboring mutant spr gene, product of gene suppresses growth phenotypes of strains harboring prc mutants.
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                                                                                                                                                                                                                                                                                                                                                                                        present invention describes an Escherichia coli strain (I) deficient
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nes 281; Conserv
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The present invention relates to a method of producing a population of activated, Cryptococcus neoformans antigen-presenting dendritic cells, comprising causing the obtained dendritic cells to present the antigen and maturing the dendritic cells. The activated, C. neoformans antigen-expressing dendritic cells are useful for treating, or as vaccines or vaccine adjuvants against, C. neoformans infection, or for generating antigen-specific T cells, The present sequence is a human protein shown in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                      Producing a population of activated, Cryptococcus neoformans antigen-
presenting dendritic cells for preventing or treating C. neoformans
infection comprises causing the obtained dendritic cells to present the
                                   C neoformans antigen expressing dendritic cell related protein #4.
                                                                    Human, fungicide, fungal infection, dendritic cell; antigen;
Cryptococcus neoformans; vaccine, immunostimulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 29-30; 32pp; English.
                                                                                                                                                                                                                               14-DEC-2001; 2001WO-US048288
                                                                                                                                                                                                                                                                04-JAN-2001; 2001US-0259653P.
(first entry)
                                                                                                                                                                                                                                                                                               (IMMV) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-674896/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 281 AA;
                                                                                                                                                          WO200266053-A2.
                                                                                                                           Homo sapiens.
                                                                                                                                                                                            29-AUG-2002.
                                                                                                                                                                                                                                                                                                                                    Thomas EK;
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DDSYNDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                             61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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100.0%; Score 281; DB 5; L
100.0%; Pred. No. 1.8e-266;
                100.0%; Pred. ...
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24-SEP-2002 (first entry)

AAU79593;

RESULT 23
AAU79593
ID AAU79
XX
AC AAU79
XX
DT 24-SE

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Certural culterentiation and acvelopment of multicellular organisms.

Apoptosis is induced by certain cytokines which include TNF and TRAIL

(also referred to as Apo-2 ligand, Apo-2L). TRAIL is a type II membrane

containing receptors, DR4 and DR5, as well as two decoy receptors, DR1

containing receptors, DR4 and DR5, as well as two decoy receptors, DR1

containing receptors, DR4 and DR5, as well as two decoy receptors, DR1

containing receptors, Interferons, induces apoptosis in tumour cells, whereas

normal cells are relatively resistant without showing significant toxic

side effects. Thus, TRAIL has the potential to be a very useful

antitumour agent. The naturally occurring sphice variants may differ in

their cellular distribution, expression levels/timing and activity.

Conternining these factors could provide possible mechanisms for the

induction of apoptosis of tumours cells. The splice variant polypeptides

and polynucleotides can be used in gene therapy, to raise antibodies, to

cheeceft the levels, distribution and ratios of expression of TRAIL, and

its splice variants, in a biological sample and to identify compounds

which bind the variant TRAIL products and modulate its activity (agonists

conduction of apoptosis of the amino acid sequences, are useful for causing a

cytotoxic effect in cancer cells and for treatment of diseases which can

control and or prevented by lowering or raising the level of

the amilorated, cured or prevented by lowering or raising the level of

the amilorated, cured or prevented by lowering or raising the level of

the amilo acid sequences. The antibodies may also have a therapeutic

cutility in blocking or decreasing the activity of the TRAIL variant

products. Diseases that may be treated include cancer, neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention discloses isolated, naturally occurring, polypeptide splice variants of human tumour necrosis factor (TNF) related apoptosis inducing ligand (TRALL). Apoptosis, or programmed cell death, occurs during normal cellular differentiation and development of multicellular organisms.
                                                              Human; cytostatic; neuroprotective; immunosuppressive; splice variant; tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand; TRAIL; apoptosis; programmed cell death; differentiation; development; cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B; type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer; therapeutic; neurodegenerative disease; autoimmune disease; aging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New splice variants of tumor necrosis factor-related apoptosis inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat diseases or disorders associated with low expression of the variants.
                     Human TNF-related apoptosis inducing ligand (TRAIL) protein.
                                                                                                                                                                                                                                                                                                                                                                 .38
te= "Transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                               39. .281
/note= "Extracellular domain"

    16
    note= "Cytoplasmic domain"

                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "TNF domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 9; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAY-2001; 2001US-00855544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAY-2000; 2000IL-00136156.
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(KHOS/) KHOSRAVI R.
(SAVI/) SAVITZKY K.
                                                                                                                                                                                                        chromosome 3q26.
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                                                                                                                                                                                                                                                      Homo sapiens.
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N-PSDB; ABX15469

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diseases, autoimmune diseases, diseases involved in the non-normal development of tissues and aging. TRAIL's gene is located on chromosome 3926. The sequence presented is the wild-type human TNF-related apoptosis inducing ligand (TRAIL) protein
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                                                                                                                                                                                                                                             DDSYWDPNDEBSWNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGFQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; Apo-2; apoptosis; induce apoptosis; inhibit apoptosis; INFR; nuclear factor-kappa B; NF-kappa B; Apo-2 ligand; AIDS; tumour acrosis factor receptor; acquired immunodeficiency syndrome; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; multiple sclerosis; rethintis pigmentosa; cerebellar degeneration; aplastic anaemia; myocardial infarction; stroke; reperfusion injury; toxin-induced liver disease; cancer; lupus; herpes virus infection.
                                                                                                                                                                 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                               MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVVYFTNBLKQMQDKYSKSGIACFLKE
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                                                                                                        Query Match
100.0%; Score 281; DB 5; L
Best Local Similarity 100.0%; Pred. No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0;
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/note= "N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Apo-2 ligand protein.
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                                                                                                       Query Match
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                                                                             Sequence 281 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-SEP-1997;
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ABG73861
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The invention relates to an Apo-3 polypeptide having an extracellular domain (ECD) sequence and a death domain sequence. The Apo-3 polypeptide domain (ECD) sequence and a death domain sequence. The Apo-3 polypeptide cateriority in mammalian cells. Human Apo-3 exhibits similarities to the tumour necrosis factor receptor (TNFR) family of polypeptides. The invention also relates to a chimeric molecule comprising an extracellular domain sequence comprising residues 1-198 of Apo-3 fused to a heterologous mainto acid sequence. The Apo-3 polypeptide is useful therapeutically to induce apoptosis in ammalian cells. Decreased levels of apoptosis has been associated with conditions such as cancer, hugus, and herpes virus infection. Increased levels of apoptosis are associated with diseases such as acquired levels of apoptosis are associated with diseases such as acquired clasease, amyorrophic lateral associated with disease, parkinson's classase, amyorrophic lateral as clerosis, multiple sclerosis, retinitis pigmentosa, cerebellar degeneration, aplastic anaemia, myocardial infarction, stroke, reperfusion injury, and toxin-induced liver disease. The Apo-3 polypeptide is also useful in non-therapeutic applications such as in quantitative diagnostic assays a control against which samples containing unknown quantities of Apo-3 may be prepared, in generating anti-bodies, as standards in assays for Apo-3 in affinity purification techniques, and in competitive-type receptor binding assays. The chimeric molecule is useful therapeutically to inhibit apoptosis or nuclear factor Apo-3 antibodies. The present sequence represents polypeptide sequence of the human Apo-2 ligand protein which is also reported to be involved in apoptotic cell death. In the current invention the apoptocit of the Apo-2 ligand protein was measured on human lymphoid cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAMMEVQGGPSIGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                           Novel isolated Apo-3 polypeptide useful for inducing apoptosis in mammalian cells, for generating antibodies, in affinity purification techniques, and in competitive-type receptor binding assays.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٥;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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100.0%; Pred. No. 1.8e-266;
ive 0; Mismatches 0;
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                                                                                                                                                Example 4; Fig 4; 52pp; English
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Best Local Similarity 100.
Matches 281; Conservative
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120 120 180 180 240

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apoptosis, or as immunogens used in control and interests the antibodies. The antibodies may be used to block excessive apoptosis, for instance in neurodegenerative disease, or to block potential autoimmune/ inflammatory effects of Apo-3 resulting from NF-kappaB activation. The nucleic acid sequences are useful as diagnostics for tissue-specific typing, for preparing Apo-3 polypeptides, or for generating transgenic or knockout animals are useful in developing and screening of therapeutically useful reagents. The present sequence represents the amino acid sequence of human Apo-2 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated Apo-3 polypeptide. The Apo-3 polypeptides are useful for stimulating or inducing apoptotic activity in mammalian cells e.g. cancer cells, or for in vivo or ex vivo gene therapy techniques. The Apo-3 chimeric molecules are useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated Apo-3 polypeptides, useful for stimulating or inducing apoptotic activity in mammalian cells, e.g. cancer cells, or for in vivo or ex vivo gene therapy techniques.
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 neurodegenerative disease; immunosuppresive; tissue typing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                    28-MAR-2002; 2002US-00112193
                                                                                                                                                                      96US-0026943P
97US-00928069
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                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                       WPI; 2003-438872/41.
N-PSDB; ACA61696.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 281 AA;
                                                                  US2003004313-A1
                                                                                                                                                                                                                                                         Ashkenazi AJ;
                                  Homo sapiens.
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11-SEP-1997;
                                                                                                  02-JAN-2003
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AC ABU7
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Human; tumour; cancer; neoplasia; liver cancer; marcoma; breast cancer; ovarian cancer; renal cancer; colorectal cancer; melanoma; uterine cancer; prostate cancer; lung cancer; bladder cancer; leukaemia;
                                                                     gastric cancer; pancreatic cancer; vulval cancer; thyroid cancer; central nervous system cancer; hepatic carcinoma; glioblastoma; central disorder; glial disorder; aetrocytal disorder; hypothalamic disorder; glandular disorder; macrophagal disorder; epithalial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; angiogenic disorder; immunologic disorder.
                   Human neoplasia inhibiting PRO polypeptide PRO1096.
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98US-0096891P.
98US-0096894P.
98US-0099803P.
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98US-0101476P.
98US-0107783P.
98US-0108849P.
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99WO-US005028.
99US-0123618P.
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99WO-US008615.
99US-0131294P.
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99US-0140650P.
99US-0141037P.
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98US-0100263P.
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99US-0115554P.
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(first entry)
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                                                                                                                                                                 US2002192209-A1.
                                                                                                                                             Homo sapiens.
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08-MAR-1999;
10-MAR-1999;
 09-JUN-2003
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22-DEC-1998
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12-JAN-1
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2000WO-US003565

11-FEB-2000;

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Claim 32; Fig 54; 186pp; English.
                                                    2000WO-US022031.
2000WO-US023522.
                         2000WO-US008439
                                                              2000US-00709238
                                                                   :000WO-US030873
                                                                                             2001US-00866034,
                                                                                                                  2001WO-US017800.
2001US-00882636.
                                                                                                                                                  2001US-00924419.
                                                                                                                                                                      29-AUG-2001; 2001WO-US027099.
04-SEP-2001; 2001US-00946374.
                                                                                                  2001WO-US017092
                                                                                                                                                                                     (GETH ) GENENTECH INC
                                                                                                                                                                                                Goddard A,
Smith V,
                                                                                                                                                                                                                WPI; 2003-328851/06.
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                                                  11-AUG-2000;
23-AUG-2000;
08-NOV-2000;
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25-MAY-2001;
01-JUN-2001;
                    15-MAR-2000;
                                        30-MAY-2000;
                                                                              28-FEB-2001;
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                                                                                                                                 29-JUN-2001;
                                                                                                                                                 06-AUG-2001;
                                                                                                                                                                 28-AUG-2001;
                                                                                                                                                                                               Baker KP, G
Shelton DL,
                                                                                                                                                                                                                                               disorders.
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Henzel W, Kabakoff RC; Gurney AL, Hebert C, Watanabe CK, Wood WI; Novel isolated PRO polypeptides e.g. PRO240, PRO381, PRO540, useful for treating tumor, preferably cancer, or for treating neuronal, glial, hypothalamic, stromal, inflammatory, angiogenic and immunologic

The invention relates to an isolated secreted and transmembrane polypeptide, designated as PRO polypeptide. PRO polypeptide lacking its associated signal peptide or PRO polypeptide extracellular domain with or without its associated signal peptide. The PRO polypeptide or an antibody binding to it is useful for inhibiting the growth of a tumor cell. A composition containing a PRO polypeptide is useful for inhibiting neoplastic cell growth or for treating a tumour, preferably cancer (such as liver, breast, ovarian, renal, colorectal, uterine, prostate, lung, cancer, hepatic carcinomas, sarcomas, glioblastomas, melanoma or leukaemia) in a mammal. The PRO polypeptide is useful for identifying its gonists. The PRO polypeptide or an antibody binding to it is useful in the preparation of a medicament for treating a condition which is composite to the PRO polypeptide or an antibody binding to it. The PRO POLYPEPTION of the preparation of a medicament for treating a condition which is constituted or an antibody binding to it. The PRO POLYPEPTION of it is also useful for treating a condition and a medicament for treating a condition which is constituted or an antibody binding to it. The PRO POLYPEPTION of the preparation of a medicament for treating a condition which is contained to the preparation of a medicament for treating a condition and the properties or an antibody binding to it. The PRO POLYPEPTION of the preparation of a medicament for treating and the preparating the properties or an antibody binding to it. The PRO PRO POLYPEPTION of the preparation of a medicament for treating and the preparation of a medicament for treating and the preparation of a medicament for treating and the preparation of a medicament for treating and the preparation of a medicament for treating and the preparating the preparation of a medicament for treating and the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the p neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelle, inflammatory, angiogenic and immunologic disorders. The present sequence represents the amino acid sequence of a PRO polypeptide of the invention

Sequence 281 AA;

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                                                                                                                                                                                              181 FYXIXSQTYFRFQEEIKENTKNDKQNVQXIXKTSYPDPILLMKSARNSCWSKDAEYGLY 240
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                                                      1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
                                       1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Human TNF-related apoptosis inducing ligand (TRAIL) protein.
               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; allergic disease; allergy; TNF; TRAIL; diagnosis;
tumour necrosis factor-related apoptosis inducing ligand;
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100.0%; Pred. No. 1.8e-266; ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                          ABG72738 standard; protein; 281 AA.
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(NIGE-) JAPAN GEN AGENCY NATION.
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                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
             281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atopic skin inflammation.
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Best Local Similarity
Matches 281; Conserv
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The invention discloses a method for examining allergic diseases, which comprises measuring the expression level of tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) gene in a specimen from the patient and comparing this level with the level in healthy persons. TRAIL gene expression is decreased in patients. The nucleic acids and polypeptide can be used to screen for agents for the treatment of allergic diseases, possibly using a transgenic rodent as a model animal for the disease, with effectiveness determined by changes in expression levels or protein activity. The method is useful for the diagnosis, examination, prevention and treatment of allergic diseases, including atopic skin inflammation. The sequence presented is the human TRAIL

Disclosure; Page 51-52; 58pp; Japanese.

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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, TNF-related apoptosis-inducing ligand, Kaposi's sarcoma; cancer, hyperproliferative disorder; rheumatoid arthritis, Parkinson's disease; meurodegenerative disorder, Alzheimer's disease; Hashinoto's disease; allergic disorder; acquired immune deficiency syndrome; ocular disease; myasthenia gravis; autoimmune disorder; Huntington's disease; vaccine; septic shock; multiple sclerosis; inflammatory disorder; liver injury; infectious disease; wayelodysplastic syndrome; cardiovascular disorder; graft-versus-host disease; thrombotic microangiopathy; aplastic anaemia; ischaemic injury; anorexia; diabetes; ulcerative colitis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel antibody against TNF-related apoptosis inducing ligand, useful for preventing, treating and ameliorating cancers and other hyperproliferative disorders, binds immunospecifically to TRAIL receptor # polypeptide.
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                                                                                      Length 281;
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                                                                                 100.0%; Score 281; DB 6; L
100.0%; Pred. No. 1.8e-266;
ive 0; Mismatches 0;
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07-MAX-2002; 2002US-0377973P.
15-AUG-2002; 2002US-0403376P.
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                                                                                                        Local Similarity
                                            Sequence 281 AA;
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  protein
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The invention relates to antibodies that immunospecifically bind to tumour necrosis factor (TMF)-related apoptosis-inducing ligand (TRAIL) receptors (TRMIL-R). Antibodies of the invention are useful for treating, preventing or antellorating cancer (e.g. cancers of pancreas, uterine, breast, colon, lung and gastrointestine and Kaposi's sarcoma) and other hyperproliferative disorders, neurodegenerative disorders (e.g. parkinson's disease, Alzheimer's disease and Huntington's disease), parkinson's disease, Alzheimer's Hashimoto's disease and immunodeficiency syndrome, inflammatory disorders (e.g. asthma, allergic disorders and relumnodeficiency syndrome), inflammatory disorders (e.g. asthma, allergic disorders and relumnode infections), myelodysplastic syndromes (e.g. aplastic anaemia') graft-versus-host disease, ischeemic injury, liver injury, toxin-induced liver disease, septic shock, cachexia, anorexia and proliferative disorders. Antibodies of the invention are also useful for treating cardiovascular disorders, cachexia, anorexia and proliferative disorders. Collabetes, coular disorders disorders, thromboric microangiopathies, and ulcerative collits and for wound healing. The invention is also used in the prepare vaccines. The present sequence is human TRAIL protein also
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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100.0%; Pred. No. 1.8e-266;
Live 0; Mismatches 0;
Example 2; Page 392-393; 405pp; English.
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The invention relates to an antibody that specifically binds: (a) the human tumor necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) protein appearing as ABU08558, (b) a soluble human TRAIL protein appearing a polypeptide; (C) a polypeptide Comprising amino acids 124-276 of ABU08558, or (d) a fragment of the TRAIL protein. Also included is an antigen-binding fragment of the antibody (a monoclonal antibody), a hybridoma cell line that produces the antibody The antibody); sused in assays to detect the presence of TRAIL polypeptides, either in vitro or in vivo, purifying TRAIL by affinity chromatography, blocking binding of TRAIL, or target cells and thus inhibiting a biological activity of TRAIL. The antibody is useful for treating disorders mediated or exacerbated by TRAIL, e.g. thrombotic microangiopathies, e.g. thrombotic transmort (TRAIL, e.g. thrombotic microangiopathies, e.g. thrombotic (TRAIL, e.g. thrombotic microangiopathies, e.g. thrombotic (Even though it can strike children as well) small blood vessel clotting disorders e.g., cardiac problems in paediatric AIDS patients and systemic uppus erythematosus (SLE). The present sequence represents human TRAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                124. .276
/note= "This region is specifically claimed in claim 20"
276. .281
/note= "C-terminal fragment specifically claimed in claim
26"
note= "N-terminal fragment specifically claimed in claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Col 45-48; 40pp; English.
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96US-00670354.
98US-00048641.
98US-00190046.
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N-PSDB; ABX93869.
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                                                                                                                                                                                                                                                                                                                  18-FEB-2003
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The invention relates to compositions comprising heterotrineric complexes of tumour necrosis factor (TNF) ligand family members, and their use in the detection, prevention and treatment of disease. In one embodiament, the heterotrimeric complex comprises full-length or extracellular to portions of TRAID and full-length or extracellular portions of other TNF ligand family members, preferably RAMIC. The heterotrimeric complexes of the invention are useful for treating an autoimmune disease, cancer or osteoporosis, and particularly for inhibiting cancer cell proliferation, increasing B cell proliferation, or inducing apoptosis of T cells. A claimed method of inducing apoptosis of T cells comprises administering a heterotrimeric complex consisting of FasL and LIGHT, TNF-alpha, theretotrimeric complex consisting of FasL and LIGHT, TNF-alpha, between the administering a heterotrimeric complex consisting of T cells comprises administering of T cells comprises administering of T cells comprises consisting of TRAIL and CD40L or RAMIC. A claimed method of treating osteoporosis of TRAIL and CD40L or RAMIC. A claimed method of treating osteoporosis comprises administering an antibody against a complex comprising RAMIC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New heteromultimeric complex having a first polypeptide member of the tumor necrosis factor (TNF) ligand family, and a second different memb of TNF ligand family, useful for treating cancer, osteoporosis or an
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                                                                                                                                                                                                                                                                                                             Human; TRAIL; tumour necrosis factor; ligand; cytostatic;
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                   241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
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100.0%; Pred. No. 1.8e-266;
ive 0; Mismatches 0;
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                                                                                                                                            ABR42313 standard; protein; 281
                                                                                                                                                                                                                                                                                                                                      immunomodulator; osteopathic.
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                                                                                                                                                                                                                                                                        Human TRAIL protein.
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DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                            Human; TRAIL receptor; tumour necrosis factor; TNF; light chain variable region TNF-related apoptosis-inducing ligand; antibody; VH; VL; cancer; heavy chain variable region; TR4; TR5; TR7; TR1; apoptosis; hyperproliferative disorder; hybridoma cell line; Kaposi's sarcoma; graft-versus-host disease; GVHD; infectious disease; AIDS; acquired immunodeficiency syndrome; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; autoimmune disorder; multiple sclerosis; Behcet's disease; lupus erythematosus; inflammatory disease; rheumatoid arthritis; psoriasis; wound healing; cardiovasculat disorder; angiogenesis; immune response;
                              RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                       121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                    FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY
                                                                                                                                              SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                                                                                                                                                                                                    Human TRAIL receptor-associated protein.
                                                                                                                                                                                                                                                ABG71905 standard; protein; 281 AA
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16-NOV-2000; 2000US-024847P.
27-NOV-2000; 2000US-025904P.
04-UUN-2001; 2001US-029501EP.
09-OCT-2001; 2001US-0327359P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chemotherapeutic agent
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CC cancers, and other hyperproliferative disorders) using the antibodies, a hybridoma cell line selected from the hybridoma cell lines contained in ATCC Deposit No. PTA-2729, PTA-268, PTA-3269, PTA-2730, PTA-2729, PTA-2289. PTA-3269, PTA-3729, PTA-2289. PTA-3269, PTA-2730, PTA-2729, PTA-2289. PTA-3269, PTA-2730, PTA-2729, PTA-2289. PTA-3269, PTA-2731 and the antibodies expressed by these contained a disease or disorder associated with increased or decreased apoptosis, e.g. cancer (such as colon, breast, uterine, carried associated with increased or decreased apoptosis, e.g. cancer (such as colon, breast, uterine, contained (ALDS), or neurodegenerative disorders (e.g. Alzieimer's contained (ALDS), or neurodegenerative disorders (e.g. Alzieimer's disease, parkinson's disease), autoimmune disorders like multiple sclerosis, Behcet's disease, lupus erythematosus, inflammatory diseases can disorders and in regulating immune response. The promoting angiogenesis, wound healing, and in regulating immune response. Many other diseases and disorders are listed in the specification. The artibody is administered in combination with a chemotherapeutic agent selected from irinotecan, paclitaxel (TRXOL (RTW), and gemcitabine. The antibody is useful as a diagnostic tool to monitor the expression of TRAIL receptor expression on cells, to detect, purify, and target the polypeptides, and in immunosasys for qualitatively and quantitatively measuring levels of TRAIL receptor polypeptides. The present sequence is a human TRAIL receptor associated protein. Note: The present sequence is included in the sequence listing but is not referred to anywhere else in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAMMEVQGGFSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-MAR-2003
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ABP60546
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Homo sapiens

acid sequence having 95 % identity to a second amino acid sequence of the variable heavy chain or light chain-complementarity determining regions (WHCDR1)/VLCDR1, VHCDR2/VLCDR2 or WHCDR3/VLCDR3 appearing as ABG71906-ABG71911 being specific for human TRAIL receptors 1-4 (TNF (tumour necrosis factor)-related apoptosis-inducing ligand receptor, also produces TR4, TR5, TR7 and TR10). Also included are an isolated cell that produces the antibody, an antibody that binds the same epitope on a TR4 polypeptide as the antibodies detailed above, detecting expression of a TR4 polypeptide (or detecting, diagnosing, prognosing or monitoring

Novel antibody for treating, or preventing disease or disorder, comprises amino acid sequence having identity to other amino acid sequence of either variable heavy/light chain-complementarity determining regions.

invention relates to an isolated antibody comprising a first amino

Disclosure; Page 366; 375pp; English.

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(HUMA-) HUMAN GENOME SCI INC.
           22-MAY-2002; 2002WO-US016106.
                24-MAY-2001; 2001US-0293100P.
                                 WPI; 2003-156740/15.
WO200294192-A2.
     28-NOV-2002.
                                               syndrome
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Novel isolated antibody that immunospecifically binds tumor necrosis factor delta, useful for treating, preventing or ameliorating Non-Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's

Disclosure; Page 216-217; 225pp; English.

The antibody of the invention has dermatological, immunosuppressive, antialibrative runner, antiarthatic, cytostatic, antianaemic, antialibratic, antiarthatic, cytostatic, antianaemic, antialibratic, antiarthatic, cytostatic, antianaemic, tuberculostatic, antialabetic, antiarthatic, antialmatic, antialabetic, antialostatic, antialabetic, antialosoriatic, anti-HIV, tuberculostatic, antialabetic, antialosoriatic, anti-HIV, antiarteriosclerotic, vasotropic, thyromimetic, and haemostatic activity. The antibody or its fragment are useful for treating, preventing or annibody at its fragment are useful for treating, preventing or human, disease or disorder such as autoimmune disease, and graft versus cythematosus, rhematodia arthritis or Sjogren's systemic lupus erythematosus, rhematodia arthritis or Sjogren's systemic lupus erythematosus, rhematodia arthritis or Sjogren's systemic lupus erythematosus, rhematodia arthritis or Sjogren's systemic lupus and disease or disorder associated with aberrant APRIL or APRIL receptor expression or aberrant function of APRIL or APRIL or APRIL or APRIL or APRIL receptor expression or aberrant function of APRIL or APR The invention relates to a novel antibody or its fragment, which immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL).

Sequence 281 AA;

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                                                                                                                              DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                         61 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                    240
                                                               1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
                                                                                            1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
                                                                                                                                                                                                                                                                                      0
100.0%; Score 281; DB 6; Length 281; 100.0%; Pred. No. 1.8e-266;
                                   0; Indels
                                                                                                                                                                                                                                                                                                                               SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                     Mismatches
                                  0
                                  Matches 281; Conservative
                    Similarity
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 Query Match
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                    Best Local
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TRAIL receptor; TR4; cancer; Kaposi's sarcoma; cerebellar degeneration; Alzheimer's disorder; neurodegenerative disorder; immume disorder; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa; Huntington's disease; amyotrophic lateral sclerosis; retinitis pigmentosa; Huntington's disease; Hashimoto's thyroiditis; biliary cirrhosis; Behcer's disease; Sologren's syndrome; asthma; biliary cirrhosis; Behcer's disease; Crohn's disease; allergic disorder; glowerulonephritis; lumune deficiency syndrome; myasthenia gravis; polymyositis; inflammatory disorder; rheumatoid arthritis; septic shock; infectious disease; acquired immunodeficiency syndrome; viral infection; infortion; no soliferative disorder; myelodysplastic syndrome; viral infection; ischaemic injury; myocardial infarction; reperfusion injury; cachexia; anorexia; stroke; cardiovascular disorder; peripheral artery disease; limb ischaemia; arrhythmia; congestive heart failure; neovascularisation; ocular disorder; wound healing; anglogenesis; transplantation; human.
                                                 AAE36258 standard; protein; 281 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        Human TR4 ligand, TRAIL protein.
                                                                                                                                                                                                                                                                                      26-JUN-2003 (first entry)
                                                                                                                                                                             AAE36258;
AAE36258
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Homo sapiens.

WO200297033-A2.

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05-DEC-2002.
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07-MAY-2002; 2002WO-US014268

2001US-0293473P 2001US-0294981P. 2001US-0309176P. 2001US-0323807P. 2001US-0327364P. 2001US-0331044P. 2001US-0331310P. 2001US-0341237P 2002US-0369860P 25-MAY-2001; 04-JUN-2001; 02-AUG-2001; 09-OCT-2001; 07-NOV-2001; 14-NOV-2001; 05-APR-2002; 21-SEP-2001; 20-DEC-2001;

(HUMA-) HUMAN GENOME SCI INC.

Vaughan TJ; Salcedo T, Ruben SM, Rosen CA, Albert VR, Dobson CL, WPI; 2003-140454/13. Novel antibody useful for treating cancers and other hyperproliferative disorders, immunospecifically binds to TRAIL receptor and comprises variable heavy or light chain complementarity determining regions.

Disclosure, Page 300-301; 301pp; English.

The present inverting terrates of the invention are useful for treating, preventing or ameliorating cancer (e.g. colon, breat, uterine, pancreatic, lung, gastrointestinal or central nervous system cancer e.g. medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in human. They are useful for detecting expression of TR4 polypeptide and detecting, diagnosing, prognosing or monitoring cancers and other hypercorrecting, diagnosing, prognosing or monitoring cancers and other hypercorrecting, diagnosing, prognosing or monitoring cancers and other hypercorrecting, preventing or ameliorating neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, cerbnitis pigmentosa, cerbelalar degeneration and Huntington's disease, immune disorders (e.g. lupus, rheumatoid arthritis, multiple sclerosis, slogren's syndrome, biliary cirrhosis, Behcet's disease, Crohn's disease, polymyositis, immune-related glomerulonephritis, myasthenia gravis, disorders (e.g. asthma, allergic disorders and rheumatoid arthritis), infectious diseases (e.g. acquired immunodeficiency syndrome (AlbS), herpes viral infections and other viral infections) and proliferative present invention relates to novel antibodies that immunospecifically

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disorders. They are also useful for treating myelodysplastic syndromes (e.g. aplastic anaemia), ischaemic injury (such as that caused by stroke, myocardial infarction and reperfusion injury), septic shock, cachexia, anorexia and toxin-induced liver diseases (such as alcohol). They are also useful for treating cardiovascular disorders including peripheral artery diseases such as limb ischaemia, arrhythmia, congestive heart failure and cardiovascular tuberculosis, diseases or disorders associated with neovascularisation and ocular disorders, for wound healing, for promoting angiogenesis and as adjuvants to enhance immune responsiveness to specific antigen e.g. viral antigen. They are also useful in the preparation or recovery from surgery, trauma, radiation therapy and transplantation. The present sequence is human TR4 ligand, TRAIL protein
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Sequence 281 AA;

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RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                 FYXIYSQTYFRFQEEIKENTKNDKQMVQXIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                             PYXIXSQTYFRFQEEIKENTKNDKQMVQXIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 240
                                                                                                                          DDSYWDPNDEESMINSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                               9
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                                                                            1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                 121 RVAAHITGIRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                  Gaps
                                0;
   Length 281;
                             0; Indels
                                                                                                                                                                                                                                                                                                                 281
                                                                                                                                                                                                                                                                                                                              SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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100.0%; Score 281; DB 6; L
100.0%; Pred. No. 1.8e-266;
iive 0; Mismatches 0;
                             Matches 281; Conservative
              Best Local Similarity
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Human TNF-related apoptosis-inducing ligand (TRAIL). AAO31151 standard; protein; 281 06-OCT-2003 (first entry) AA031151; RESULT 34

complementarity determining region; CDR; light chain variable domain; VL; TRAIL receptor 7; TR7; tumour necrosis factor; KILLER; death receptor 5; TRAIL receptor 7; TRAIL-R2; TNF-related apoptosis-inducing ligand; Kaposi's sarcoma; central nervous system, medulloblastoma; neuroblastoma; graft versus host disease; antibody therapy; noorropic; AIDS; acquired immune deficiency syndrome; neurodegenerative disorder; immunosuppressive; neuroprotective; antibody therapy; antibody. Human; protein coordinate data; heavy chain variable domain; VH; cancer;

20-DEC-2001; 2001US-0341237P. 05-APR-2002; 2002US-0369877P. 04-JUN-2002; 2002US-0384828P. 18-JUL-2002; 2002US-0396591P. 15-AUG-2002; 2002US-0403370P. 19-DEC-2002; 2002WO-US040597 WO2003054216-A2 03-JUL-2003.

Homo sapiens

Human TNF-related apoptosis inducing ligand TRAIL Incyte 059509CD1

(first entry)

05-SEP-2003

Z

ABO25125 standard; protein; 281

AB0251;

Human; DNA methylation; cancer; colon cancer.

US2003013099-A1

Homo sapiens.

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61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                      VHCDR1 (heavy chain variable domain complementarity determining region), VHCDR2, VLCDR3, VLCDR1 (light chain variable domain complementarity determining region), VLCDR2 or VLCDR3. The antibody or its fragment immunospecifically binds TRALL (tumour necrosis factor; TNF-related apoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as TRALL receptor 2 (TRAIL.R2), death receptor 5 (DR5) and KILLER. The antibody or its fragment is useful for treating, preventing or ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or gastrointestinal cancer or Kaposi's sarcoma or cancer of the central nervous system such as medulloblastoma, neuroblastoma or giloblastoma or graft versus host disease, AIDS (acquired immune deficiency syndrome) or a neurodegenerative disorder. The invention is useful in antibody therapy. The present sequence is human TRAIL
                                                                                                                                                                                                               lung or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated antibody or its fragments such
                                                                                                                                                                                 New antibody or its fragment, useful for treating, preventing or ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lur gastrointestinal cancer, or Kaposi's sarcoma or, graft versus host
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                                                                                           Rosen CA, Humphreys R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                        Disclosure; Page 297-298; 301pp; English.
13-NOV-2002; 2002US-0425737P.
                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281; Conservative
                                                                                           Salcedo I, Albert VR,
                                                                                                                                       WPI; 2003-569250/53.
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                                                                                                                                                                                                                                                       disease, AIDS.
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09 9

WO2003029420-A2

Homo sapiens.

native; human.

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expressed in a disorder or process associated with DNA methylation. The combination and cDNAs are useful for diagnosing, staging, treating or monitoring treatment of cancer, e.g. colon cancer and for detecting changes in expression of genes encoding proteins that are associated with DNA methylation. The protein is useful for screening molecules or compounds to identify at least one ligand that binds to the protein and for producing an antibody. The present sequence represents the amino acid sequence of a protein expressed in a disorder or process associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLLRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                           process associated with DNA methylation, useful for diagnosing, staging, treating or monitoring treatment of cancer, e.g. colon cancer.
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                                                                                                                                                                                                                                                                           New combination comprising cDNAs that are expressed in a disorder or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 281;
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                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 56-57; 66pp; English.
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                                  07-MAR-2002; 2002US-00093766.
                                                                       19-MAR-2001; 2001US-0277380P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281; Conservative
                                                                                                                                                                                  Lasek AKW, Jones DA,
                                                                                                      (LASE/) LASEK A K W. (JONE/) JONES D A. (KARP/) KARPF A R.
                                                                                                                                                                                                                       2003-503249/47.
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                                                                                                                                                                                                                                        N-PSDB; ACD42246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA methylation
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16-JAN-2003
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The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence to polypeptide having a sequence that differs from the native sequence polypeptide having 281 amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions at tesidue positions identified from x-ray crystal structure of the DRS.Apo2L complex. The polypeptide having the substitutions made at residue position(s) selected from 20 positions such as S96C, 8101C, 8110C, 8115C, 8115C, 8115C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8134C, 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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100.0%; Pred. No. 1.8e-266;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 1; 92pp; English.
                                                                                                                                                                                                  01-OCT-2002; 2002WO-US031210.
                                                                                                                                                                                                                                                    02-OCT-2001; 2001US-0326622P.
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                                                                                                                                                                                                                                                                                                                                                          Lindstrom
                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-541400/51.
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Best Local Similarity
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                                                                                                                                                  10-APR-2003.
                                                                                                                                                                                                                                                                                                                                                       Kelley RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281;
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181 FYXIYSQTYFRFQBEIXENTKUDKQMVQXIYKYTSYPDPILLMKSARNSCWSKDAEYGLY

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The invention relates to an isolated nucleic acid molecule encoding a isolated antibody or its fragment is used for treating an individual in need of decreased level of endokine alpha activity. The endokine alpha polypeptide present in a heterotrimeric complex is used for treating an individual having a disorder associated with excessive bone resorption, e.g. osteoporosis, paget's disease or arterial calcification. Treating an individual having a disorder associated with insufficient bone resorption, comprises administering an endokine alpha antagonist, which is the antibody that binds specifically to endokine alpha polypeptide. The present sequence represents the amino acid sequence of a tumour necrosis factor family ligand. 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 240 treating a 9 New Endokine alpha gene useful for preparing a composition for treating disease associated with excessive or insufficient bone resorption e.g., osteoporosis, Paget's disease or arterial calcification. 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 0; Gaps human; tumour necrosis factor; TNF ligand; endokine alpha; excessive bone resorption disorder; osteoporosis; Paget's disease; arterial calcification. Query Match 100.0%; Score 281; DB 7; Length 281; Best Local Similarity 100.0%; Pred. No. 1.8e-266; Matches 281; Conservative 0; Mismatches 0; Indels SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281 Disclosure; SEQ ID NO 20; 145pp; English. Nardelli B; Human TNF ligand family member #10. ADC35202 standard; protein; 281 AA. 16-AUG-2001; 2001US-0312542P. 30-OCT-2001; 2001US-0330761P. 15-AUG-2002; 2002US-00218547. (first entry) Ni J, Rosen CA, WPI; 2003-696072/66. NARDELLI B. (YUGG/) YU G. (NIJJ/) NI J. (ROSE/) ROSEN C A. N-PSDB; ADC35201. US2003100074-A1. Sequence 281 AA; Homo sapiens. 18-DEC-2003 29-MAY-2003. ADC35202; 241 (NARD/) Yu G, à q à

DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVERGPQ 120

1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE

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The present invention describes a predictor set comprising a plurality of polymucleotides or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase pathway. Also described: (1) predicting whether a compound is capable of pathway. Also described: (1) predicting whether a compound is capable of cells, comprising obtaining a sample of cells, cerrelating the expression of the markers to the compound's ability to correlating the expression of the markers to the compound's ability to correlate the activity of the cells; (2) a plurality of cell lines for identifying polymucleotides and polypeptides whose expression levels correlate with compound sensitivity or resistance of cells associated with a disease state; and (3) identifying polymucleotides and a disease state; and (3) identifying polymucleotides that predict compounds, analysing the expression pattern of a microarray of polymucleotides or polypeptides that predict the sensitivity or cell lines to one or more compounds, analysing the expression pattern of the microarray. The polymucleotides are compounded with a disease state by using the expression pattern of the microarray. The polymucleotides are cytostatic activities, and can be used in gene therapy. The polymucleotides and polypeptides are useful in predicting the
61 DDSYWDPNDEESWNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                              181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                       121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predictor set; protein tyrosine kinase activity modulator;
protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;
gene therapy; drug sensitivity; genetic profile; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides and polypeptides for predicting the activity of compounds that interact with protein tyrosine kinases and/or protein
                                                                                                                                                                                                                                                  241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                           241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human src biomarker polypeptide SEQ ID NO:269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shaw P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; SEQ ID NO 269; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  ADD14080 standard; protein; 281 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huang F, Fairchild CR, Lee FY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JAN-2002; 2002US-0350061P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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N-PSDB; ADD14676.
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                                                                                                                                                                                                                                                                                                                                                                   RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                    121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                        FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLIMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New substantially purified polypeptide, useful for diagnosing or treating a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
activity of compounds that interact with protein tyrosine kinases and/or protein tyrosine kinase pathways. These may be used in determining drug sensitivity in patients to allow the development of individualized genetic profiles which aid in treating diseases and disorders (e.g. cancer) based on patient response at a molecular level. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                           1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
                                                                                                                                                                                                                                                             1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiarteriosclerotic; vilnerary; gene therapy; hypoxia-regulated condition; tumourigeneshs; angiogenesis; apoptosis; inflammation; erythropoiesis; glycolysis; gluconeogenesis; glucose transportation; catecholamine synthesis; iron transport; infile iron categories is glucose; iron transport; retinopathy; neonatal stress; pre-eclampsia; atherosclerosis; inflammatory condition; wound healing.
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0
                                                                                                                                                           Length 281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                          ; Score 281; DB 7; L; Pred. No. 1.8e-266; 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human disease related protein SegID499.
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                                                                                                                                                      100.0%;
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2001GB-00024037.
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                                                                                                                                                                          Best Local Similarity 100.
Matches 281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kingsman SM, White J,
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                                                                                                                                                                        Similarity
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                                                                                                                           Sequence 281 AA;
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05-OCT-2001;
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                                                                                                                                                          Query Match
Best Local 9
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implicated in certain disease states. Compounds which modulate the proteins of the invention may have cytostatic, antiinflammatory, oppthalmological, antiatreficelerotic or vulnerary activities. The sequences of the invention may be useful for gene therapy. The invention may be useful for gene therapy. The invention may be useful for gene therapy. The invention may be useful for diagnosing or treating a hypoxia-regulated condition, such as tumourigenesis, angiogenesis, apoptosis, inflammation, erythropolesis, or the biological response to hypoxia conditions including processes such as glycolysis, gluconeogenesis, glucose transportation, catecholamine synthesis, iron transport or nitric oxide synthesis. The disease includes cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis, inflammatory conditions or wound healing. The present sequence is that of a disease related protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; liver disorder; hyperlipidaemia; hypertension; type II diabetes; tumour; liver; inflammatory disorder; immune response disorder; high-throughput screening; differential gene expression; gene therapy.
                                                                                         invention relates to novel human genes and gene product which are cated in certain disease states. Compounds which modulate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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   or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
 injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 281;
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 281; DB 7; I
Pred. No. 1.8e-266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                    Claim 25; SEQ ID NO 499; 424pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 281; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KASE/) KASER M R.
                                                                                                                                                                                                                                                                                                                                                                           Sequence 281 AA;
                 wound healing.
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The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidaemia, hypertension, type II diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of screening several molecules or compounds to identify a ligand which specifically binds a CDNA. A protein encoded by the CDNA is useful for a high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the CDNA with several of molecules or compounds under conditions to allow specific binding a ligand which specifically binds the protein. The composition is useful for detecting and molecule or compound, therefore identifying a ligand which specifically binds the protein. The composition is useful for detecting and communate prognosis and to design a treatment regimen and to monitor the efficacy of treatment. The present sequence represents the amino acid sequence of a protein encoded by a CDNA differentially expressed in a
                                                                                                             Composition comprising several cDNAs that are differentially expressed in treated human C3A liver cell cultures, useful for treating liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FYXIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DDSYWDPNDEESMNGPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVVYFTNELKQMQDKYSKSGIACFLKE
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100.0%; Pred. No. 1.8e-266;
ive 0; Mismatches 0;
                                                                                                                                                                                                             Claim 1; SEQ ID NO 118; 41pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human TL2 (TRAIL), ligand for TR5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 281; Conservative
                                            WPI; 2004-031227/03.
N-PSDB; ADE76952.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           liver disorder
                                                                                                                                                              disorders.
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AAW76332
ID AAW76
XX
AC AAW76
XX
DT 11-JA
XX
XX
KW TL2;
KW arthr
KW infla
KW infla
KW infla
KW brain
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This is the amino acid sequence of human TL2 (also known as TRAIL), which has newly been discovered to be a ligand of human tumour necrosis related receptor TR5 (see AAWF6311). This TR5 polypeptide of the invention and TL2 can be used in screening processes for compounds which bind the receptor, or its ligand, and which activate (agonists) or inhibit (antagonists) the receptor or TL2. Treatment of a subject with the need to inhibit TR5 polypeptide activity comprises administering an antagonist to the polypeptide, administering a nucleic acid that inhibits the expression of the nucleotide sequence encoding the polypeptide and/or administering a polypeptide that competes with the polypeptide for its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYNDPNDEESMNSPCMOVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSI 240
                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide encoding TR5 polypeptide - used to diagnose, prevent and treat e.g. inflammation, arthritis, septicaemia, autoimmune diseases, infections, stroke, ischaemia, ARDS, psoriasis, restenosis, brain injury,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ligand, substrate or receptor. The active agents on be used for the treatment of chronic and acute inflammation, arthritis, septicaemia, autoimmune diseases (-g. inflammatory bowel disease, psoriasis), transplant rejection, graft vs host disease, infection, stroke, ischaemia, acute respiratory disease syndrome, restenosis, brain injury, AIDS, bone diseases, cancer (e.g. lymphoproliferative disorders), atherosclerosis and Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SYWDENDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 MMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 YIYSQTYFRFQEEIKENTKNDKQMVQXIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSI
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Alzheimer's disease; human; therapy; diagnosis; ligand.
                                                                                                                                                                                                                                                                                                                   Lyn SDP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 17-18; 22pp; English.
                                                                                                                                                                                                                                                                           (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                     Truneh A,
                                                                                                                                                                                                               97US-00795910.
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nes 279; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIDS and bone diseases.
                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-497862/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 279 AA;
                                            Homo sapiens
                                                                                                                                                                    04-FEB-1998;
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28-JUL-1997;
                                                                                  EP867509-A2
                                                                                                                            30-SEP-1998
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AAW95032

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to identifying agonists or antagonists to tumour necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2 and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a candidate compound in the presence of TL4 or (ii) contacting TL2 or TL4 with a candidate compound in the presence of TR1; and (b) assessing the ability of the candidate compound to compete with TR1 or TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful for treating diseases caused by imbalance of TL or TR polypeptide levels, which cause: chronic and acute inflammation, arthritis, septicemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRV 122
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                                                                                                                                  Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL2; TL4; arthritis; inflammation; septicemia; autoimmune disease; transplant rejection; arfatt vs. host disease; infection; stroke; ischemia; brain injury; AIDS; acute respiratory disease syndrome; restenosis, bone disease; cancer; athersclerosis; Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying agonists and antagonists to tumour necrosis factor receptor (TNF-R) related polypeptides (LR1, LR2, LT2 and LT4) - useful for treating stroke, Alzheimer's disease and AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 MMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                  Tumour necrosis factor receptor (TNF-R) related polypeptide TL2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 14-15; 18pp; English.
AAW95032 standard; protein; 279 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                           97US-0055513P.
97US-0056980P.
                                                                                                                                                                                                                                                                                                                                            98EP-00304424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Young PR;
                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-134308/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brigham-Burke MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 279 AA;
                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                          04-JUN-1998;
                                                                   13-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                              26-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                             29-AUG-1997;
                                                                                                                                                                                                                                                                        BP897114-A2
                                                                                                                                                                                                                                                                                                        17-FEB-1999
                                 AAW95032;
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(Apo-21). The Apo-21 polypeptide can be produced by standard recombinant methodology. Apo-21 is useful for inducing apoptosis in mammalian cancer cells. This is useful for the treatment of cancer. Apo-21 can be used to induce apoptosis for pathological conditions characterized by decreased to induce apoptosis for pathological conditions characterized by decreased mediated glomerular nephritis and cancer. Apo-21 and its nucleic acid coding sequence can also be used in quantitative and screening diagnostic techniques. Anti-Apo-21 antibodies can be used for treating diseases associated with increased apoptosis. Sequences AAY27016-19 represent specific examples of Apo-21 variants. Note: This sequence is not provided in the specification. It has been created by modifying the wild-type Apo-21 sequence provided in Fig 1A
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181 YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytokine, designated Apo-2 ligand, useful for inducing apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to a novel human cytokine, designated Apo-2 ligand
                                                                                                                                                                                                                                                                                  Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder; lupus; immune-mediated glomerular nephritis; human; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAMMEVOGGPSLGQTCVLIVIFTVILQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pitti RM, Schwall RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                    /label= D269A
/note= "wild-type Asp is replaced with Ala"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                    241 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.4%; Score 268; DB 2; Le
100.0%; Pred. No. 9.6e-254;
ive 0; Mismatches 0;
                                 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                                                                                                                                                                                                                                 Human Apo-2 ligand (Apo-2L) variant D269A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O'connel MT,
                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                AAY27018 standard; protein; 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US001039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-00007886
98US-00060533
                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kelley RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in mammalian cancer cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
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Matches 268; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                       sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9936535-A1
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15-APR-1998;
                                                                                                                                                                                                                     24-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUL-1999
                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                   AAY27018;
                                 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence having 281 amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions at residue positions identified from x-ray crystal structure of the DRS.Apo2L complex. The polypeptide having the substitutions made at residue position(s) selected from 20 positions such as S9CC, 510IC, 511IC, V114C, R115C, E116C, N134C, E144C, N152C, S153C, R170C, S111C, V114C, R115C, E116C, N134C, E25C, E263C, H264C, such that the residue position is, outside of the receptor contact region of the DRS.Apo2L complex, and displays high solvent accessibility in the crystal structure of the DRS.Apo2L complex. The Apo-2 ligand variant polypeptide and further compositions have the following activities: cytostatic, antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
                                                                                                            180
                                   61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRISEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                               180
                                                                                                                                                                                                                                              240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apo-2 ligand, DR5.Apo21 complex, receptor contact region,
high solvent accessibility; oyrostatic; antiathritic; neuroprotective;
trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
lung; breast; immune-related disease; arthritis; multiple sclerosis;
                                                                                                                                            RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                                       FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
/note= "Native residue of His is substituted by Cys"
                                                                                                                                                                                                                                                                                                                                                                                                            SIYQGGIFELKENDRIFVSVTNEHLIDM 268
                                                                                                                                                                                                                                                                                                                                                                         241 SIYQGGIFELKENDRIFVSVTNEHLIDM 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Apo-2 ligand protein mutant H264C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADB61495 standard; protein; 281 AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; mutant; mutein.
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an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for inducting apoptosis in mammalian cells, by exposing mammalian cells expressing a receptor selected from DR4 receptor and DR5 receptor to a therapeutically effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, the Apo-2 ligand variant polypeptide, the Apo-2 ligand variant polypeptide, the Apo-2 ligand variant polypeptide, colon or colorectal cancer) or immune-related disease (such as arthritis or multiple sclerosis) in a mammal, by administering to the mammal an effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. This sequence represents the human Apo-2 ligand mutant H264C protein of the invention. NOTE: This sequence is not shown in the specification. It has been created from information provided in claim 1 and from the sequence in Fig 1 of the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 FYXIXSQTYFRFQEBIKENTKNDKQMVQXIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                          Length 281;
                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
                                                                                                                                                                                                                                                                                                                                                    93.6%; Score 263; DB 7; Lv
100.0%; Pred. No. 7.5e-249;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Apo-2 ligand protein mutant E263C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIYOGGIFELKENDRIFVSVTNE 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 SIYQGGIFELKENDRIFVSVINE 263
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                                                                                                                                                                                                                                                                                                                                                                                          Matches 263; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                     Sequence 281 AA;
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02-OCT-2001; 2001US-0326622P.

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The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence to polypeptide having as equence that differs from the native sequence comparing as animo acide given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having the substitutions at the polypeptide having the substitutions at the polypeptide having the substitutions and at the polypeptide having the substitutions and the polypeptide having the substitutions and and at the polypeptide having the substitutions and the polypeptide having the substitutions and an are a selected from 20 positions such as $960, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100, $1100
                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from the sequence in Fig 1 of the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page; 92pp; English.
                                                                                                                                   Kelley RF, Lindstrom SH;
(GETH ) GENENTECH INC.
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Sequence 281 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVAAHIIGIRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLAMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                             1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
                                                                                                                                                                                                                                                                                                                                                                                              1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                             93.2%; Score 262; DB 7; Length 281; 100.0%; Pred. No. 7.2e-248; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIYQGGIFELKENDRIFVSVTN 262
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                                                                                                                                                                                                                                                                                                                                                                              Matches 262; Conservative
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ADB61493 standard; protein; 281 AA.
RESULT 46
                  ADB61493
ID ADB6
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ADB61493;
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04-DEC-2003 (first entry)

Human Apo-2 ligand protein mutant R255C.

nigh solvent accessibility; cytostatic; antiarthritic; neuroprotective; trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer; lung; breast; immune-related disease; arthritis; multiple sclerosis; Apo-2 ligand; DR5.Apo2L complex; receptor contact region; human; mutant; mutein.

Homo sapiens Synthetic.

Location/Qualifiers Misc-difference 255

/note= "Native residue of Arg is substituted by Cys"

WO2003029420-A2.

10-APR-2003

01-OCT-2002; 2002WO-US031210.

02-OCT-2001; 2001US-0326622P

(GETH) GENENTECH INC.

Kelley RF, Lindstrom SH;

WPI; 2003-541400/51.

Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.

Claim 1; Page; 92pp; English.

The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence having a sequence that differs from the native sequence having all amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions at residue positions identified from 20 positions such as S96C, S101C, S12C, W14C, R115C, R1

Sequence 281 AA;

Query Match

Length 281; DB 7; 90.4%; Score 254;

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FR2766713-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence having 281 amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions at residue positions identified from x-ray crystal structure of the DRS.Apo2L complex. The polypeptide having the substitutions made at
                                                                                                                                                      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                          181 FYYIXSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLLMKSARNSCWSKDAEYGLY
                                                                                 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                             FYYIYSQTYFRFQEEIKENTKNDKQMVQXIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                    1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                        1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, compamino acid substitutions in the native sequence of the Apo-2 ligand.
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             Indels
  red. No. 4.8e-240;
Mismatches 0;
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  Pred.
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Misc-difference 249
                                                                                                                                                                                                                                                                                                         ADB61492 standard; protein; 281 AA.
 al Similarity 100.0%; P. 254; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page; 92pp; English
                                                                                                                                                                                                                                               241 SIYÖGGIFELKEND 254
                                                                                                                                                                                                                          241 SIYQGGIFELKEND 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; mutant; mutein.
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Best Local Similarity
Matches 254; Conserv
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cc residue position(s) selected from 20 positions such as $96C, $101C, $111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, $155C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R170C, R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein associated with neurodegenerative and autoimmune diseases.
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100.0%; Pred. No. 3.6e-234;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY01516 standard; peptide; 281 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 SIYQGGIF 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAY-1999
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                                                                                                                                                                                                            The specification describes the use a polypeptide corresponding to at least the primary sequence of part of the present sequence to produce a diagnostic, prophylactic or therapeutic composition useful in cases of degenerative, autoimmus and inflammatory diseases. The polypeptides can be used in treatment of neurodegenerative disease, The polypeptides can rhuematoid arthritis, and SEP. The polypeptides are apoptotic in central nervous system cells, antigenic and specifically recognise the surface receptor of the TRAIL protein. The polypeptide is a marker of disease and a therapeutic target, e.g. its apoptotic activity can be blocked with an anti-TRAIL antibody or a TRAIL equivalent that binds to specific receptors, inhibiting formation of natural complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                   Use of polypeptide derived from TRAIL protein for diagnosis of degenerative disease - autoimmunity and inflammation, also useful in prevention or treatment, and similar use of corresponding ligand and nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; attenuated tumour-targetted bacteria; effector molecule; tumour necrosis factor; TNF; anti-angiogenic factor; cytotoxic polypeptide; tumour inhibitory enzyme; therapy; carcinoma; melanoma; lymphoma; sarcoma; metastasis; cytostatic; fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                          Score 244; DB 2; Length 281; Pred. No. 3e-230;
                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OmpA signal peptide-human TRAIL fusion protein.
                                                                                                                                                                                                                                                                                                                                                                  86.8%; Scor.
100.0%; Pred. No. sc.
100.0%; Pred. No. sc.
0; Mismatches
                                                                                         Perron H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY72935 standard; protein; 266 AA.
                                                                                                                                                                                           Claim 1; Page 13; 21pp; French.
                      97FR-00010176
                                            97FR-00010176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              Matches 244; Conservative
                                                                                         Belliveau JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
                                                                  (INMR ) BIO MERIEUX.
                                                                                                              WPI; 1999-156177/14.
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIYQ 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIYO 244
                                                                                                                                                                                                                                                                                                                                                    Sequence 281 AA;
                      04-AUG-1997;
                                            04-AUG-1997;
  05-FEB-1999
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                                                                                         Rieger F,
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tumour-targetted bacteria, such as, eg., Salmonella, as a vector for the delivery of one or more primary effector molecules and secondary effector molecules to the site of a solid tumour. The primary effector molecules of the invention include members of the tumour necrosis factor (TMP), anti-angiogenic factors, cytotoxic polypeptides and tumour inhibitory enzymes. They induce a local immune response at the site of the tumour that results in the inhibition of growth of a tumour or tumour cells. The primary effector molecules are used for the treatment of solid tumours such as acroinomas, melanomas, lyaphomas, sarcomas or metastases derived from these tumours. The present sequence is ompa signal peptide-mature human TMF-alpha-related apoptosis-inducing ligand (TRAIL) fusion protein. The fusion of Ompa signal peptide to the amino terminus of TRAIL effector molecule enhances the periplasmic localisation and subsequent processing of the effector molecule. (Updated on 11-SEP-2003 to standardise OS
                                                                                                                                                                                                                                                                                                220 ILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 ISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 ISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to the preparation and use of attenuated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Attenuated tumor-targeted bacteria comprising nucleic acids encoding primary and secondary effector molecules, useful for the treatment of e.g. carcinomas, melanomas, lymphomas and sarcomas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 GHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 NELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRISEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 GHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Belcourt M;
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INF-alpha-related apoptosis-inducing ligand; TRAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match
Local Similarity 100.0%; Pred. No. 2.6e-228;
es 242; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clairmont CA, Lin SL,
                                                                                                                                                                                                                                         .. .21
/label= OmpA_signal_peptide
                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 7; Fig 6; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0157500P.
99US-0157581P.
99US-0157637P.
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                                                                                                                                                                                                                                                                                                                                                                     ligand"
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                                                                                                                                                                                                                                                                                                                                                                                                                               WO200125397-A2.
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04-OCT-1999;
04-OCT-1999;
                                                                 Homo sapiens
Escherichia
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                                                                                                                                  Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                   Region
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The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence having 281 amino acids given in specification. The Apo-2 ligand variant oblypeptide is selected from a polypeptide having substitutions at residue positions identified from x-ray crystal structure of the DRS-Apo2L complex. The polypeptide having the substitutions ande at residue position(s) selected from 20 positions such as S96C, S101C, S111C, V114C, R170S, R179C, D234C, R25C, E263C, H264C, such that the residue position is, outside of the receptor contact region of the DRS-Apo2L complex, and displays high solvent accessibility in the crystal structure of the DRS-Apo2L complex. The Apo-2 ligand variant polypeptide and thather compositions have the following activities: cytosfatic, and thather than neuroprotective. The Apo-2 ligand variant polypeptide, an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for inducting apoptosis in mammalian cells, by exposing mammalian cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expressing a receptor selected from DA4 receptor and DR5 receptor to a heargebulfoally effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are colon or colorectal cancer cells. The Apo-2 ligand trimer is useful for treating cancer (such as lung, breast, colon or colorectal cancer) or an immune-related disease (such as arthritis or multiple sclerosis) in a
205 ILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFL 264
                                                                                                                                                                                                                                                                                                                                           Apo-2 ligand, DRS.Apo2L complex; receptor contact region; high solvent accessibility; cytostatic; antiarthritic; neuroprotective; trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer lung; breast; immune-related disease; arthritis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Native residue of Asp is substituted by Cys"
                                                                                                                                                                                                                                                                                                       Human Apo-2 ligand protein mutant D234C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                               ADB61491 standard; protein; 281 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-OCT-2001; 2001US-0326622P
                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kelley RF, Lindstrom SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                              human; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-541400/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 234
                                                                            VG 266
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                                      VG 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                            265
                                                                                                                                                                                                                          ADB61491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                      280
                                                                                                                                          RESULT 50
                                                                                                                                                              ADB61491
ID ADB
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                                                                                                                                                                                                                                                                                                                                                           RVAAHITGIRGENILSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                           61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                             1 MAMMEVQGGPSLGQTCVLIVIFTVILQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel human cytokine, designated Apo-2 ligand (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
mammal, by administering to the mammal an effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. This sequence represents the human Apo-2 ligand mutant D234C protein of the invention. NoTE: This sequence is not shown in the specification. It has been created from information provided in claim 1 and from the sequence in Fig 1 of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder; lupus; immune-mediated glomerular nephritis; human; variant.
                                                                                                                                                                                                            1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                    181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "wild-type Asp is replaced with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schwall
                                                                                                                                              Length 281;
                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pitti RM,
                                                                                                                                              Score 233; DB 7; L
Pred. No. 1.7e-219;
                                                                                                                                                          100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Apo-2 ligand (Apo-2L) variant D218A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY27017 standard; protein; 281 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Page; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= D218A
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                                                                                                                                                82.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n mammalian cancer cells.
                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                Sequence 281 AA;
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Synthetic.
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methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer cells. This is useful for the treatment of cancer. Apo-2L can be used to induce apoptosis for pathological conditions characterized by decreased levels of apoptosis, e.g. autoimmune disorders like lupus and immune-mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid coding sequence can also be used in quantitative and screening disquestive techniques. Anti-Apo-2L antibodies can be used for treating dispositive techniques. Anti-Apo-2L antibodies can be used for treating diseases associated with increased apoptosis. Sequences AAY27016-19 represent in the specification. It has been created by modifying the wild-type Apo-2L sequence provided in Fig 1A
                                                                                                                                                                                                                                                                                                                                        DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSERTISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                  DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                    RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                               121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                               1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
                                                                                                                                                                                                                                                                                                Cytokine; Apo-2 ligand, Apo-2L; apoptosis; cancer; autoimmune disorder; lupus; immune-mediated glomerular nephritis; human; variant.
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                  77.2%; Score 217; DB 2; Length 281; 100.0%; Pred. No. 8e-204; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= D218A
/note= "wild-type Asp is replaced with Ala"
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/note= "wild-type Asp is replaced with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Apo-2 ligand (Apo-2L) variant D203A, D218A, D269A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FYXIXSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYP 21.7
                                                                                                                                                                                                                           100.0%; Prec. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= D203A
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98US-00060533.
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 218
                                                                                                                                                                                     Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
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The invention relates to a novel human cytokine, designated Apo-2 ligand (Apo-21). The Apo-21 polypeptide can be produced by standard recombinant methodology. Apo-21 is useful for inducing apoptosis in mammalian cancer cells. This is useful for the treatment of cancer. Apo-21 can be used to induce apoptosis for pathological conditions characterized by decreased levels of apoptosis, e.g. autoimmune disorders like lupus and immunemediated glomerular nephritis and cancer. Apo-21 and its nucleic acid coding sequence can also be used in quantitative and screening dispassed techniques. Anti-Apo-21 antibodies can be used for treating diseases ssociated with increased apoptosis. Sequences AAY27016-19 represent specific examples of Apo-21 variants. Note: This sequence is not provided in the specification. It has been created by modifying the wild-type Apo-21 sequence provided in Fig 1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRISEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A movel cytokine, designated Apo-2 ligand, useful for inducing apoptosis in mammalian cancer cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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   Schwall RH;
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
 Pitti RM,
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 71.9%; Score 202; DB 2; L. Best Local Similarity 100.0%; Pred. No. 3.8e-189; Matches 202; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Apo-2 ligand (Apo-2L) variant D203A.
 O'connel MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FYYIYSQTYFRFQEEIKENTKN 202
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                                                                                                                 Claim 12; Page; 86pp; English.
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Kelley RF,
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                                 WPI; 1999-444397/37
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 281 AA;
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 Ashkenazi AJ,
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The invention relates to a novel human cytokine, designated Apo-2 ligand (Apo-21). The Apo-21 is useful for inducing apoptosis in mammalian cancer cells. This is useful for inducing apoptosis in mammalian cancer induce apoptosis for pathological conditions characterized by decreased to induce apoptosis for pathological conditions characterized by decreased mediated glomerular nephritis and cancer. Apo-21 and its nucleic acid coding sequence can also be used in quantitative and screening disappositic techniques. Anti-Apo-22 antibodies can be used for treating diseases associated with increased apoptosis. Sequences AAY27016-19 represent specific examples of Apo-21 variants. Note: This sequence is not provided in the specification. It has been created by modifying the wild-type Apo-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis in mammalian cancer cells.
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                                                                         Schwall RH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; tumour related apoptosis inducing ligand; Trail;
Trail prokaryotic expression system; tumour cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human tumour related apoptosis inducing ligand (Trail).
                                                                         Pitti RM,
                                                                         O'connel MT,
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                                                                                                                                                                                                                                                                                                                                                                                     2L sequence provided in Fig 1A
98US-00007886.
98US-00060533.
                                                                                                                                                                          Claim 9; Page; 86pp; English.
                                                                         Ashkenazi AJ, Kelley RF,
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                                           (GETH ) GENENTECH INC
                                                                                                   WPI; 1999-444397/37
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Best Local Similarity
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 15-JAN-1998;
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            15-APR-1998;
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                                                                                                                                                                                                                                                                                                                                 tumour related apoptosis inducing ligand (Trail), and the Trail protein. The Trail full length CDNA is cloned, and is utilised to create a Trail protein. The Trail full length CDNA is used to respectively clone cDNA of soluble ectocytic segment Trail109 and Trail 114, and respectively clone cDNA of sculple ectocytic segment Trail1109 and Trail 114, and respectively create Trail109 cDNA and Trail114 cDNA prokaryotic expression systems. The prokaryotic expression systems created greatly increase the expression and quantity of the Trail 109, and Trail114 proteins, and may be useful in a new preparation for killing tumour cells. The present sequence represents the full length human Trail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 RVAAHITGIRGRSNILSSPNSKNEKALGRKINSWESSRSGHSFLSNIHLRNGELVIHEKG
                                                                                                                                                                                                                                                                                                                The present invention relates to the isolation of CDNA encoding human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                       Tumor death induction ligand gene, gene expression protein and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 199; DB 5; Le
Pred. No. 3.3e-186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human TRAIL splice variant 8, rpl-6-6, protein.
                                                                                                                                                                                                                                                                              Claim 7; Page 10 (disclosure); 17pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.8%; Scor.
100.0%; Pred. No. 3...
... 0; Mismatches
                                                                                        (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU99301 standard; protein; 212 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 FYYIYSQTYFREQEEIKEN 199
                                                     30-NOV-2001; 2001CN-00132371.
                 30-NOV-2001; 2001CN-00132371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 FYYIYSQTYFRFQEEIKEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome 3q26; rp1-6-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 199; Conservative
                                                                                                                                                                 WPI; 2002-751439/82.
                                                                                                                                                                                                                                             preparation method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                       N-PSDB; ABX14391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 281 AA;
                                                                                                                            Hu Y, Yao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU99301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 55
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Location/Qualifiers

Key

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Side effects. Thus, TRAIL has the potential to be a very useful antitumour agent. The naturally occurring splice variants may differ in their cellular distribution, expression levels/timing and activity.

Their cellular distribution, expression levels/timing and activity.

Determining these factors could provide possible mechanisms for the induction of apoptosis of tumours cells. The splice variant polypeptides and polymucleotides can be used in gene therapy, to raise antibodies, to detect the levels, distribution and ratios of expression of TRAIL, and its splice variants, in a biological sample and to identify compounds which bind the variant TRAIL products and modulate its activity (agonists of and antagonists). Pharmaceutical compositions, comprising an expression vector or any of the amino acid sequences, are useful for causing a cytotoxic effect in cancer cells and for treatment of diseases which can be ameliorated, cured or prevented by lowering or raising the level of the amino acid sequences. The antibodies may also have a therapeutic cutility in blocking or decreasing the activity of the TRAIL variant condiseases, diseases involved in the non-normal and any and any and any activity of the family and any and any activity of the reached any and any and any activity of the reached any activity of the non-normal and any activity of its normal and any activity of its normal and any activity of the reached any activity of the reached any activity of the reached any activity of the reached any activity of any activity of any activity of any activity of any activity of any activity of any activity of any activity of any activity of any activity of any activity of any activity of any activity of any activity of any activity of any activity of any activity of any activity of any activity of any activity of any activity of any activity of any activity of any activity of any activity and any activity of any activity and any activity and any activity and any activity and any activity and any activity and any activi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention discloses isolated, naturally occurring, polypeptide splice variants of human tumour necrosis factor (TNF)-related apoptosis inducing ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal cellular differentiation and development of multicellular organisms.

Apoptosis is induced by certain cytokines which include TNF and TRAIL also referred to as Apo-2 ligand, Apo-21). TRAIL is a type II membrane protein which induces apoptosis and nuclear factor-B (NF-B) activation in many tissues and cells. Receptors for TRAIL include two death domain proceptors, DR4 and DR5, as well as two decoy receptors, DCRI and DCR2, lacking receptors, induces apoptosis in tumour cells, whereas normal cells are relatively resistant without showing significant toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diseases, unterdommune diseases, diseases involved in the controlled on chromosome development of tissues and aging. TRAIL's gene is located on chromosome development of tissues and aging. TRAIL's gene is located on chromosome 3q26. The sequence presented is the human TNF-related apoptosis inducing 3q26. The sequence presented is trol-6-6, protein which has had an C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New splice variants of tumor necrosis factor-related apoptosis inducing ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat diseases or disorders associated with low expression of the variants.
                                                                                                                                                                                                                /note= "Encoded by in-frame stop codon"
                                                            note= "Extracellular domain"
                                note= "Cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Savitzky K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Fig 8; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                16-MAY-2001; 2001US-00855544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAY-2000; 2000IL-00136156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yelin R, Khosravi R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (YELI/) YELIN R.
(KHOS/) KHOSRAVI R.
(SAVI/) SAVITZKY K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-479259/51.
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                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                             US2002061525-A1
                                                                                                                                                                                                                                                                                                                                          23-MAY-2002.
                                                            Domain
      Domain
                                                                                                                         Domain
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1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
    68.7%; Score 193; DB 5; Length 212; 100.0%; Pred. No. 2e-180; Live 0; Mismatches 0; Indels
Query Match
Best Local Similarity 100.
Matches 193; Conservative
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Claim 18; Fig 3; 41pp; English

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121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                               DDSYWDPNDEESWNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New tumor necrosis factor related apoptosis inducing ligand polypeptides for treating viral infections (e.g. bovine viral diarrhea or human immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27. .29
/note= "Tripeptide corresponding to an oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Tripeptide corresponding to an oligonucleotide employed in vector construction"
                                                                                                                                                                                                                                                                                                             Human, tumour necrosis factor, TNF, cytokine; cytostatic; virucide, TNF related apoptosis inducing ligand; TRAIL; cancer, viral infection, human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma; melanoma; growth hormone; GH; leucine zipper; fusion protein;
                       DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                                                                                                                                        GH-derived leader peptide-leucine zipper-human TRAIL fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Human TRAIL protein fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "GH-derived leader peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          employed in vector construction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Leucine zipper peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                              AAE11037 standard; protein; 253 AA.
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95US-00548368.
96US-00670354.
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                                                                                                                        181 FYXIYSQTYFRFQ 193
                                                                                                                                                 181 FYYIYSOTYFRFO 193
                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note=
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N-PSDB; AAD18398.
                                                                                                                                                                                                                                                                                                                                                                 chimeric protein.
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
Unidentified.
Chimeric.
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01-NOV-1995;
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10-NOV-1998;
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                                                                                                                                                                                                                                       AAE11037;
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The invention relates to a cytokine designated as tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis of certain target cells, including cancer cells and virally infected cells. The TRAIL polypeptides are useful in killing cancer cells, in treating viral infections (e.g. bovine viral diarrhoea or human immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and melanoma), as a research reagent useful in studying apoptosis including the regulation of programmed cell death. TRAIL DNA sequences may be employed in developing a gene therapy approach to treating disorders mediated by defective or insufficient amounts of TRAIL, in the production of TRAIL polypeptides and as probes or primers in polymerase chain reactions (PCR). The present sequence is growth hormone (GH)-derived leader peptide-leucine zipper-human TRAIL fusion protein
                                                                                                                                                                                                                                                                                                                                                                            ESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                            186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumour necrosis factor; apoptosis; hāemostatic; immunosuppressive; antiinflammatory; dermatological; thrombotic microangiopathy; thrombotycomotic thrombotytopaenic purpura; TTP; HUS; SLB; clotting disorder; adult haemolytic uraemic syndrome; cardiac problem; paediatric AIDS; systemic lupus erythematosus; growth hormone; leucine zipper.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF
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                                                                                                                                                                                                                                                                                                                            Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Growth hormone/leucine zipper/TRAIL 95-281 fusion protein.
                                                                                                                                                                                                                                                                                     66.5%; Score 187; DB 4; Length 253; 100.0%; Pred. No. 1.7e-174; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; TNF related apoptosis inducing ligand; TRAIL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU08564 standard; protein; 253 AA.
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95US-00548368.
96US-00670354.
98US-00048641.
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                                                                                                                                                                                                                                                                                                                       Matches 187; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FGAFLVG 281
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                       Sequence 253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6521228-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUN-1995;
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25-JUN-1996;
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human tumor necrosis factor (TNF) related apoptosis inducing ligand
(TRAIL) protein appearing as ABU08558; (b) a soluble human TRAIL
polypeptide, (c) a polypeptide comprising amino acids 124-276 of
polypeptide, (c) a fragment of the TRAIL protein. Also included is an antigen-binding fragment of the antibody (a monoclonal antibody), a hybridoma cell line that produces the antibody. The antibody is used in assays to detect the presence of TRAIL polypeptides, either in vitro or in vivo, purifying TRAIL by affailty chromatography, blocking binding of TRAIL to target cells and thus inhibiting a biological activity of TRAIL.
TRAIL e.g. thrombotic microangiopathies, e.g. thrombotic
thrombocytopaenic purpura (TTP), adult haemolytic uraemic syndrome (HUS)
(even though it can strike children as well) small blood vessel clotting
disorders e.g., cardiac problems in paediatric AIDS patients and systemic
lupus erythematosus (SLB). The present sequence represents a growth
commone signal peptide/leucine zipper/TRAIL 95-281 fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 ESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 TSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 TSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 ESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 SYPDPILLMKSARNSCWSKDAEYGLYSTYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 246
                                                                                                                              Novel antibody which binds to human tumor necrosis factor related apoptosis inducing ligand protein, useful for inhibiting TRAIL-mediated apoptosis of a target cell, or blocking binding of TRAIL to a target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; tumour necrosis factor; TNF; cytokine; cytostatic; virucide; TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection; human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma; melanoma; cytomegalovirus; CWV; leucine zipper; fusion protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CMV-derived leader peptide-leucine zipper-human TRAIL fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                           The invention relates to an antibody that specifically binds: (a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.5%; Score 187; DB 6; Length 253; 100.0%; Pred. No. 1.7e-174; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE11038 standard; protein; 256 AA
                                                                                                                                                                                                                                                Disclosure; Fig 3; 40pp; English.
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                       Goodwin RG;
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                                                                WPI; 2003-340628/32.
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                                                                                        N-PSDB; ABX93872.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 253 AA;
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Unidentified.
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                     Wiley SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE11038;
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The invention relates to an antibody that specifically binds: (a) the human tumor necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) protein appearing as ABU08558; (b) a soluble human TRAIL polypeptide: (c) a polypeptide comprising amino acids 124-276 of ABU08558, or (d) a fragment of the TRAIL protein. Also included is an antiqen-binding fragment of the antibody (a monoclonal antibody), a hybridoma cell line that produces the antibody. The antibody is used in vivo, purifying TRAIL by affinity chromatography, blocking binding of TRAIL to target cells and thus inhibiting a biological activity of TRAIL. C. The antibody is useful for treating disorders mediated or exacerbated by TRAIL, e.g. thrombotic microangiopathies, e.g. thrombocic thrombotic microangiopathies, e.g. thrombocic chromotic microangiopathies, e.g. thrombocic chromotic purpura (TTP), adult haemolytic uraemic syndrome (HUS) (even though it can strike children as well) small blood vessel clotting disorders e.g. cardiac problems in paediatric AIDS patients and systemic lupus erythematosus (SLB). The present sequence represents a CMV (human proper in the partial peptide/leucine zipper/TRAIL 95-281 fusion
                                                                                                                                    The invention relates to a cytokine designated as tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis of certain target cells, including cancer cells and virally infected cells. The TRAIL polypeptides are useful in killing cancer cells, in treating viral infections (e.g. bovine viral diarrhoea or human immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and melanoma), as a research reagent useful in studying apoptosis including the regulation of programmed cell death. TRAIL DNA sequences may be employed in developing a gene therapy approach to treating disorders mediated by defective or insufficient amounts of TRAIL, in the production of TRAIL polypeptides and as probes or primers in polymerase chain reactions (PCR). The present sequence is a DNA encoding cytomegalovirus (CMV)-derived leader peptide-leucine zipper-human TRAIL fusion protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 TSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New tumor necrosis factor related apoptosis inducing ligand polypeptides for treating viral infections (e.g. bovine viral diarrhea or human immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
                                                                                  /note= "Tripeptide corresponding to an oligonucleotide employed in vector construction"
                                                                                                                                                                                       /note= "Tripeptide corresponding to an oligonucleotide employed in vector construction"
70. .256
/note= "Human TRAIL protein fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                        'note= "CMV-derived leader peptide"
                                                                                                                                                 "Leucine zipper peptide"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Fig 4; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-00548368.
96US-00670354.
98US-00048641.
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N-PSDB; AAD18399.
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Disclosure, Fig 4; 40pp; English.

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tumour necrosis factor; apoptosis; häemostatic; immunosuppressive; antiinflammatory; dermatchogical; thrombotic microangiopathy; thrombotic thrombotic thrombotic thrombotic thrombotic thrombotic thrombotic upon adult haemolytic uraemic syndrome; cardiac problem; paediatric AIDS; systemic lupus erythematosus; leucine zipper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel antibody which binds to human tumor necrosis factor related apoptosis inducing ligand protein, useful for inhibiting TRAIL-mediated apoptosis of a target cell, or blocking binding of TRAIL to a target
                                                                                                                                                                                                                                                                                                                CMV sig. pep./leucine zipper/TRAIL 95-281 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                   Human; TNF related apoptosis inducing ligand; TRAIL; CMV;
                                                                                                                                                                  ABU08565 standard; protein; 256 AA.
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95US-00548368.
96US-00670354.
98US-00048641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cytomegalovirus.
Unidentified.
                           FGAFLVG 256
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FGAFLVG
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26-MAR-1998;
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07-SEP-2001; 2001WO-EP010364.
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/note=
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                                                                                                                                                                       Similarity
                                                                                                                                               Sequence 461 AA;
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                                                                                                                                                                               187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammation
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  receptor.
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                                                              70 TSBETISTVQBKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 129
                                                                                                 130 ESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT 189
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                                                                                                                                             249
                                                                                                                                                                                                                                                                                              Antibody-cytokine fusion protein; proapoptotic; immunomodulatory; cancer. immune disease; multiple sclerosis; rhematoid arthritis; cytostatic; antiflammatory; antirheumatic; antiathritic; antibacterial; virucide; procesoacide; antiallergic; antidabetes; infection;
                                                                                                                          SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF
                                                                                                                                     190 SYPDPILLMKSARNSCWSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASF
                                                     95 TSEETISTVOEKOONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW
                                                                                       155 ESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide prodrug, useful e.g. for treating tumors, comprises cytokine, oligomerization domain and antibody specific for cytokine
                                   ;
0
                66.5%; Score 187; DB 6; Length 256; 100.0%; Pred. No. 1.7e-174; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "human TRAIL protein fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                               domain,
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                                                                                                                                                                                                                                                                                                                                                                                                          "ScFv antibody fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "immunoglobulin CH3
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                                                                                                                                                                                                                                                                                                                                                                                1. .19
/note= "signal peptide"
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/note= "linker peptide"
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                                                                                                                                                                                                                                                                              Antibody-cytokine fusion protein #3.
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                                                                                                                                                                                                                          AAO17496 standard; protein; 461 AA.
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/note= "c
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/note= "hu
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                                   Matches 187; Conservative
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                                                                                                                                                                              250 FGAFLVG 256
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                Query Match
Best Local Similarity
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Sequence 256 AA;
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                                                                                                                                                                                                                                                                                                                                   inflammation.
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                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                                                                                                                                            AA017496;
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The present invention relates to proteins comprising a segment with biological activity for a specific target molecule, a peptide linker, and a segment that is an antibody (or fragment) that recognises a specific target molecule on a cell surface. In absence of site-specific and/or segment bas no biological activity. The proteins are useful in the treatment of cancers, infections (bacterial, viral or protozol), metabolic diseases, inflammatory states (including allergy and transplant rejection), and autoimmune diseases, especially rheumatic/arthritic diseases but also multiple sclerosis and diabetes. The present sequence is a fusion protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                395 SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.5%; Score 187; DB 5; Le
100.0%; Pred. No. 2.7e-174;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "linker peptide"
Disclosure; Page 38-39; 45pp; German.
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'note=
                                                                                                                                                                                                                                                                          N-PSDB; AAL46270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 614 AA;
                                                                                                                 WO200222680-A2.
                                                                                                                                                                                                                   (WAJA/) WAJANT
                                                                                                                                       21-MAR-2002
                                                                                                                                                                                                                                                                                                                        receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB28692;
                Region
                                     Region
                                                                                Region
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ID AAB2
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AC AAB2
    SXXCCCCCCCCXXXXIIIIXXBXXBXXBXXBXXBXXBXIIIIII
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                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                            The present invention relates to proteins comprising a segment with biological activity for a specific target molecule, a peptide linker, and a segment that is an antibody (or Iragment) that recognises a specific target molecule on a cell surface. In absence of site-specific and/or selective binding of the antibody to the target, the biologically active segment has no biological activity. The proteins are useful in the treatment of cancers, infections (bacterial, viral or protozoal), metabolic diseases, inflammatory states (including allergy and transplant rejection), and autoimmune diseases, especially rheumatic/arthritic diseases but also multiple sclerosis and diabetes. The present sequence is a fusion protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                  95 TSETIISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 154
                                                                                                                                                                                                                                                                                                                                                                                               BSSRSGHSFLSNLHIRNGELVIHEKGFYXIYSQTYFRFQEEIKENTKONDKQMVQYIYKYT 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody-cytokine fusion protein; prospoptotic; immunomodulatory; cancer; immune disease; multiple sclerosis; rheumatoid arthritis; cytostatic; antiinflammatory; antirheumatic; antiarthritic; antibacterial; virucide; protozoacide; antiallergic; antidiabetic; diabetes; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
                                                                                                                                                                                                                                                                                                                                                                                                                               ESSRSGHSFLSNIHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT
                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                           New polypeptide prodrug, useful e.g. for treating tumors, comprises cytokine, oligomerization domain and antibody specific for cytokine
                                                                                                                                                                                                                                                                                                                                          Length 480;
                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                      66.5%; Score 187; DB 5; Le
100.0%; Pred. No. 2.8e-174;
ive 0; Mismatches 0;
                                                         Wueest
                                                       Moosmayer D,

    19
    /note= "signal peptide"
    20. .274

                                                                                                                                                        Disclosure; Page 36-37; 45pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody-cytokine fusion protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA017494 standard; protein; 614 AA.
15-SEP-2000; 2000DE-01045591.
                                                       Wajant H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                             Matches 187; Conservative
                     PFIZENMAIER K.
WAJANT H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FGAFLVG 480
                                                                            WPI; 2002-362336/39
                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                      N-PSDB; AAL46271
                                                                                                                                                                                                                                                                                                                  Sequence 480 AA;
                                                     Pfizenmaier K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                               155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA017494;
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                     (PFIZ/)
(WAJA/)
                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                   Local
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The present invention relates to proteins comprising a segment with biological activity for a specific target molecule, a peptide linker, and as esgment that is an antibody (or fragment) that recognises a specific target molecule on a cell surface. In absence of site-specific and/or selective binding of the antibody to the target, the biologically active segment has no biological activity. The proteins are useful in the treatment of cancers, inflections (bacterial, viral or protozoal), metabolic diseases, inflammatory states (including allergy and transplant rejection), and autoimmune diseases, especially rheumatic/arthritic diseases but also multiple sclerosis and diabetes. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 TSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   548 SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide prodrug, useful e.g. for treating tumors, comprises cytokine, oligomerization domain and antibody specific for cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.5%; Score 187; DB 5; Length 614; 100.0%; Pred. No. 3.5e-174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                      "human TRAIL protein fragment"
                                                                                                                      /note= "immunoglobulin CH3 domain"
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"ScFv antibody fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moosmayer D,
                        275. .314
/note= "linker peptide"
                                                                                                                                               419. .427
/note= "linker peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 33-35; 45pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is a fusion protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                              07-SEP-2001; 2001WO-EP010364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-SEP-2000; 2000DE-01045591.
                                                                                .418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfizenmaier K, Wajant H,
                                                                                                                                                                                                    .614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 187; Conservative
                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGAFLVG 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-362336/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PFIZ/) PFIZENMAIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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154 487 547 274 607 high solvent accessibility; cytostatic; antiarthritic; neuroprotective; trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer; lung; breast; immune-related disease; arthritis; multiple sclerosis;

human; mutant; mutein.

Synthetic

Apo-2 ligand; DR5.Apo2L complex; receptor contact region;

Human Apo-2 ligand protein mutant S96C.

(first entry)

04-DEC-2003

ADB61476;

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antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV; human immunodeficiency virus; apoptosis; proliferative disorder; cancer; hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder; transplant rejection; cardiovascular disease; arteriosclerosis; Fc-huAGP-1; fusion protein.
                                                                                                                                                                                                                                                                                                                   Fusion protein of AGP-1 protein and an Fc region, used to treat proliferative disorders, immune disorders, and virally-induced disorders.
                                            Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;
                    Fc-huAGP-1 (95-281) fusion protein.
                                                                                                                                                                                                                                                                                                                                                     Disclosure, Fig 3; 93pp; English.
                                                                                                                                                                                           24-MAR-2000; 2000WO-US008004.
                                                                                                                                                                                                                99US-00293245.
                                                                                                                                                                                                                                                                                  WPI; 2000-665240/64.
N-PSDB; AAC67832.
                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                           Hsu H, Meng S;
                                                                                                                                               WO200063253-A1.
                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                16-APR-1999;
                                                                                                                                                                    26-OCT-2000.
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The present sequence is an AGP-1 fusion protein. AGP-1 is a type II transmembrane protein. The fusion proteins comprise an Fc immunoglobulin region fused to the N-terminal portion of the AGP-1 protein. The fusion proteins can be used to induce apoptosis in a tissue, and to treat proliferative disorders, immune disorders, or virally-induced disorders, proliferative disorders include cancers, such as breast, prostate, lung or colon cancer. The viral infections include hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune disorders may be autoimmune disorders or transplant rejection. Cardiovascular diseases such as arteriosclerosis may also be treated. The AGP-1 containing fusion proteins used in prior art therapies

Sequence 441 AA;

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TSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 315
                                                                                                                            214
                                                                                                                                                          375
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                                                                                                                                                                                                        SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 435
                                                              TSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 154
                                                                                                                         ESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT
                                                                                                                                                        316 ESSRSGHSFLSNIHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT
                                                                                                                                                                                       SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF
                                Gaps
                                  .
0
 Score 186; DB 3; Length 441;
                               Indels
              100.0%; Pred. No. 2.5e-173; ive 0; Mismatches 0;
 66.28;
                             Matches 186; Conservative
                                                                                                                                                                                                                                                    FGAFLV 280
                                                                                                                                                                                                                                                                                 FGAFLV 441
              Local Similarity
                                                              95
                                                                                           256
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Query Match
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RESULT 64
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ADB61476 standard; protein; 281 AA.

Length 281;

65.8%; Score 185; DB 7; L 100.0%; Pred. No. 1.7e-172;

Query Match Best Local Similarity

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The invention trainers to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence baving 281 amino acids given in specification. The Apo-2 ligand variant polypeptide lawing substitutions at residue positions identified from x-ray crystal structure of the residue positions identified from x-ray crystal structure of the residue position(s) selected from 20 positions such as 396°, 810°C, 811°C, V114°C, 811°C, V114°C, 811°C, V114°C, 811°C, V114°C, 811°C, V114°C, 811°C, V114°C, 811°C, V114°C, 811°C, V114°C, 811°C, V114°C, 811°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81°C, 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.
                                                                                                                                                                                                                                                                                                                                                                                               /note= "Native residue of Ser is substituted by Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel isolated Apo-2 ligand variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and from the sequence in Fig 1 of the specification.
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002; 2002WO-US031210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-2001; 2001US-0326622P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kelley RF, Lindstrom SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-541400/51.
                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 96
                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003029420-A2.
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                                                                                                                                                                                                                                                                                                      Homo sapiens,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide having a sequence that differs from the native sequence having 281 amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions at residue positions identified from r-yatal structure of the DRS.Apo2L complex. The polypeptide having the substitutions made at residue position(8) selected from 20 positions such as S96C, S101C, S111C, V114C, R115C, B116C, N134C, R14C, R14C, S153C, R170C, R170K, R170S, R179C, D234C, E249S, R255C, E263C, H264C, such that the residue position is, outside of the receptor contact region of the DRS.Apo2L complex, and displays high solvent accessibility in the crystal
                         156
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                                                                                                                                           217 PDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTINEHLIDMDHEASFFG 276
                                                                                                                                                                                                                                                                                                                                                         Apo-2 ligand; DR5.Apo2L complex; receptor contact region; high solvent accessibility; cytoetatic; antiarthritic; neuroprotective; trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer; lung; breast; immune-related disease; arthritis; multiple sclerosis;
                                                                                      SRSGHSFLSNLHLRNGELVIHEKGFYXIXSQTYFRFQEIKENTKNDKQMVQYIYKYTSY
                        97 EETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWES
                                                                      SRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRPDEEIKENTKNDKQMVQYIYKYTSY
                                                                                                                      PDPILLIMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG
  Gaps
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0; Indels
0; Mismatches
                                                                                                                                                                                                                                                                                                                                  Human Apo-2 ligand protein mutant R115C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                           ADB61480 standard; protein; 281 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002; 2002WO-US031210.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kelley RF, Lindstrom SH;
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           human; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 115
                                                                                                                                                                       AFLVG 281
                                                                                                                                                                                             277 AFLVG 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
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and further of the DRS.Apo2L complex. The Apo-2 ligand variant polypeptide and further compositions have the following activities: cytostatic, antiatrhritic and neuroprocective. The Apo-2 ligand variant polypeptide, an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for cytostasing a receptor selected from DR4 receptor and DR5 receptor to a therapeutically effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, the Apo-2 ligand composition or Apo-2 ligand trimer is useful for treating cancer (such as lung, breast, colon or colorectal cancer) or immune-related disease (such as arthritis or multiple sclerosis) in a mammal, by administering to the mammal an effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand composition or Apo-2 ligand composition or Apo-2 ligand composition or Apo-2 ligand for the Apo-2 ligand composition or Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand for the Apo-2 ligand mutant R115C protein of the invention. Word: This sequence is not shown in the sequence in Fig 1 of the specification provided in claim 1
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high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
lung; breast; immune-related disease; arthritis; multiple sclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDABYGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAMMEVOGGPSLGOTCVLIVIFTVLLOSLCVAVTYVYFTNELKOMODKYSKSGIACFLKE
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Best Local Similarity 99.6%; Pred. No. 1.3e-167;
Matches 280; Conservative 0; Mismatches 1;
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01-OCT-2002; 2002WO-US031210.
                                   02-OCT-2001; 2001US-0326622P.
                                                                                                                    Lindstrom SH;
                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                          WPI; 2003-541400/51.
                                                                                                                    Kelley RF,
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Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand. Claim 1; Page; 92pp; English.

The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence polypeptide having a sequence that differs from the native sequence having all amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions at the polypeptide having the substitutions and the polypeptide having the substitutions and the polypeptide having the substitutions and the polypeptide having the substitutions made at cresidue position(s) selected from 20 positions subtained at 20 positions with the polypeptide having the substitutions made at creature position(s) selected from 20 positions as 596C, S101C, S111C, V114C, R115C, E116C, N134C, N149C, E149C, E255C, E263C, H264C, such that the creature position is, outside of the receptor contact region of the DRS.Apo2L complex. The Apo-2 ligand variant polypeptide, and further compositions have the following accivities: cytostatic, and harden composition or an Apo-2 ligand variant polypeptide, antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide, conducing apoptosis in mammalian cells, by exposing mammalian cells are colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand variant polypeptide, colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, colon or colorectal cancer cells. The Apo-2 ligand decreases) or an immune-related disease (such as arthritis or multiple sclerosis) in a mammal by broad and ministering to the mammal an effective amount of the Apo-2 ligand composition or Apo-2 ligand composition or Apo-2 ligand composition or Apo-2 ligand composition or Apo-2 ligand composition or the mammal and colorectal cancer (such as arthritis color or colorectal cancer cells and colorectal cancer cells and composition or Apo-2 ligand composition or Apo-2 ligand composition or Apo-2 ligand composition or co specification. It has been created from information provided in claim 1 and from the sequence in Fig 1 of the specification.

Sequence 281 AA;

Claim 1; Page; 92pp; English.

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FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                PYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                          DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                         61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                            RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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                                                                       1 MAMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                      Gaps
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 64.1%; Score 180; DB 7; Length 281; 99.6%; Pred. No. 1.3e-167;
                                    1; Indels
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Query Match
Best Local Similarity 99.6
Matches 280; Conservative
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Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.
                                                                                 Apo-2 ligand, DR5.Apo2L complex, receptor contact region;
high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
lung; breast; immune-related disease; arthritis; multiple sclerosis;
                                                                                                                                                                                        /note= "Native residue of Glu is substituted by Cys"
                                                               Human Apo-2 ligand protein mutant E144C.
                                                                                                                                                                      Location/Qualifiers
        ADB61484 standard; protein; 281 AA
                                                                                                                                                                                                                                                 01-OCT-2002; 2002WO-US031210.
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                                             (first entry)
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                                                                                                                          human; mutant; mutein.
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                                                                                                                                                                               Misc-difference 114
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                                                                                                                                                      Homo sapiens.
                                              04-DEC-2003
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                          ADB61484;
ADB61484
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The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence that differs from the native sequence comparing a sequence that differs from the native sequence comparing all amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions at the polypeptide having the substitutions and eat comparing the substitutions and eat comparing the substitutions and eat comparing the substitutions and eat comparing the substitutions and eat comparing the substitutions and eat comparing the receptor contact region of the DRS.Apo2L complex. The Apo-2 ligand variant polypeptide composition is outside of the receptor contact region of the compositions have the following activities: cytostatic, and further compositions have the following activities: cytostatic, and Apo-2 ligand compositions are useful for contact receptor selected from DR4 receptor and DR5 receptor to a natiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide, contacting apoptosis in mammalian cells, by exposing mammalian cells are colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, the Apo-2 ligand variant polypeptide, colon or colorectal cancer cells. The Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand variant polypeptide, colon or colorectal cancer cells. The Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the

and from the seguence in Fig 1 of the specification.

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Homo sapiens
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Matches
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                                                                                                                                                   RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                            FYYIYSQTYFREQEEIKENTKNDKQMVQYIYKYTSYPDPILLLMKSARNSCWSKDAEYGLY 240
                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                        trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer; lung; breast; immune-related disease; arthritis; multiple sclerosis;
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                                                                                                                                                                                                           181 FYYIYSQIYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                              1 MAMMBVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNBLKQMQDKYSKSGIACFLKE
                                                                                   1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYPTNELKQMQDKYSKSGIACFLKE
                                                                                                         DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                          Gaps
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                                          ö
                     Length 281;
                   Score 180; DB 7; Length 28:
Pred. No. 1.3e-167;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                     SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                           SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                                                                                                                                                                                ADB61478 standard; protein; 281
                     64.1%;
99.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lindstrom SH;
                                         280; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             human; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 111
                              Similarity
Sequence 281 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                   Query Match
Best Local (
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                                         Matches
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cc polypeptide is selected from a polypeptide having substitutions at residue positions identified from x-ray crystal structure of the DRS.Apo2L complex. The polypeptide having the substitutions made at residue position(s) selected from X-ray crystal structure of the polypeptide from X-ray crystal structure of the RISC, RIJGC, M134C, N140C, E144C, N152C, S153C, RIJOC, S111C, V114C, RIJSC, RIJGC, M134C, N140C, E144C, N152C, S153C, RIJOC, RIJOC, RIJOC, RIJOC, RIJOC, RIJOC, E249C, R255C, E263C, H264C, such that the creatidue position is, outside of the receptor contact region of the residue position is, outside of the receptor contact region of the RIS.Apo2L complex. The Apo-1 ligand variant polypeptide and further compositions have the following activities: cytostatic, and have the following activities: cytostatic, and neuroprotective. The Apo-2 ligand variant polypeptide, an Apo-2 ligand composition or an Apo-2 ligand variant polypeptide, conducing apoptosis in mammalian cells, by exposing mammalian cells are therapeutically effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, the Apo-2 ligand composition or the Apo-2 ligand variant polypeptide, colon or colorectal cancer (such as lumi), breach, colon or colorectal cancer) or immune-related disease (such as archritis or multiple sclerosis) in a mammal, by administering to the mammal an effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand composition or the Apo-2 ligand wariant sill colorected contacted from information provided in claim in the specification. It has been created from information. Colorected in Fig 1 of the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 FYYIYSQIYFRFQEBIKENIKODKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKOMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.1%; Score 180; DB 7; I 99.6%; Pred. No. 1.3e-167; iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Apo-2 ligand protein mutant El16C.
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The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence having a sequence that differs from the native sequence having all amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions at the polypeptide having the substitutions at the polypeptide having the substitutions and the polypeptide having the substitutions and the treatide position(s) selected from 20 positions such as 596c, S101C, S111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C, R170K, R170S, K179C, D234C, E249C, R25C, E263C, 1264C, such that the residue position is, outside of the receptor contact region of the DRS.Apo2L complex, The Apo-2 ligand variant polypeptide and further compositions have the following accivities: cytostatic, and Apo-2 ligand compositions have the Apo-2 ligand variant polypeptide, an Apo-2 ligand composition or an Apo-2 ligand variant polypeptide, charapeutically effective amount of the Apo-2 ligand variant polypeptide, charapeutically effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or the Apo-2 ligand variant polypeptide, colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, colon or colorectal cancer cells. The Apo-2 ligand composition or the Apo-2 ligand variant polypeptide, colon or colorectal cancer cells. The Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand variant polypeptide, and mammal an effective amount of the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specification. It has been created from information provided in claim 1 and from the sequence in Fig 1 of the specification.
                                                    /note= "Native residue of Glu is substituted by Cys"
Location/Qualifiers
                                                                                                                                                                                                          01-OCT-2002; 2002WO-US031210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page; 92pp; English.
                                                                                                                                                                                                                                                            02-OCT-2001; 2001US-0326622P
                                                                                                                                                                                                                                                                                                                                                                 Kelley RF, Lindstrom SH;
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                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-541400/51.
                           Misc-difference 116
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Best Local Similarity
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DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRISEETISTVQEKQQNISPLVRCRGPQ 120 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRISEETISTVQEKQQNISPLVRERGPQ 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 0; Gaps Length 281; 1; Indels Score 180; DB 7; I Pred. No. 1.3e-167; 0; Mismatches 1; ч 121 121 61 엄 d ð ò 셤

181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240

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120

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Dispeptide having a sequence that differs from the native sequence having all minoractions at the native sequence having about the native sequence having about the native sequence having 281 amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions at residue positions identified from x-ray crystal structure of the DRS.Apo2L complex. The polypeptide having the substitutions made at residue position(s) selected from 20 positions such as 586C, 810C, 8101C, 811C, R115C, R15C, R249C, R255C, E263C, H264C, such that the residue position is, outside of the receptor contact region of the DRS.Apo2L complex, and displays high solvent accessibility in the crystal structure of the DRS.Apo2L complex. The Apo-2 ligand variant polypeptide and tharther compositions have the following activities: cytostatic, and neuroprotective. The Apo-2 ligand variant polypeptide, an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for inducing apoptosis in mammalian cells, by exposing mammalian cells are therapeutically effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, the Apo-2 ligand composition or Apo-2 ligand variant polypeptide, the Apo-2 ligand composition or the Apo-2 ligand variant polypeptide, the Apo-2 ligand composition or the Apo-2 ligand variant polypeptide, the Apo-2 ligand composition or the Apo-2 ligand variant polypeptide, the Apo-2 ligand composition or the Apo-2 ligand variant polypeptide, the Apo-2 ligand composition or the Apo-2 ligand variant polypeptide, the Apo-2 ligand composition or the Apo-2 ligand variant polypeptide, the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand variant polypeptide, the Apo-2 ligand composition or the Apo-2 ligand variant polypeptide, the Apo-2 ligand composition or colo

The invention relates to a novel isolated Apo-2 ligand variant

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Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.
181 FYXIXSQTYFRFQEEIKENTKNDKQNVQXIXKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                 high solvent accessibility; cytostatic; antiarthritic; neuroprotective; trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer; lung; breast; immune-related disease; arthritis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                              /note= "Native residue of Arg is substituted by Cys"
                                                                                                                                                                                                     Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
                                   SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                       241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                Human Apo-2 ligand protein mutant R170C.
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                                                                                                             ADB61487 standard; protein; 281
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                                                                                                                                                                                                                                                                                                                                                                                              FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                         181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                               1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
                                                                                                                                                                                                                                  Apo-2 ligand; DR5.Apo2L complex; receptor contact region; high solvent accessibility; cytostatic; antiarthritic; neuroprotective; trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer; lung; breast; immune-related disease; arthritis; multiple sclerosis;
immune-related disease (such as arthritis or multiple sclerosis) in a mammal, by administering to the mammal an effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. This sequence represents the human Apo-2 ligand mutant R170C protein of the invention, NOTE: This sequence is not shown in the specification. It has been created from information provided in claim 1 and from the sequence in Fig 1 of the specification.
                                                                                                                                                                                      Gaps
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                                                                                                                                                                                      ;
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                                                                                                                                                     Length 281;
                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                   Score 180; DB 7; I
Pred. No. 1.3e-167;
0; Migmatches 1;
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                                                                                                                                                                 99.68;
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                                                                                                                                                                                 Matches 280; Conservative
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                                                                                                                                                                   Similarity
                                                                                                                       Sequence 281 AA;
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The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence having 281 amino acids given in specification. The Apo-2 ligand variant collypeptide having substitutions at residue positions identified from x-ray crystal structure of the DAY-Poptide positions identified from 20 positions such as 596C, S101C, V114C, R115C, B116C, M134C, M140C, E144C, M152C, S153C, R170C, S111C, V114C, R115C, E116C, M134C, R255C, E263C, H264C, such that the CRIVOK, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the CRIVOK, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the CRIVOK, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the CRIVOK, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the CRIVOK, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the CRIVOK, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the CRIVOK, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the CRIVOK, R170S, M19C, D234C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E340C, E34
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cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.
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                                                                                                                           invention relates to a novel isolated Apo-2 ligand
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Best Local Similarity 99.6%; Pred. No. 1.3e-167;
Matches 280; Conservative 0; Mismatches 1;
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high solvent accessibility; cytostatic; antiarthritic; neuroprotective; trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer; lung; breast; immune-related disease; arthritis; multiple sclerosis; bundan; mutant; mutein.

Synthetic

Homo sapiens

Location/Qualifiers Misc-difference

/note= "Native residue of Lys is substituted by Cys"

WO2003029420-A2.

10-APR-2003

01-OCT-2002; 2002WO-US031210.

02-OCT-2001; 2001US-0326622P.

(GETH) GENENTECH INC.

Lindstrom SH; Kelley RF,

WPI; 2003-541400/51.

Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.

Claim 1; Page; 92pp; English

The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence having 281 amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions dat casique positions identified from x-ray crystal structure of the residue positions identified from x-ray crystal structure of the DRS.Apo2L complex. The polypeptide having the substitutions and residue positions is elected from x-ray crystal structure of the residue position; selected from x-ray orystal structure of the TATOK, RITOS, E116C, N134C, N134C, N140C, E144C, N152C, S133C, R170C, S111C, V114C, R115C, E116C, N134C, N145C, E146C, S115C, S133C, R170C, S111C, V114C, R115C, E116C, N134C, N255C, E263C, E263C, E264C, such that the residue position is, outside of the receptor contact region of the DRS.Apo2L complex. The Apo-2 ligand variant polypeptide and further compositions have the following activities: cytostatic, antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide, antiariar are useful for inducing apoptosis in mammalian cells, by exposing mammalian cells are therapeutically effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are colorectal ancer cells. The Apo-2 ligand variant polypeptide, the Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are colorectal ancer cells. The Apo-2 ligand variant polypeptide, the Apo-2 ligand variant polypeptide, the Apo-2 ligand variant polypeptide, the Apo-2 ligand variant polypeptide, the Apo-2 ligand variant polypeptide, the Apo-2 ligand variant polypeptide, the Apo-2 ligand variant polypeptide, the Apo-2 ligand variant polypeptide, the Apo-2 ligand variant polypeptide, the Apo-2 ligand variant polypeptide, the Apo-2 ligand variant polypeptide, the Apo-2 ligand variant polypeptide, the Apo-2 ligand variant polypeptide, the Apo-2 ligand variant polypeptide, the Apo-2 ligand variant polypepti the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for treating cancer (such as lung, breast, colon or colorectal cancer) or an immune-related disease (such as arthritis or multiple sclerosis) in a mammal, by administering to the mammal an effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. This sequence represents the human Apo-2 ligand mutant K199C procesin of the invention. NOTE: This sequence is not shown in the specification. It has been created from information provided in claim 1 and from the sequence in Fig 1 of the specification.

Sequence 281 AA;

.. Score 180; DB 7; Length 281; Pred. No. 1.3e-167; 0; Mismatches 1; Indels 64.18; 99.68; Matches 280; Conservative Similarity Query Match Local

9 9 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120

1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFINELKQMQDKYSKSGIACFLKE 1 MAMMEVOGGEPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE

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RVAAHITGIRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHECG 180 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240 DDSYWDPNDEESMNSPCWOVKWOLROLVRKMILRTSEETISTVOEKOONISPLVRERGPO 120 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281 181 181 121 원 à d ò ò

RESULT 73 ADB61477

ADB61477 standard; protein; 281 AA.

ADB61477;

(first entry) 04-DEC-2003

Human Apo-2 ligand protein mutant S101C.

Apo-2 ligand, DR5.Apo2L complex, receptor contact region, high solvent accessibility, cytostatic; antiarthritic, neuroprotective, trimer, apoptosis, DR4 receptor, DR5 receptor; colon, colorectal cancer, lung, breast; immune-related disease, arthritis, multiple sclenosis; numan; mutant; mutein.

Synthetic

Homo sapiens.

Location/Qualifiers

Misc-difference 101

/note= "Native residue of Ser is substituted by Cys"

WO2003029420-A2.

10-APR-2003.

01-OCT-2002; 2002WO-US031210.

02-OCT-2001; 2001US-0326622P.

(GETH) GENENTECH INC.

Kelley RF, Lindstrom SH;

WPI; 2003-541400/51.

Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.

Claim 1; Page; 92pp; English.

The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence that differs from the native sequence below a cids given in specification. The Apo-2 ligand variant oplypeptide is selected from a polypeptide having substitutions at residue positions identified from x-ray crystal structure of the DRS.Apo2L complex. The polypeptide having the substitutions made at residue positions is selected from 20 positions such as S96C, S10C, S11C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S13C, R170C, R1

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an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for inducing apoptosis in mammalian cells, by exposing mammalian cells expressing a receptor selected from DR4 receptor and DR5 receptor to a therapeutically effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, treating cancer (such as lung, breast, colon or colorectal cancer) or an immune-related disease (such as arthritis or multiple sclerosis) in a mammal, by administering to the mammal an effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. This sequence represents the human Apo-2 ligand mutant Sillic protein of the invention. NOTE: This sequence is not shown in the appecification. It has been created from information provided in claim 1
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Sequence 281 AA;

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                                                                            102 TVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGH 161
                                                                                                                                    SFLSNIHLRNGELVIHEKGPYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPIL 221
                                                                                                                                                                             LMXSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                               102 TVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGH
                                0; Gaps
64.1%; Score 180; DB 7; Length 281; 100.0%; Pred. No. 1.3e-167;
                             0; Indels
         100.0%; Pred. ....
                             Matches 180; Conservative
Query Match
Best Local Similarity
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Human Apo-2 ligand protein mutant V114C. ADB61479 standard; protein; 281 AA. (first entry) 04-DEC-2003 ADB61479; RESULT 74 ADB61479

Apo-2 ligand, DR5.Apo2L complex, receptor contact region, high solvent accessibility; cytostatic; antiarthritic; neuroprotective; trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer; lung; breast; immune-related disease; arthritis; multiple sclerosis; human; mutant; mutein.

Homo sapiens Synthetic

/note= "Native residue of Val is substituted by Cys" Location/Qualifiers Misc-difference 114

WO2003029420-A2

10-APR-2003.

01-OCT-2002; 2002WO-US031210.

32-OCT-2001; 2001US-0326622P.

(GETH) GENENTECH INC.

Kelley RF, Lindstrom SH;

WPI; 2003-541400/51.

Novel isolated Apo-2 ligand variant polypeptide useful for treating

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The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence having a sequence that differs from the native sequence having all amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions at residue positions identified from x-ray crystal structure of the DRS.Apo2L complex. The polypeptide having the substitutions made at residue position(s) selected from 20 positions such as 596c, S101c, S111c, V114c, R115c, E116c, N134c, N140c, E144c, N152c, S153c, R170c, R170s, K179c, D214c, E249c, R255c, E263c, H264c, such that the recidue position is, outside of the receptor contact region of the DRS.Apo2L complex, and displays high solvent accessibility in the crystal structure of the DRS.Apo2L complex. The Apo-2 ligand variant polypeptide and further compositions have the following activities: cytostatic, and houroprotective. The Apo-2 ligand variant polypeptide, an Apo-2 ligand composition or an Apo-2 ligand variant polypeptide, an Apo-2 ligand composition or an Apo-2 ligand variant polypeptide, colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, the Apo-2 ligand composition or Apo-2 ligand variant polypeptide, the Apo-2 ligand composition or the Apo-2 ligand variant polypeptide, the Apo-2 ligand composition or the Apo-2 ligand variant polypeptide, the mammal, by administering to the mammal an effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or the Apo-2 ligand composition or the Apo-2 ligand wariant polypeptide, trimer. This sequence represents the human Apo-2 ligand mutant V114c protein of the invention. NOTE: This sequence in Pig 1 of the specification. It has been created from information.
cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.
                                                                                        Claim 1; Page; 92pp; English.
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Sequence 281 AA;

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                                                                                                                                                                                                                                                                                                61 DDSYWDPNDEESWNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLCRERGPQ 120
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                                                                                                                     1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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64.1%; Score 180; DB 7; Length 281; 99.6%; Pred. No. 1.3e-167; ive 0; Mismatches 1; Indels
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                                                              Matches 280; Conservative
                                  Local Similarity
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   Query Match
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ADB61486

ADB61486;

ADB61486 standard; protein; 281 AA

04-DEC-2003 (first entry)

Human Apo-2 ligand protein mutant S153C.

Apo-2 ligand; DR5.Apo2L complex; receptor contact region;

us-10-662-429-2.oligo.rag

Synthetic

trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer; lung; breast; immune-related disease; arthritis; multiple sclerosis; bunman; mutant; mutein. high solvent accessibility; cytostatic; antiarthritic; neuroprotective; /note= "Native residue of Ser is substituted by Cys" Location/Qualifiers 02-OCT-2001; 2001US-0326622P. 01-OCT-2002; 2002WO-US031210. Lindstrom SH; (GETH) GENERATECH INC. WPI; 2003-541400/51. Misc-difference 153 WO2003029420-A2 Homo sapiens. 10-APR-2003. Kelley RF,

Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.

Claim 1; Page; 92pp; English.

The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence complex by a sequence that differs from the native sequence baring 281 amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions at residue positions identified from x-ray crystal structure of the cresidue position is, outsided from 20 positions such as S96C, 1810C, 1815C,

Sequence 281 AA;

Query Match

à ద ð

1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60 9 Gaps ; 64.1%; Score 180; DB 7; Length 281; 99.6%; Pred. No. 1.3e-167; ive 0; Mismatches 1; Indels Best Local Similarity 99.6 Matches 280; Conservative Similarity

61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120

181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINCWESSRSGHSFLSNLHLRNGELVIHEKG 180 181 FYYIYSQIYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281 121 ò 8 요 à g

Search completed: March 23, 2004, 09:22:12 Job time : 64 secs us-10-662-429-2.oligo.rspt

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Q897/K6 xanthomonas
Q82uj6 nitrosomona
Q81ud0 arabidopsis
Q81ud0 arabidopsis
Q80v44 bradyrhizob
Q8dfn8 vibrio vuln
Q96d11 toxoplasma
Q9ezk4 staphylococ
Q95d2 staphylococ
Q95d2 staphylococ
Q91d6 staphylococ
Q81wub bacillus an
Q81wub bacillus an
Q81wub bacillus an
Q81y10 mus musculu
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Q15e1 salmonlla
Q8wpj2 mytilus edu
Q91se1 salmonlla
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09ybc2 aeropyrum p
083tul staphylococ
09n8d4 trypanosoma
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Q8kiu0 pseudomonas
Q8nsf0 homo sapien
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Q81835 treponema p
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Q9kc2 thermoplasm
Q8kuc2 corynebacte
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Q9r23 deinococcus
Q9r37 plasmodium
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Oglv97 arabidopsis
                                                                          March 23, 2004, 09:19:40; Search time 45 Seconds (without alignments) 1970.236 Million cell updates/sec
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1 MAMMEVQGGPSLGQTCVLIV......NEHLIDMDHEASFFGAFLVG
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Q8rn38 Q8rn13 Q8rn23 Q8rj26

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Length 304;

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Sayed A.A., Horiuchi H.H., Furusawa S., Matsuda H.;
"Identification and Charachterization of Chicken TNF-Superfamily
Ligand 8 (D130 Ligand) and 10 (Tumor Necrosis Factor Related Apoptosis
Inducing Ligand TRAIL).",
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AB114678, BAC79267.1;
SEQUENCE 304 AA; 34658 MW; DFC128B517747C96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma
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Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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Thermoplasmataceae; Thermoplasma.
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SEQUENCE 465 AA; 51450 MW; 74E47FAPF0C44BSA CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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Pred. No. 8.7e-05;
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4.6%; Score 13; DB
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Matches 13; Conservative 0; Mismatches
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MEDLINE=20479972; PubMed=11029001;
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Nature 407:508-513 (2000).
EMBL, AL445065, CACI1817.1;
InterPro; IPR007272; DUP395.
Pfam; PF04143; DUF395; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical membrane protein.
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   TISSUE=Spleen;
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OBC4D5 mus musculu
OBC4U6 vibrio chol
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OBWSM Caenchlabdi
OBWSM Caenchlabdi
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves; Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
TNF-related apoptosis inducing ligand.
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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"Rattus norvegicus TNF-related apoptosis inducing ligand (TRAIL).";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AX115578; AAM497971. -.

GO; GO:0016020; C:membrane; IEA.

GO; GO:000164; F:tumor necrosis factor receptor binding; IEA.

GO; GO:0006955; P:mmune response; IEA.

InterPro; IPR008993; TNF_like.

InterPro; IPR008993; TNF_like.

InterPro; IPR003656; TNF_subf.
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Pred. No. 1.7e-21;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annocation update)
Tumor necrosis factor related apoptosis inducing ligand.
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                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-077-2002 (TrEMBLrel. 22, Created)
01-077-2002 (TrEMBLrel. 22, Last seq
01-077-2003 (TrEMBLrel. 25, Last ann
                                                                                      Q9CQ72
Q8CDP5
Q8PQI5
Q9KTU6
Q8KI43
Q8EVG2
Q8WSN8
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ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
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PROSITE; PS50049; TNF 2; 1.
SEQUENCE 287 AA; 32979 M
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SEQUENCE FROM N.A.
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NCBI_TaxID=9031;
\begin{array}{c} \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \end{array}
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Q7T1F2;
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RESULT 5

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STRAIN=RI / ATCC 13939 / DSM 20539 / NCIB 9279;
MEDLINE=20036896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Woffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makazrova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TICR, DRA0061; ...
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0015520; F:tetracycline:hydrogen antiporter activity; IEA.
GO; GO:0015520; F:ternasporter activity; IEA.
GO; GO:0015916; F:transporter activity; IEA.
GO; GO:0015916; P:transport; IEA.
GO; GO:0015916; P:transport; IEA.
InterPro; IPR00439; Efflux EmrB.
InterPro; IPR005828; Sub_transporter.
InterPro; IPR00184; TCR_TetB.
InterPro; IPR001911; TCR_TetB.
InterPro; IPR001911; TCR_TetB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=FCC1/HN; Ma C.L., Yu X.B., Shan Z.X., Li X.R.; Ma C.L., Yu X.B., Shan Z.X., Li X.R.; "Polymorphisms in the genes are linked to Chloroquine-Resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.8%; Score 8; DB 16; Length 643;
100.0%; Pred. No. 27;
                                                                                                                                                                                                           Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales; Deinococcaceae; Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              643 AA; 67778 MW; 4168A0998E467A63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                         Last sequence update)
Last annotation update)
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                                              643 AA.
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PRINTS; PRO1036; TCRTETB.
TIGRFAMs; TIGR00711; efflux_EmrB; 1.
PROSITE; PS50850; MFS; 1.
COMPLETE protecome.
SEQUENCE 643 AA; 67778 MW; 4168A
                                                                               01-WAY-2000 (TrEMBLrel. 13, Created) 01-WAY-2000 (TrEMBLrel. 13, Last seq 01-OCT-2003 (TrEMBLrel. 25, Last ann Drug transport protein, putative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AE001862; ARF12254.1; --
PIR; G75599; G75599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.08;
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                                                                                                                                                                                       Deinococcus radiodurans.
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nes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fraser C.M.;
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Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
Jin S.S., Koo H., Jemann V., Haiao J., Blunt S., Vanaken S.S.,
Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.,
"Oryza sativa chromosome 10 BAC OSJNBa00/3161 genomic sequence.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                       Gaps
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               "The entire genomic sequence of Corynebacterium efficiens YS-314."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

BMBL, AP065214; BAC16908.1; -

Hypothetical protein; Complete proteome.

SEQUENCE 473 AA; 52745 MW; 9BBFBDBDBAA8E249 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Enrhartoideae, Oryzeae, Oryza.
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The Rice Chromosome 10 Sequencing Consortium;
"In-depth view of structure, activity, and evolution of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Nipponbare;
Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC092548; AAM18732.1; -
EMBL; AE017083; AAP53323.1; -
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                                                                                                                                               DB 16; Length 473;
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                                                                                                                                             / Match
2.8%; Score 8; DB 1
Local Similarity 100.0%; Pred. No. 21;
les 8; Conservative 0; Mismatches
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Interpro; IPR00652; Kalch_rep.
Pfam; PF00144; Kelch; 2.
SWART; SW00256; FBOX; 1.
SWART; SW00125; Kelch; 2.
PROSITE; PS50181; FBOX; 1.
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  Usuda Y., Sugimoto S.;
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paraga V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S., Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
6M03003p (GM01206)
BCDNA:GM01206 OR BCDNA:GM03003.
Drosophila melanogater (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Bukaryota, Edopteray, Arthropoda, Hexapoda, Insecta, Pterygota, Ephydroidea; Drosophila.
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EMBL; AY060851; AAL28373.1; -.
ELYBASE; EBGN0047295; BEDNA; 4446 NW; 432F8F340E895DC6 CRC64;
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EMBL; BX294142; CAD74279.1; --

Hypothetical protein; Complete proteome.

SEQUENCE 73 AA; 8265 MW; EF2C586B58E7443F CRC64;
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Last annotation update)
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100.0%; Pred. No. 27;
tive 0; Mismatches
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(TrEMBLrel. 25, I
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          133 SNTLSSPN 140
                                                    670 SNTLSSPN 677
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Su X., Kirkman L.A., Fujioka H., Wellems T.E.;
"Complex polymorphisms in an approximately kDa protein are linked to
chloroquine-resistant P. falciparum in Southeast Asia and Africa.";
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AL844506; CAD5043.1; -.
SEQUENCE 1248 AA; 146629 WW, FDBE0EBF1DF769C2 CRC64;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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                                                                                                                                             2.8%; Score 8; DB 5; Length 939;
100.0%; Pred. No. 38;
tive 0; Mismatches 0; Indels
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Plasmodium falciparum in China.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AP260819; APR69511.; ----
InterPro; IRR09011; Man 6 P R bind.
SEQUENCE 939 AA; 109367 WW; EB96972DC096412D CRC64;
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SEQUENCE 950 AA; 110601 WW; ED19FEA3B517A378 CRC64;
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Last annotation update)
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Last annotation update)
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100.0%; Pred. No. 38;
iive 0; Mismatches
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EMBL; AF030690; AAC47851.1; -..
PIR; T09076; T09076.
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                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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PF07 0035,
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Berry C., O'Niel S., Ben-Dov E., Jones A.F., Murphy L., Quail M.A., Harris D., Zaritsky A., Parkhill J.;

"The complete sequence and organisation of pBtoxis, the toxin-coding plasmid of Bacillus fluiringiensis subsp. israelensis.";

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AL731825; CAD30135.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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100.0%; Pred. No. 55;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 92;
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                                                                                                                                                                                                                                          Bacillus thuringiensis (subsp. israelensis).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang Z., Dietrich F.S.;
"YNLOGGW (STN4) mRNA.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases:
EMBL; AY245796; AAP04346.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 AA; 10480 MW; 545BF0363F697398 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 AA; 9444 MW; 6AA4C3BE7C157E67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
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Pred. No. 57;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                       88 AA.
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Best Local Similarity 100.
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Matches 7; Conservative
                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4932;
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Q9HSN3
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MEDINE=20504483; PubMed=11016950; MEDINE=20504483; PubMed=11016950; MG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Swarzaell S., R., Baliga N.S., Thorseon V., Sbrogna J., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.P., Pohlechroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; Forc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).

EMBL, AE004981; AAG18770.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xanthomonas axonopodis (pv. citri).Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;Xanthomonadaceae; Xanthomonas.
                                                                  Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.5%; Score 7; DB 17; Length 93; 100.0%; Pred. No. 57; 0; Indels tive 0; Mismatches 0; Indels
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EMBL, AE011781; AAM36362.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 94 AA; 11253 MM; A54AD81C115FBF2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
SEQUENCE 93 AA; 9680 MW; AE96B8359F340B49 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                               Halobacteriaceae; Halobacterium.
NCBI TaxID=64091;
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nes 7; Conservative
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DB 17; Length 107; 0; Indels

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al protein; Complete proteome.
107 AA; 12018 MW; 9471937E9819A836 CRC64;
                                                                                                                        Query Match
2.5%; Score 7; DB 17
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches
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      Pfam; PF04143; DUF395; 1.
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SYNW0353.
                                   Hypothetical
SEQUENCE 10
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STRANN=ATCC 35092 / DSM 1617 / P2;

MEDLINE=21332296; PubMed=11427726;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

A wayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

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Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Median N., Peng X.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Charlebois R.L., Doolittle W.F., Duguet M., Gasterland T.,

A garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

BEBBL, AE006762; AAK41690.1; -.

BRBL, REDOGO562; AAK41690.1; -.
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                                                                    Gaps
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Spermatophyta; Magnoliophyta; eudicotyledone; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL TaxID=3702;
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Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
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Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
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      DB 16; Length 94;
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SEQUENCE 106 AA; 12377 MW; A85ECD52EF507B4C CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last amontation update)
Genomic DRA, chromosome 5, Pl clone:MXX3.
Arabidopsis thaliana (Mouse-ear cress).
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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vative 0; Mismatches
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Local Similarity 100.0%; Pred. No. 64;
les 7; Conservative 0; Mismatches
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"" Res. 7:31-63(2000)
                                                                                                                               253 NDRIFVS 259
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                                                                                                                                                                                65 NDRIFVS 71
                                   Best Local Similarity
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      Query Match
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBL_TaxID=84588;
[1]
                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                   Staphylococcus aureus (strain Mu50 / ATCC 700699).
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
112 AA.
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Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches
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PROSITE; PS00397; RECOMBINASES_1; 1.
PROSITE; PS00398; RECOMBINASES_2; 1.
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236 EYGLYSI 242
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   FROM N.A.
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Q9YBC2;
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                 Palenik B., Brahamba W., Larimer F. W., Land M., Hauser L., Chain P., Lamerdin J., Regala W., Allen B.E., McCarren J., Paulsen I., Lamerdin J., Partensky F., Webb B.A., Waterbury J.;

"The genome of a motile marine Synechococcus.";

Nature 424:1037-1042(2003).

BMBL; BX569689; CARG6868.1;

Hypothetical protein; Complete proteome.

SEQUENCE 121 AA; 13842 MW; CE9C3284C63811F5 CRC64;
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Rhabditidae, Peloderinae, Caenorhabditis.
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Bacteria; Protobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
                                                                                                                     2.5%; Score 7; DB 16; Length 121; 100.0%; Pred. No. 72; tive 0; Mismatches 0; Indels
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Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
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125 AA; 12834 MW; 92D8F57FD4493496 CRC64;
                                                                                                                                                                                                                                                             01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
Hemolysin A homolog (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                           125 AA.
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           MEDLINE=22825697; PubMed=12917641;
                                                                                                                                                                                                                                                                                                                                                                        STRAIN=22491;
MEDLINE=97008141; PubMed=8855317;
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                                                                                                                  Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                120 QRVAAHI 126
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                                                                                                                                                                                     76 ORVAAHI 82
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=487;
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P72087
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Q8MM82
SWERFERE
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Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Nagai Y., Nishijiam K., Nakazawa H.,
Takamaya M., Mauda S., Fuunahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
orenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1399).
BRIR; AP000062; BAA80676.1; -.
BRIR; A72548; G72548.
Hypothetical protein; Complete proteome.
SEQUENCE 155 AA; 16841 MW; 1AA47C685D52939B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                        "Genome sequence of the nematode C.elegans: A platform for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 134;
                                                                                                                                                                                                         Lloyd C.R.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; Z38112; CAD36484.1; --
EMBL; Z35603; CAD36484.1; JOINED.
EMBL; Z35603; CAD36486.1; --
EMBL; Z35603; CAD36496.1; --
EMBL; Z38112; CAD36496.1; --
EMBL; Z38112; CAD36496.1; JOINED.
WOXMPEP; T02C12.4; CE30825.
SEQUENCE 134 AA; 15340 MW; 1DB9A0AD8814E477 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales; Desulfurococcaceae; Aeropyrum.
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Last sequence update)
Last annotation update)
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MEDLINE=99069613; PubMed=9851916;
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(TrEMBLrel. 24, L
(TrEMBLrel. 24, L
                                                                                     investigating biology.";
Science 282:2012-2018(1998)
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Last annotation update)

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01-OCT-2003 (TrEMBLrel. 25, L. Hypothetical protein XCC2605.
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Best Local Similarity
                                                                   NCBI TaxID=340;
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Q82UJ6
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A Atkin R.J., Barron A.J., Bart-Delabesse E.N., Bowman S.,
Bray-Allen S.P., Bringaud F., Clark L.N., Corton C.H., Cronin A.,
Davies R., Doggett J., Fraser A., Gruter E., Hall S., Harper D.A.,
A Rabbinowitsch B., Rutherford K., Sasse J., Sharp S., Shownkeen R.,
Gull K., Barrell B.G., Melville S.E.;
"The sequence and analysis of the highly polymorphic chromosome I of
I The African trypanosoma brucel.";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
R GJ: GO:0008080; F:Nacctyltransferase activity; IEA.
R GJ: GO:0016740; F:transferase activity; IEA.
R InterPro; IPR000182; GCNSactyl trans.
R Pfam; PF00583; Acetyltransf; 1.
                                                               STRAIN-Newman, and ISP479C;
Steinhuber A., Goerke C., Bayer M.G., Doring G., Wolz C.;
Steinhuber A., Goerke C., Bayer M.G., Doring G., Wolz C.;
"Molecular architecture of the regulatory locus sae of Staphylococcus aureus and its impact on the expression of virulence factors.";
Submitted (ARR-2003) to the EWBL/GenBank/DDBJ databases.
EMBL, AJ556794; CAD89113.1;
EMBL, AJ556795; CAD89113.1;
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Trypanosoma brucei.
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
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                                                                                                                                               Hypothetical protein.
SEQUENCE 157 AA; 17665 MW; AF973D8D95D5963E CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Acetyltransferase, possible.
TB927.1.4490.
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Last sequence update)
         Stāphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
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100.0%; Pred. No. 97;
tive 0; Mismatches
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100.0%; Pred. No. 90;
tive 0; Mismatches
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                                                                                                                                                                      Query Match
Best Local Similarity 100.
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Hypothetical protein.
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                                                      SEQUENCE FROM N.A.
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ID Q8
AC Q8
DT 01
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 23913 / NCPPB 528;

MEDINE=20202145; PubMed=12024217;

MEDINE=20202145; PubMed=12024217;

A Bargio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

Raia J.B., Ferreira A.J.S., Ferreira R.C.C., Farro M.T.,

Ratia J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,

Ratsuyama A.M., Kishi L.T., Lelte R.P., Lemos B.G.M., Lemos M.V.F.,

Martins E.C., Machadus M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Machadus M.A., Manck C.F.M., Miyaki C.Y., Moon D.H.,

Rations E.C., Machadus M.A., Okura V.K., Oliveira M.C., Oliveira W.R.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Tarkita M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D.,

Ratindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Setubal J.C., Kitajima J.P.;

T. "Comparison Of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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STRAIN-ATCC 19718 / IFO 14298;
MEDLINE-22586410; PubMed=12700255;
MEDLINE-22586410; PubMed=12700255;
Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M., Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A., Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
Complete genome sequence of the ammonia-oxidizing bacterium and obligate chemolithoautoroph Nitrosomonas europaea.";
J. Bacteriol. 185:2759-2773 (2003).
EWBL; BX31861; CAD85399.1;
GO: 00016874; Filiqase activity; IEA.
GO: GO: 0009107; Filipoate biosynthesis; IEA.
Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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Hypothetical protein; Complete proteome.
SEQUENCE 193 AA; 22001 MW; F00A357929414027 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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LIPB OR NE1488.
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NCBI_TaxID=915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             host specificities.";
Nature 417:459-463(2002).
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clones.";
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091100
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 702145; PubMed=12024217;

MEDINE=20212145; PubMed=12024217;

A a Silva A.C.R., Ferro d-1.202417;

A da Silva A.C.R., Ferro d-1.202417;

A da Silva A.C.R., Ferro d-1.20., Van Sluys M.A., Almeida N.F., Alves L.M.C., do Amaral A.M., Betrolini M.C., Camargo L.E.A.,

A camarotte G., Cannavan F., Cutano Sanco J.R., El-Dorry H., Ferral J.B., Ferral A.B., Ferral R.C.C., Ferro M.I.T.,

A ratia J.B., Ferral C.B., Van Sluys M.A., Lemos B.G., Greggio C.C., Gruber A.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

A Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

B.C. Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Machado M.A., Mack C.F.M., Miyaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sana J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Tamita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Sctubal J.C., Kitajima J.P., f.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.";
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Xanthomonas axonopodis {pv. citri}.
Bacteria; Fortebacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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                                                                                                                                                              2.5%; Score 7; DB 16; Length 204; 100.0%; Pred. No. 1.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.5%; Score 7; DB 16; Length 216; 100.0%; Pred. No. 1.2e+02; tive 0; Mismatches 0; Indels
      GO; GO:0006464; P:protein modification; IEA.
InterPro; IPR004143; BPL LipA LipB.
InterPro; IPR00644; LipOate B.
Pfam; PF03099; BPL LipA LipB; 1.
ProDom; PD006086; LipOate B; 1.
IGRPAMS; TIGR00214; LipB; 1.
PROSITE; PS01313; LIPB; 1.
Ligase; Complete proteome.
SEQUENCE 204 AA; 22764 MW; A83F6EF5F0346E61 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein XAC2766.
                                                                                                                                                                                                                                                                                                                                         216 AA.
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EMBL, ABOL1917, AAM37611.1; -.
InterPro; IPR006839; DUF615.
InterPro; IPR001232; Skpl.
InterPro; IPR008945; Skpl.Skp2.
                                                                                                                                             Query Match
Best Local Similarity 100...
Lag 7; Conservative
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                                                                                                                                                                                                                                                           97 ROLVRKM 103
                                                                                                                                                                                                                              85 RQLVRKM 91
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Q8PIX9
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161 QLRQLVR 167

RESULT 28

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"Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
features of the regions of 4,504,864 bp covered by sixty Pl and TAC
                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
02-0CT-2003 (TrEMBLrel. 25, Last annotation update)
03-0CT-2003 (TrEMBLrel. 25, Last annotation update)
03-0CT-2003 (TrEMBLrel. 25, Created)
04-0CT-2003 (TrEMBLrel. 25, Created)
04-0CT-2003 (TrEMBLrel. 25, Created)
05-0CT-2003 (TrEMBLrel. 25, Created)
06-0CT-2003 (TrEMBL
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MEDLINE=22484998; PubMed=12597275;
Raneko T., Nakamura Y., Saro S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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DNA Res. 9:189-197(2002).
EMBL; AP005939; BAC46479.1; -.
INTERPRO; IPRO00437; PROKALIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tabata S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 217;
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100.0%; Pred. No. 1.2e+02;
trive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Ta
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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EMBL; AB025608; BAA95731.1; -.

InterPro; IPR008637; HR lesion.

Pfam; PF05514; HR lesion;

SEQUENCE 217 AA; 25219 WW; F88CDEIA0BEABC4F CRC64;
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Last annotation update)
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   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20277480; PubMed=10819329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.0
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 SFFGAFL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Columbia;
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
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Staphylococcus aureus.
                                                                                                                                                                                                                                                            Rot-like protein Rlp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 RIFVSVT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                        09EZK4;
01-MAR-2001
01-JUN-2001
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RESULT 32
Q9EZK4
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Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
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"Molecular characterization of TgMICS, a proteolytically processed antigen secreted from the micronemes of Toxoplasma gondii.";
Mol. Biochem. Parasitol. 11:51-66(2000).

EMBL; Y09782; CAA70921.1; -.
SEQUENCE 231 AA; 25984 MW; 9C5B0E4690B36314 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H., Choy H.E.;
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5. 1.2e+02;
cches 0; Indels
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5. 1.3e+02;
cches 0; Indels
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016797; AAO08706.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 AA; 24807 MW; 94A0EF9F43F33FAD CRC64;
                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                           222 AA.
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Best Local Similarity 100.0%; Pred. No. 1.3
Matches 7; Conservative 0; Mismatches
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2.5%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 1.2
Matches 7; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                               113 LVRERGP 119
                                                                                             110 LVRERGP 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio vulnificus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome. SEQUENCE 222 AA;
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SETAINEMUSO, and N315;

MEDLINE=21311952; PubMed=11418146;

MEDLINE=21311952; PubMed=11418146;

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MEDLINE=22040717; PubMed=12044378;
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Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramateu K.;
"Genome and virulence determinants of high virulence community-
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
SARH2 OR SAV2499 OR SA2287 OR MW2418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.5%; Score 7; DB 2; Length 247; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF288788; AAG45334.2; --
SEQUENCE 247 AA; 29792 MW; D078366866F60B2B CRC64;
                                   01-WAR-2001 (TrEMBLrel. 16, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus (strain Mu50 / ATCC 700699), Staphylococcus aureus (strain N315), and Staphylococcus aureus (strain NW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus. NCBI_TaxID=1558078, 158879, 196620;
                                                                                                                                                                               Bacteria; Firmicutes; Bacillales; Staphylococcus
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2.5%; Score 7; DB 16; Length 253; 100.0%; Pred. No. 1.4e+02; tive 0; Mismatches 0; Indels

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Hypothetical protein, Complete proteome.
SEQUENCE 253 AA; 27656 MW; 358A4F06B9B66C8E CRC64;
     Pfam; PF00990; GGDEF; 1.
SMART; SM00267; DUE; 1.
TIGREAMS; TIGR00254; GGDEF; 1.
PROSITE; PS50887; GGDEF; 1.
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EMBI, AP003005; BAB51407.1; -
InterPro, IPR00106; G3DEC.
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Phyllobacteriaceae, Mesorhizobium.
                                                                                                                                                  Ouery Match 2.5%; Score 7; DB 16; Length 247; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 7; Conservative 0; Mismatches 0; Indels
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Complete proteome.
SEQUENCE 247 Aa; 29793 MW; 90AE3B0F7A87CC35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetacese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein mll4839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
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MEDLINE=21082930; PubMed=11214968;
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Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                             255 RIFVSVT 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The genome sequence of Bacillus anthracis Ames and comparison to
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2.5%; Score 7; DB 16; Length 271
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                              Bacillus anthracis (strain Ames).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=198094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Complete proteome.
SEQUENCE 271 AA; 31338 MW; D01E8F4D025FF187 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0016707; F:hydrolase activity; IEA.
GO; GO:006725; P:araneatic compound metabolism; IEA.
InterPro; PR0000073; A/b hydrolase.
InterPro; IPR003089; AB_hydrolase.
InterPro; IPR003089; Ser_estrs.
Pfam; PR00551; abhydrolase; 1.
PRINTS; PR00111; ABHYDROLASE.
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Last annotation update)
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                                                                                                                                                                                                                   01-JUN-2003 (TIEMBLREL: 24, Created) 01-JUN-2003 (TIEMBLREL: 24, Last seq 01-OCT-2003 (TYEMBLREL: 25, Last annitydrolase, alpha/beta fold family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        closely related bacteria.";
Nature 423:81-86(2003).
EMBL; AE01/036; AAP27611.1; -.
TIGR; BA3877; -.
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                           PRELIMINARY;
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168 FGAFLVG 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S., Wessels M.R., Paulsen I.T., Nelson K.B., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherry S.C., DeBOY R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
                                                                                                                                                                                                                                                                                                                       Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek I., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                      Kunst F.,; "Genome sequence of Streptococcus agalactiae, a pathogen causing
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100.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus agalactiae (serotype V).
Bacteria, Firmicutes, Lactobacillales; Streptococcaceae;
                                                                                                                                  Streptococcus agalactiae (serotype III).
Bacteria, Pirmicutes, Lactobacillales, Streptococcaceae,
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298 AA; 32452 MW; 5BF7720198133368 CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                            Last sequence update)
Last annotation update)
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                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Microbiol. 45:1499-1513(2002).
EMBL; AL766853; CAD47435.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=NEM316 / Serotype III;
MEDLINE=22242508; PubMed=12354221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=2603 V/R / Serotype V;
MEDLINE=22222988; PubMed=12200547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE014270; AAN00594.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                       invasive neonatal disease.";
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23,
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Best Local Similarity الاست
الا كانت
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                                            01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                        01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sagalist; gbs1776; -. Hypothetical protein;
                                                                                        Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=216466;
                                                                                                                                                                                   Streptococcus.
NCBL_TaxID=216495;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of Chlamydophila caviae (Chlamydia psittaci GPIC): examining the role of niche-specific genes in the evolution of the Chlamydiaceae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22569155; PubMed=12682364;
Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A.
Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
Fraser C.M.;
Hypothetical protein (Fragment).

Was musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydophila caviae.
Bacteria, Chlamydiae, Chlamydiales, Chlamydiaceae, Chlamydophila.
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                                                                                                                                                                                                                                                                                                                                                2.5%; Score 7; DB 11; Length 293; 100.0%; Pred. No. 1.5e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                   Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC026645; AAH26645.1; -.
Hypothetical protein.
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TIGRRAMs, TIGR00544; lgt; 1.
Lipoprotein; Transferer Complete proteome.
SEQUENCE 296 AA; 33457 WW; 1E148CA397939E64 CRC64;
                                                                                                                                                                                                                                                                                                 293 AA; 33723 MW; 642B913C78884195 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-UTN-2003 (TrEMBLrel. 24, Created)
01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 31:2134-2147(2003).

EMBL, AEG1695; AAP05216.1; -.

TIGR, CCA00471; -.

GO, GO:0016020; C:membrane; IEA.

GO, GO:0015740; F:transferase activity; IEA.

GO, GO:0009249; P:protein-lipoylation; IEA.

InterPro; IPR001640; LGI.
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 LRTSEET 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01790; LGT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 LRTSEET 11
                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                     [1]
SEQUENCE FROM N.A.
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                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                  TISSUE=Colon;
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WEDLINE=CO196006; Pubmed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
A Adams M.D., Celniker S.E., Holt R.A.,
A Adams M.D., Celniker S.E., Holt R.A.,
A Gorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.K., Yandell M.D., Zhang Q., Chen L.X.,
A Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bellew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Bouck J., Broklerein P., Brottler P.,
Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
                                                                                                                                                                                                                                                                                                                            Phelan M., Farmer A.; "Cloning of human full-length CDSs in BD Creator(TM) System Donor
                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
Similar to cAMP responsive element binding protein-like 1.
                                                                                                                                                                                                                                                                                                                                                                                                                             2.5%; Score 7; DB 4; Length 318;
100.0%; Pred. No. 1.6e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC008394; AAH08394.1; -.
EMBL; BT007042; AAP35691.1; -.
SEQUENCE 318 AA; 33894 MW; D70E20D5409C165B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 322 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
                                                                             PRT;
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Matches 7; Conservative
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                                                                            PRELIMINARY;
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                                                                                                                                                        Homo sapiens (Human)
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92 VLLOSLC 98
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                                                                                                                                                                                                                                     TISSUE=Prostate;
                                                                                                                                                                                              NCBI_TaxID=9606;
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01-MAY-2000
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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kammel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liu X., Mattei B., McIntosh T.C., Morris J., McPherson D.,
Liu X., Mallshina N.V., Mobarry C., Morris J., Moshrefi A.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Nelson D.K., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.W.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Krämos I., Simpson M., Skrupski M.P., Smith T.,
Shue B.C., Siden-Krämos I., Simpson M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q., Zheng I.,
RA Benome Sequence of Drosophila melanogaster.";
RT "The genome sequence of Drosophila melanogaster.";
R. Science 287:2185-2195(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farian D., Frise B., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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100.0%; Pred. No. 1.7e+02;
tive 0; Mismatches 0; Indels
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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EMBL; AY089235; AAL6973.1; -.
FlyBase; FBGM037455; CG2336.
SEQUENCE 322 AA; 36891 MW; D8680A7A63BBS988 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein Xf0992.
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MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xanthomonadaceae; Xylella.
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132 RSNTLSS 138
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084846
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Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
A Frieger T.E., Kuranne B.E., Laigret F., Lambais M.R., Leite L.C.,
Lemos B.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Martino U.L.,
Marchado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
Marques M.V., Martins E.A.L., Martins E.M.F., Matchkuma A.Y.,
Marques M.V., Marcaca E.C., Miyaki C.Y., Monteiro-Vitoriello C.B.,
Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
Moni A.Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
Moon D.H., Nepraira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
A Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
A da Silva A.C.R., da Silva F.R., Silva W.A., Jr.,
A da Silva A.C.R., Van Silva M.M., Taai S.N., Tsuhako M.H.,
A vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
Nature 406:151-159(2000).
M. RIMEL, AR003937; AAR93802.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDILTE=99120557; PubMed=9923682;
MEDILTE=99120557; PubMed=9923682;
All R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
Trust T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.5%; Score 7; DB 16; Length 327 100.0%; Pred. No. 1.7e+02; ive 0; Mismatches 0; Indels
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Hypothetical protein; Complete proteome.
SEQUENCE 327 AA; 35553 MW; 96A5841EB1A08E90 CRC64;
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01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Matches
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MEDLINE=22709201; PubMed=12810954;
MEDLINE=22709201; PubMed=12810954;
Merbhaum S., Josenhans C., Sterzenbach T., Drescher B., Brandt P.,
Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A.,
Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,
Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
"The complete genome sequence of the carcinogenic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                   Helicobacter hepaticus.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of an obligate intracellular pathogen of humans:
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Bacteria, Chlamydiae, Chlamydiales, Chlamydiaceae, Chlamydia
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Pfam, PF03739; YJgP_YJgQ; 1.
Hypothetical protein; Complete protecme.
SEQUENCE 354 AA; 40065 MW; AD79C8F2CD59F4E5 CRC64;
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                                                                                                                                                                                                                                    01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) DTDP-D-glucose 4,6-dehydratase (EC 4.2.1.46).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter hepaticus.";
Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).
EMBL; AE017144; AAP76696.1; -.
Lyase; Complete proteome.
                                                                                                                                                    343 AA.
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                                                                                                                                                                            Q7VJZ3;
01-OCT-2003 (TrEMBLrel. 25, Created)
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Les 7; Conservative
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46 RSNTLSS
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NCBI_TaxID=813;
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2.5%; Score 7; DB 16; Length 354;

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                                                   Gaps
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OSTATC OR B1080D07.14.
OSTATC OR B1080D07.14.
EURAryotat Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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MEDLINE=21140310; PubMed=11244106;
Agrawal G.K., Yamazaki M., Kobayashi M., Hirochika R., Miyao A.,
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Nucleic Acids Res. 28:1397-1406(2000).
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Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
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100.0%; Pred. No. 1.8e+02; ive 0; Mismatches 0; Indels
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InterPro; IPR005495; YigP_YigQ.
Pfam, PF03739; YigP_YigQ: 1.
Hypothetical protein; Complete proteome.
SEQUENCE 354 AA; 40145 MW; E6A1317A124C10D1 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein TC0227.
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Best Local Similarity 100.
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Best Local Similarity 100.
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Mount D.B., Gamba G.;
Mount D.B., Gamba G.;
Mount D.B., Gamba G.;
Mount D.B., Gamba G.;
Partial sequence of xKCC, a K-Cl cotransporter from Xenopus laevis.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF325505; AAK28520.1; -..
GO; GO:00105215; Fitransporter activity; IEA.
GO; GO:0006811; P:ion transport; IEA.
InterPro; IPR000622; KCl_Cotransport.
Pfam; PF03522; KCl_Cotranspli.
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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0
                                                                       STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
"Loryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
clone:B1080D07.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ABOS0885; BAB39766.1;
GEMBL, ABOS0303; BAB64068.1;
Gramene; Q9AVE6; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.5%; Score 7; DB 10; Length 359; 100.0%; Pred. No. 1.8e+02; Ative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           359 AA; 38763 MW; D25349B32FE1B540 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Endo-1,4-mannanase precursor (EC 3.2.1.78).
Mytilus edulis (Blue mussel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Plant Physiol. 125:1248-1257(2001).
                                                                                                                                                                                                                                                                            InterPro, IRR008277; Tat C.
InterPro, IPR02033; Translocase.
Pfam, PF00902; TatC; 1.
IGRFAMS; TIGR00945; tatC; 1.
PROSITE; PS01218; TATC; 1.
SEQUENCE 359 AA, 38763 MW; D2:
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 DRIFVSV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 DRIFVSV 147
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                                                    SEQUENCE FROM N.A.
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SEQUENCE
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Q8WPJ2;
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NCBI_TaxID=601;
                                                                    PLASMID=R2
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Palenik B., Brahamsha B., Larimer F.W., Land M., Hauser L., Chain P.,
Lamerdin J., Regala W., Allen E.E., McCarren J., Paulsen I.,
Dufresne A., Partensky F., Webb E.A., Waterbury J.;
"The genome of a motile marine Synechococcus.";
Mature 424.1037-10421(2003)
BMBL; BX569695; CAE08826.1; -.
                                                                                                         TISSUE-Gill;

Xu B., Janson J.C., Sellos B.;

"An endo-1,4-beta-d-mannanase gene isolated from mytilus edulis.";

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ271365; CAC81056.1;

GO; GO:0016798; F.:Mydrolase activity, acting on glycosyl bonds; IEA.

GO; GO:0016985; F.:mannan endo-1,4-beta-mannosidase activity; IEA.

GO; GO:0016985; F.:mannan endo-1,4-beta-mannosidase activity; IEA.

GO; GO:0016985; F.:mannan endo-1,4-beta-mannosidase activity; IEA.

GO; GO:0016986; F.:mannan endo-1,4-beta-mannosidase activity; IEA.

GO; GO:0016986; F.:mannan endo-1,4-beta-mannosidase activity; IEA.

GO; GO:0016986; F.:mannan endo-1,4-beta-mannosidase activity; IEA.

FOOTON: UNINNANANEE.
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Plasmid R27, and Plasmid pHCMI.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
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100.0%; Pred. No. 1.9e+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     DB 5; Length 367; . 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        374 AA; 41775 MW; A1FFC8CE06FBB444 CRC64;
                                                                                                                                                                                                                                                                                                                                    18 367 ENDO-1,4-MANNANASE.
367 AA; 40956 MW; B364E0341BD2EA86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synechococcus sp. (strain WH8102).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
0rf, hypothetical protein (Hypothetical protein).
R0207 OR HCMI.114.
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Last annotation update)
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100.0%; Pred. No. 1.9
tive 0; Mismatches
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01-0CT-2003 (TrEMBLrel. 25, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
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                            Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity luv...
7; Conservative
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Matches 7; Conservative
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SEQUENCE 374 AA;
                                                                                           SEQUENCE FROM N.A.
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                                              NCBI_TaxID=6550;
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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DENGEMENT FROM N.T.

STRAIN=CT16; PLASMID=PHCM1;

MEDLINE=21534947; PubMed=11677608;

MEDLINE=21534947; PubMed=11677608;

MEDLINE=21534947; PubMed=11677608;

MEDLINE=21534947; PubMed=11677608;

MEDLINE=21534947; PubMed=11677608;

Mingall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,

Cronin A., Davies R., Davies R.M., Dowd L., White N., Farrar J.,

Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,

Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,

Whitehead S., Barrell B.G.; Amoultiple drug resistant Salmonella

"Complete genome sequence of a multiple drug resistant Salmonella
                                                          MEDINE-20280091; PubMed=10773089;
Sherburne C.K., Lawley T.D., Gilmour M.W., Blattner F.R., Burland V.,
Grotbeck E., Rose D.J., Taylor D.E.;
"The complete DNA sequence and analysis of R27, a large IncHI plasmid
from Salmonella typhi that is temperature sensitive for transfer.";
Nucleic Acids Res. 28:2177-2186(2000).
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EMBL; AF250878; AAF70043.1; -.

EMBL; AL513383; CAD09712.1; -.

GO; GO:0046821; C:extrachromosomal DNA; IEA.

Hypothetical protein; Plasmid; Complete protecome.

SEQUENCE 375 AA; 42554 NW; 98669AIE335525C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             375 AA; 41620 MW; 3A9F8E7BB626464C CRC64;
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01-0UN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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InterPro, IPR008934, AcPase VanPerase.
InterPro, IPR002803; DUF100.
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STRAIN=AV19 / DSM 6324 / JCM 9639;
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Best Local Similarity 10v...
7; Conservative
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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NCBI_TaxID=2320;
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2.5%; Score 7; DB 17; Length 375;

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RESULT 57
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                                                                                              Gaps
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 24, Last annotation update)
4-nitrophenylphosphatase-like.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
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Raneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
Tabata S.;
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Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
NCBI_TaxID=375;
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100.0%; Pred. No. 1.9e+02;
Live 0; Mismatches 0; Indels
                                                                                     Indels
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Complete protecome.
SEQUENCE 379 AA; 40061 MW; 30D67BCB25880B61 CRC64;
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Last annotation update)
                                        1.9e+02;
hes 0;
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                                                                                     Mismatches
                                            Pred. No.
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InterPro; IPRO06357; HAD_SF_IIA.
InterPro; IPR006334; Hydrolase.
InterPro; IPR006349; PGP-cuk.
Pfam; PF00702; Hydrolase; 1.
TIGRFAMS; TIGR01460; HAD-SF-IIA; 1.
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100.08; P1
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Best Local Similarity 100.0
7; Conservative
                                                                                     7; Conservative
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                                                                                                                                                                      169 LRNGELV 175
                                                                                                                                                                                                                                                       307 LRNGELV 313
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                                        Best Local Similarity
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Q89SW4
                                                                                     Matches
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Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
Simpson A.J.G., Reinach F.C., Arruda P., Baia G.S., Baptista C.S.,
A Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Carraro D.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., El-Dorry H.,
Raga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
Raga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
Bachiella J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
Rrieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
Rrieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
Rrieger J.E., Martins E.A.L., Martins E.M.F., Marchado J.R.,
Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y.,
Mannado M.A., Madeira A.M.B.N., Martins E.M.F., Matsukuma A.Y.,
Mannado M.A., Nascimento A.L.T.O., Netto L.E.S.,
Nhani A.Jr., Nobrega F.G., Miyaki C.Y., Monteiolio-Vitorello C.B.,
Nhani A.Jr., Nobrega F.G., Miyaki C.Y., Monteiolio-Vitorello C.B.,
A G. Silva A.C.R., de Sallva A.M., da Silva A.M. A. Jr.,
A da Silva A.C.R., da Silva A.M., da Silva A.M. A. Jr.,
A da Silva A.C.R., da Silva A.M., L.Z., Siqueira W.J., Tsuhako M.H.,
A da Silva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A Zago M.A., Zatz M., Meidanis J., Setubal J.C.,
Mature Genome sequence of the plant pathogen Xylella fastidiosa.";
H. Fahria a. Napalana.
                                                                                                                                                                    Gaps
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                                                                                                   Length 389;
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100.0%; Pred. No. 2e+02;
trive 0; Mismatches 0; Indels
TIGRFAMB; TIGR01452; PGP_euk; 1.
SEQUENCE 389 AA; 43131 NW; 96E3D9A7BC4E0583 CRC64;
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InterPro; IRR008928; Glyco trans 6hp.
Hypothetical protein; Complete proteome.
SEQUENCE 401 AA; 46935 MW; B773581D85270510 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein Xf1611.
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vative 0; Mismatches
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                                                                                                                              Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         xylella fastidiosa.
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Matches
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MEDLINE-22421331; PubMed=12533478;

MEDLINE-22421331; PubMed=12533478;

MAYAKI C.Y. Purlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,

Nayaki C.Y. Purlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,

Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,

Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Derry H., Teai S.M.,

Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,

A Carrer H., Carraro D.M., Abreu I.L., Alves L.R., of Amaral A.M.,

Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,

Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,

da Cunha A.P., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,

Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.T., Sena J.A.D.,

de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,

Kitajima J.P.,

Kitajima J.P.,
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EMBL, ARCJAG933; BABL5032.1; -.

EMBL, ARCJAG933; BABL5032.1; -.

Hypothetical protein.

SEQUENCE 402 AA; 46254 MW; 716C111B5B794DC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Comparative analyses of the complete genome sequences of Pierce's disease and citrus variegated chlorosis strains of Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                      PD1162.

Xylella fastidiosa (strain Temeculal / ATCC 700964).

Bacteria; Froteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.

NCBI_TaxID=183190;
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels.
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BMBL, AE012557; AA029015.1;
InterPro, IPR008928; Glyco trans_Ghp.
Hypothetical protein; Complete proteome.
SEQUENCE 401 AA; 46925 MW; 2380EA4DB84D2944 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 25, Last annotation update)
Hypothetical.protein FLJ21240.
Homo sapiens (Human).
                                                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                              401 AA.
                                                                                                                                                  Conserved hypothetical protein.
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                              PRELIMINARY;
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Best Local Similarity
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Q87CC1
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DT Q1-JUN-
DT Q1-JUN-
DE CONSERV
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SEQUENCE FROM N.A.

STRATN=ATC 35092 / DSM 1617 / P2;

MEDLINE=21332296; PubMed=11427726;

MEDLINE=21332296; PubMed=11427726;

A RAGYEZ M.J., Chan-Welher C.C.-Y., Clausen I.G., Curtis B.A.,

A RAGYEZ M.J., Chan-Welher C.C.-Y., Clausen I.G., Curtis B.A.,

A Heikamp-de Jong I., Jeffrise A.C., Kozera C.J., Medina N., Peng X.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.,

The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

Proc. Natl. Acad. Sci. U.S.A. 98:7815-7840(2001).

PHOSPHRIBOSYLTRANSFERASE FAMILY.
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EMBL, AE006691; AAK40942.1; -.
PIR; G90210; G90210.
HSSP; P004497; 1GPH.
GO; GO:0004044; F:amidophosphoribosyltransferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
GO; GO:0016757; P:transferase activity, GO; GO:0008152; P:metabolism; IEA.
GO; GO:0008152; P:metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SERAINS-ATCC 35092 / DSW 1617 / P2;

MEDLINE-20165948; PubMed=10701121;

Charlebois R.L., Singh R.K., Chan-Weiher C.C.-Y., Allard G., Chow C.,

Confalonieri F., Curtis B., Duguet M., Brauso G., Faguy D.,

Gasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C.,

Kushwaha N., Lafleur E., Medina N., Peng X., Penny S.L., She Q.,

St Jean A., van der Oost J., Young F., Zivanovic Y., Doolittle W.F.,

Ragan M.A., Sensen C.W.,

"Gene content and organization of a 281-kbp contig from the genome of

the extremely thermophilic archaeon, Sulfolobus solfataricus P2.";
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Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
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PURF-2 OR SSO0633 OR CO8_016.
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
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Pfam; PF00156; Pribosyltran; 1.
PROSITE; PS00103; PUR PNR PR TRANSFER; 1.
G1yCOSyltransferase; Transferase; Complete proteome.
SEQUENCE 404 AA; 44839 MW; DFFF4D11A07FD8A0 CRC64;
                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Amidophosphoribosyltransferase (ATASE) (Glutamine
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InterPro; IPR002375; Pr/py rp_transf.
InterPro; IPR000836; PRTransferase.
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Matches 7; Conservative
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94 RISEETI 100
                                                                      29 RTSEETI 35
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49 YSKSGIA 55

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83 QLRQLVR 89
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Matches 7; Conserv
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     HID DE RELEASE DE LA COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCOCO COCCO COCOCO COCOCO COCCO COCCO COCCO COCCO COCCO COCCO COCOCO COCCO COCCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAINE-SF370 / ArCC 700294 / Serotype M1;

MEDLINE-21192684; PubMed=11296296;

A Ferretti J. J., McShan W.M., Ajdic D.J., Savic G., Lyon K.,

Primeaux C., Seazte S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,

Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,

A vian X., Clifton S.W., Roe B.A., McLaughlin R.;

"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";

Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

RMBL; AE006631; AAK34765.1; -.

RO; GO:0005215; Fitzansporter IEA.

RO; GO:0005215; Fitzansporter IEA.

RO; GO:0006810; Pitzansporter IEA.

RITEPPO; IPR005828; Sub_transporter.

InterPro; IPR005828; Sub_transporter.

REPPO: ARC PROSESS; Sub_transporter.

REPPO: ARC PROSESS; Sub_transporter.

REPPO: ARC PROSESS; Sub_transporter.

REPPO: ARC PROSESS; Sub_transporter.

REPPO: ARC PROSESS; Sub_transporter.

REPPO: ARC PROSESS; Sub_transporter.

REPPO: ARC PROSESS; Sub_transporter.

REPPO: ARC PROSESS; Sub_transporter.

REPPO: ARC PROSESS; Sub_transporter.

REPPO: ARC PROSESS; Sub_transporter.
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MEDLINE=21927593; PubMed=11917108;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
Sylva G.L., Sturdevant D.E., Ricklefe S.M., Porcella S.F.,
Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
"Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
outbreaks.";
Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Putative integral membrane protein.
SPYMI8_2178.
                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
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                                                                                                                               PRELIMINARY;
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35 YSKSGIA 41
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SEQUENCE 406 AA,
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Q8NZ26;
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Matches
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HERE TO BE THE SET OF

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C STRAIN-SSI-1 / Serotype M3;

Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,

Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,

Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,

Hayashi H., Hamada S.,

"The genome of invasive Streptococcus pyogenes; a comparative analysis of S. Pyogenes SSI-1, SF370 and MGASB232.";

E. Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AR014171; AAM80411.1; -.

DR GO; GO:0016020; E:membrane; IEA.

GO; GO:0016020; F:transporter activity; IEA.

RO; GO:0008215; F:transporter activity; IEA.

RO; GO:0008215; F:transporter.

RICEPTO; IPR001682; Sub_transporter.

RICEPTO; IPR001682; Sub_transporter.

RICEPTO; IPR001682; Sug_transporter.

RICEPTO; IPR001682; Sug_transporter.

RICEPTO; IPR001682; Sug_transporter.
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MEDLINE=22133808; PubMed=1212206;
MEDLINE=22133808; PubMed=12122206;
Bareas S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlibevert P.M., Musser J.M.;
"Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
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EMBL, AE010119; AAL98622.1; -.

GO; GO:0016220; C:membrane; IEA.

GO; GO:0005215; F:transporter activity; IEA.

GO; GO:0006810; P:transport; IEA.

InterPro; IPR007114; MFS.

InterPro; IPR008428; Sub_transporter.

InterPro; IPR008428; Sug_transporter.

PEAM; PF00083; sugar_tr; 1.

R PROSITE; PS50850; MFS; 1.

R PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.

R COMPJETE; DS00216; SUGAR_TRANSPORT_1; 1.

R COMPJETE; PS00216; SUGAR_TRANSPORT_1; 1.
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Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Laft sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative integral membrane protein.
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272 ASFFGAF 278
272 ASFFGAF 278
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SEQUENCE 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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100.0%; Pred. No. 2.1e+02;
ive 0; Mismatches 0; Indels
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP003335: BAB90033.1; --Gramene; Q8S179; --
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InterPro, IPROM806; RNA_pol_Rpc82.
Fram; PF05645; RNA_pol_Rpc82; 1.
SEQUENCE 414 AA, 47142 MW; EB95244618E143DD CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0UN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to glycosyl transferases group 1.
Pseudomonas aeruginosa.
                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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EMBL, AF498403, AAM27604.1; --
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:009058; P:biosynthesis; IEA.
InterPro; IPR001296; Glyco_trans_1.
Pfam; PF00534; Glycos_trans_1.
Transferase.
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Best Local Similarity 100.0%; Pred. No. 2.1r
Marches 7; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last seq 01-OCT-2003 (TrEMBLrel. 25, Last ann Putative RNA polymerase III subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=22053227; Pubmed=12057956;
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                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          322 LVRERGP 328
  83 OLROLVR 89
                                              OLROLVR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=39947;
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ID Q8S179
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MEDLINE=22555705; PubMed=12368864;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Gardner M.J., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angluoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
                                                                                                                                                                                                                                                                      MEDLINE=22053227; PubMed=12057956; Raymond C.K., Sime B.H., Kas A., Spencer D.H., Kutyavin T.V., Ivey R.G., Zhou Y., Kaul R., Clendenning J.B., Olson M.V.; Genetic Variation at the O-Antigen Biosynthetic Locus in Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 2.5%; Score 7; DB 2; Length 417; Local Similarity 100.0%; Pred. No. 2.1e+02; nes 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417 AA; 46410 MW; 2265075495ABCE78 CRC64;
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01-MAR-2003 (TEMBLrel. 23, Created)
10-MAR-2003 (TEMBLrel. 23, Last sequence update)
01-MAR-2003 (TEMBLrel. 23, Last annotation update)
Hypothetical protein.
01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF498415; AAM27788.1; -.
GO; GO:0016740; Fitransferase activity; IEA.
GO; GO:0009058; P:biosynthesis; IEA.
InterPro; IPR001296; Glyco_trans 1.
Pfam; PF00534; Glycos_transf_1; 1.
                                                                                    Similar to glycosyl transferases group 1.
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J. Bacteriol. 184:3614-3622(2002).
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                                                                                                             Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
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SEQUENCE FROM N.A.
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                   thaliana.";
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QBLP64;
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A Nishikawa T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Takhashi Fulii A., Hara H.,

A Tanase T., Nomura Y., Togiya S., Kawai F., Hara R., Takeuchi K.,

A rita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

A Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;

INEDO human cDNA sequencing project.";

Submitted (FEB-2000) to the EmBL/GenBank/DDBJ databases.

C -!- SIMILARITY: BELONGS TO THE BZIP FAMILY.

E FMBL; AK000938; BAA91431.1; -.

R GO: GO:0005634; C:mucleus; IRA.

GO: GO:0005634; C:mucleus; IRA.

GO: GO:0005634; C:mucleus; IRA.

R GO: GO:0005634; T:DZIP.

R HITEPPRO: IPR004827; T:DZIP.

R FMAN; FROM PRO170; DZIP; 1.

R FMAN; FROM PRO070; DZIP; 1.
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Ar2g38590 protein.
Ar2g38590
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brasslcales; Brasslcaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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100.0%; Pred. No. 2.1e+02;
tive 0; Mismatches 0; Indels
                                                                     2.5%; Score 7; DB 5; Length 420;
100.0%; Pred. No. 2.1e+02;
live 0; Mismatches 0; Indels
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PROSITE, PS00036; BZIP_BASIC, 1.
Hypochetical protein; DNA-binding; Nuclear protein.
SEQUENCE 423 AA; 46463 MW; 348ASEFECSALE977 CRC64;
2E57639FCA8F985C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-077-2000 (TrEMBLrel. 15, Created)
01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                423 AA.
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MEDLINE=20083487; PubMed=10617197;
49697 MW;
                                Ouery Match
Best Local Similarity 100...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
                                                                                                                                                                                                                                 196 IKENTKN 202
                                                                                                                                                                                                                                                                                                               294 IKENTKN 300
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Les 7, Conserv
    420 AA;
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SEQUENCE
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Croin L.A., Shen M., VanAber S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.;
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"Phylogenetic analysis of Brassicaceae plants based on the nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.5%; Score 7; DB 10; Length 424 100.0%; Pred. No. 2.1e+02; tive 0; Mismatches 0; Indels
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Required (DEC-2001) to the EMBL/GenBank/DDBJ databases.

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AB075409; BAB97357.1; ...

GO; GO:0005529; F:sugar binding; IEA.

InterPro; IPR001480; B lectin.

InterPro; IPR001689; SIccus glycop.

Pfam; PF01453; Agglutinin; 1.

Pfam; PF00154; S locus glycop; 1.

SMARI; SM00108; B_lectin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; H84806; H84806.
InterPro; IPR001810; F-box.
InterPro; IPR008652; F-box assoc 1.
InterPro; IPR008645; Skpl Skpl.
Fram; PF00646; F-box; 1.
SWART; SM00256; PBOX; 1.
TIGRPAMS; FIGR01640; F-box assoc 1; 1.
PROSITE; PS50181; PBOX; 1.
SRQUENCE 424 AA; 50354 MW; 9DA14E4F834BE340 CRC64;
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425 AA; 48418 MW; CIED97DAE305CF15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
8-locus-related I (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.5%; Score 7; DB 10; Le
100.0%; Pred. No. 2.1e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AC005499; AAC67359.1;
                                                                                                                                                                                                                                                                                            Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
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AE002218; AAF38415.1; -.
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                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                 156 SSRSGHS 162
                                                                                                                                                                                                        237 SSRSGHS 243
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                                                                                                          SEQUENCE
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Q9Z913
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MEDINTE-20504483; PubMed=11016950;
MG W.V., Kennedy S.P., Maliga N.S., Thorsson V., Sbrogna J.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
"Genome sequence of Halobacterium species NRC-I.";
                                                                                                                                                                                                                            Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Venter K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                           Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
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                                                                                                                                                                                                                                                                                                                  "Complete genome seguence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.5%; Score 7; DB 16; Length 427;
100.0%; Pred. No. 2.1e+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        427 AA; 45732 MW; 0B5247CDBFA901AD CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UND-2003 (TrEMBLrel. 24, Last annotation update)
Zinc metalloproteinase homolog.
CAAX OR VNG0329G.
                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                        GO, GO:0008483, F:transaminase activity; IEA GO; GO:0008152; P:metabolism; IEA.
                                                                                  Created)
                                                                                                                      Nitrogen fixation protein (NIFS-2).
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                                                                                                                                                                                                          STRAIN=Nichols;
MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                      EMBL; AE001256; AAC65826.1; -. PIR; G71272; G71272.
                                                                               01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                         Science 281:375-388(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 TGTRGRS 133
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 171 LGRKINS 177
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nes 7; Conserv
                                                                                                                                           Treponema pallidum.
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                TIGR; TP0863; -.
                                                                                                                                                                  NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                spirochete.";
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                                                                      083835;
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                                                            083835
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Geng M.M., Schuhmacher A., Muehldorfer I., Bensch K.W., Schaefer K.P., Schneider S., Pohl T., Essig A., Marre R., Melchers K., "The genome sequence of Chlamydia pneumoniae TW183 and comparison with other Chlamydia strains based on whole genome sequence analysis."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AE001604, AAD18324.1; --
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
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Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
2.5%; Score 7; DB 17; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000).

EMBL; AE004992; AAG18905.1; -

PIK; E84192; E84192.

GO; GO: 10016020; C: membrane; IEA.

GO; GO: 0004222; F: metalloendopeptidase activity; IEA.

GO; GO: 0004222; F: metalloendopeptidase activity; IEA.

InterPro; IPRO01915; Peptidase M48.

Pfam; PF01435; Peptidase M48; I.

Complete protecome.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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GUAA OR CPN0171 OR CP0599 OR CPB0173.
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MEDLINE=20330349; PubMed=10871362;
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MEDLINE=99206606; PubMed=1019238B;
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                                                                                                                                                              GO:0005524; F:ATP binding; IEA.
GO:0003824; F:catalytic activity; IEA.
GO:0003922; F:GMP synthage (glutamine-hydrolyzing) activity; IEA.
GO:0006177; P:GMP biosynthesis; IEA.
GO:0006164; P:purine nucleotide biosynthesis; IEA.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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100.0%; Pred. No. 2.1e+02;
iive 0; Mismatches 0; Indels
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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01-070-2003 (TrEMBLrel. 24, Last sequence update)
01-071-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR006220; Anch synthil.
InterPro; IPR000991; GATase 1.
InterPro; IPR001674; GMP synth C.
InterPro; IPR004739; GMP synth C.
Pfam; PF00117; GATase; 1.
Pfam; PF00588; GMP synt C; 1.
PRINTS; PR00099; ANTSNTHASEII.
PRINTS; PR00096; GATASE.
TIGREAMS; TIGR00888; guaA_Nterm; 1.
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Pfam; PF00036; efhand; 2.
SMART; SM00054; EFh; 2.
Hypothetical protein.
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2003 (TrEMBLrel. 24,
RH55021p (CG12344-PA).
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PIR; B72109; B72109.
PIR; C86512; C86512.
HSSP; P04079; 1GPM.
TIGR; CP0599; -.
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EMBL; ANO49438; AMF1291.1; ---

EMBL; ANO49438; AMF1291.1; ---

EMBL; AE003828; AAF58743.3; ---

EMBL; AE003828; AAF58743.3; ---

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EMBL; AE003828; F: cint cyrity; IEA.

GO; GO:0005220; F: cint channel activity; IEA.

GO; GO:0005216; F: cint channel activity; IEA.

GO; GO:0005216; F: cint channel.

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Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
Chillingworth T., Collins M., Cronin A., Davis P., Doogett J.,
Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
"Comparative analysis of the genome sequences of Bordetella pertussis,
Bordetella parapertussis and Bordetella bronchiseptica.";
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                                                                                   FlyBase;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Transmembrane.
SEQUENCE 449 AA; 51258 MW; 79EE29E409FDC648 CRC64;
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
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SEQUENCE 457 AA, 50053 MW; 21C76EBD1CB46265 CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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EMBL; BX640438; CAE30876.1; -.
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1 TNELKÇMQDKYSKSGIACFL.....NEHLIDMDHEASFFGAFLVG 243
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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61 SNLHLRNGELVIHEKGFYXIXSQTYERFQEBIKENTKNDKQMVQXIYKYTSYPDPILLMK 120
                                                          SNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMK 186
                                                                                                                                                                                                                                                                                                                        APPLICANT: Shu, Hong-Bing
TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 RVAAHITGIRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 142
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187 SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 2.1e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Preq. ...
                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/565,423
CURRENT APPLICATION NUMBER: US/09/565,423
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: UNKNOWN
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/132,892
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09105343A Patent No. 6207642 GENERAL INFORMATION:
APPLICANT: WILEY, S.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : Abbott Laboratories
100 Abbott Park Road
                                                                                                                                                                                                                                                                    Sequence 7, Application US/09565423
Patent No. 6475987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 100 ALTY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60064-6050
                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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US-09-105-343A-8
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                                                            127
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APPLICANT: Hsu, Hailing
APPLICANT: Wooden, Scott K
APPLICANT: Wooden, Scott K
APPLICANT: Boyle, William J
TITLE OF INVENTION: Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family
FILE REFERENCE: 01017/35550A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 EKOONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 SNLHLRNGELVIHEKGFYYIYSQTYFRFQEE-----IKENTKNDKQMVQYIYKYTSYPD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NHVLFRNGELVIEQEGLYXIYSQTYFRFQBABDASKWVSKDKVRTKQLVQXIXKYTSYPD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 ERGPQRVAAHITGTRGRSNTLSSPNSKOREKALGRKINSWESSRSGHSFLSNLHLRNGELV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EKOLSTPPLPRGGRPQKVAAHITGITRRSNSALIPISKDGKTLGQKIESWESSRKGHSFL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 50.8%; Score 654; DB 3; Length 18:
Best Local Similarity 68.7%; Pred. No. 5.6e-60;
Matches 125; Conservative 22; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.7%; Score 446; DB 4; Length 85; 100.0%; Pred. No. 7.1e-39; Live. 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/632,287A
CURRENT FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/147,294
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEC ID NOS: 22
                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER:
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: BECKER, Cheryl L.
REGISTATION NUMBER: 35,441
REFERRNCE/DOCKET NUMBER: 6048.US.P2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                       6048.US.P2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,343A
FILING DATE: 12-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/09632287A Patent No. 6521422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear _
MOLECULE TYPE: No. 6207642e
                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                    183 amino acids
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                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 183 amino ació
                                                                                                                                                                                                                                                                                                      TELEFAX: 847-938-2623
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                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT FILING DATE: 1999-05-26
EARLIER APPLICATION NUMBER: 09/190,046
EARLIER APPLICATION NUMBER: 09/048,641
EARLIER FILING DATE: 1998-111-10
EARLIER FILING DATE: 1998-03-26
EARLIER FILING DATE: 1996-06-25
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 08/548,368
EARLIER APPLICATION NUMBER: 08/548,368
EARLIER FILING DATE: 1995-11-01
EARLIER FILING DATE: 1995-11-01
EARLIER FILING DATE: 1995-106-29
NUMBER OF SEC 1D NOS: 25
SOFTWANE: PATCHILIN VEF. 2.0
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Patent No. 6521228
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Best Local Similarity 100.0
Matches 52; Conservative
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Best Local Similarity
REFERENCE: 2835-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            LENGTH: 101
TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: human
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1 ERGPQRVAAHITGIRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
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                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Kathryn A. Anderson, Immunex Corporation STREET: 51 University Street
                                                                                                                                                                                              Sequence 4, Application US/08670354
Patent No. 5763223
GENERAL INFORMATION:
APPLICANT: Steven R. Wiley and
APPLICANT: Raymond G. Goodwin.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09320424
Patent No. 6284236
GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
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Pred. No. 1.1e-22;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-JUN-1996
CLASSIFICATION: 435
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PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-UTN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ANGERSON, KALHYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELECHMUNICATION INFORMATION:
TELEPAK: (206) 587-04430
                                                  138 IHEKGFYYIYSQTYFRQEEIKENT 162
                                                                                           61 IHEKGFYYIYSQTYFRFQEEIKENT 85
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TELEX: 756822
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 101 amino acids
amino acid
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Best Local Similarity 100.
Matches 52; Conservative
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; MOLECULE TYPE: protein
US-08-670-354-4
                                                                                                                                                                                                                                                                                                                                                                                                                          Seattle
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                                                                                                                                                                                    US-08-670-354-4
                                                                                                                                                              RESULT
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                                                             Gaps
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                                                                                                                 1 TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRK 52
                                                                                                                                                                     39 TNELKOMODKYSKSGIACFLKEDDSYMDPNDEESMNSPCWQVKWQLRQLVRK 90
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22.6%; Score 291; DB 3; Length 101; 100.0%; Pred. No. 1.1e-22; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wiley, Steven R.
PEDLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE KEFEKEMET 2031

CURRENT PEDELICATION NUMBER: US/09/825,563

CURRENT FILING DATE: 2001-04-02

PRIOR APPLICATION NUMBER: 09/320,424

PRIOR FILING DATE: 1990-05-26

PRIOR FILING DATE: 1990-11-10

PRIOR FILING DATE: 1990-11-10

PRIOR PILING DATE: 1996-03-26

PRIOR FILING DATE: 1996-06-25

PRIOR FILING DATE: 1996-06-25

PRIOR FILING DATE: 1996-06-25

PRIOR FILING DATE: 1996-06-25

PRIOR FILING DATE: 1996-06-25

PRIOR FILING DATE: 1996-06-25

PRIOR FILING DATE: 1996-06-25

PRIOR FILING DATE: 1995-11-01

PRIOR FILING DATE: 1995-06-29

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PATENTIN VET: 2.0

SEQ ID NO 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
PCT-US96-10895-4
; Sequence 4, Application PC/TUS9610895
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81 PORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHE 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYY 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 IYSQTYFRFQEBIKENTKNDKQMVQYIYKYT-SYPDPILLMKSARNSCWSKDABYGLYSI 204
                                                                                                                                                                             US-09-396-937-10

Sequence 10, Application US/09396937

Patent No. 6645500

GENERAL INFORMATION:

APPLICANT: M&E Biotech A/S

APPLICANT: HALNIER, Torben

TITLE OF INVENTION: Activity

TITLE OF INVENTION: Activity

FILE REPRENCE: 22021 PC. 1

CURRENT APPLICATION NUMBER: US/09/396,937

CURRENT FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 35

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 10

LENGTH: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 AHLT-----INAASIPSGSHKVTL---SSWYHDR-GWAKISNMTLSNGKLRVNQDGFYY
                                                                                                        3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Gaps
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APPLICANT: MAE Biotech A/S
APPLICANT: HAANING, Jesper
TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
TITLE OF INVENTION: Activity
TITLE REFERENCE: 22021 PC 1
CURRENT APPLICATION NUMBER: US/09/396,937
CURRENT FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: DNA encoding ; OTHER INFORMATION: murine OPGL, residues 158-316, fused to His tag US-09-396-937-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.8%; Score 228.5; DB 4; Length 173; 34.2%; Pred. No. 7.4e-16; tive 31; Mismatches 62; Indels 11.
                                                    Query Match
Best Local Similarity 65.8%; Pred. No. 4.7e-18;
Matches 50; Conservative 9; Mismatches 14; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 NVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/09396937
Patent No. 6645500
                                                                                                                                                                                                                                         141 KGFYYIYSQTYFRFQE 156
                                                                                                                                                                                                                                                                                        64 E---YIYSOTYFRFOE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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         US-09-632-287A-13
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US-09-396-937-12
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APPLICANT: Wooden, Scott K
APPLICANT: Wooden, Scott K
APPLICANT: Boyle, William J
TITLE OF INVENTION: Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family
FILE REFERENCE: 01017/35550A
CURRENT PILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/147,294
PRIOR APPLICATION NUMBER: US 60/147,294
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 TNELKQWQDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
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              APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                       ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-UN-1995
CLASSIFICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ANGERSON, KATHYN A.
REGISTRATION NUMBER: 32,172
REFERNEM/ED/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPRX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-09-622-287A-13
Sequence 13, Application US/09632287A
Patent No. 6521422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELERAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 101 amino acids
amino acid
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GENERAL INFORMATION:
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CITY: Seattle
                                                                                                                                                                                                           USA
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ORGANISM: Mouse
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                                                                                                                                                                                                           COUNTRY:
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LENGTH: 87
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APPLICANT: HALKIER,
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LENGTH: 188
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                                                                                                                                                                                                                                                                                                                                                            146 IYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSI 204
                                                                                                                                                                                                                                                                                               22 AHLT----INAASIPSGSHKVTL---SSWYHDR-GWAKISNWTLSNGKLRVNQDGFYY 71
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                                                                                                                                                                                                                           62; Indels 11; Gaps
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APPLICANT: MAE Biotech A/S
APPLICANT: HALKIER, Torben
APPLICANT: HALKIER, Torben
APPLICANT: HALKIER, Torben
APPLICANT: HARNING, Jesper
TITLE OF INVENTION: Activity
FILE OF INVENTION: Activity
FILE REFERENCE: 22021 PC 1
CURRENT APPLICATION NUMBER: US/09/396,937
CURRENT FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PLECHIN Ver. 2.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Synthetic PCR CTER INFORMATION: product with optimum codons for E. coli and P. CTER INFORMATION: pastoris expression US-03-396-937-8
                                                                 Fusion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 11;
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                                                                                                                                                                             Query Match
17.8%; Score 228.5; DB 4; Length 173;
Best Local Similarity 34.2%; Pred. No. 7.4e-16;
Matches 54; Conservative 31; Mismatches 62; Indels 11
                                                               OTHER INFORMATION: Description of Artificial Sequence: Fusical CHER INFORMATION: murine OPGL, residues 158-316 with C to S CTHER INFORMATION: mutation, and His tag US-09-396-937-12
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  TYPE: PRT
ORGANISM: Artificial Sequence
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                                              FEATURE:
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86 AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSCHSFLSNLHLRNGELVIHEKGFYY 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 AHLT-----INAASIPSGSHKVTL----SSWYHDR-GWAKISNMTLSNGKLRVNQDGFYY 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: HALKIER, Torben
APPLICANT: HALKIER, Torben
APPLICANT: HALKIER, Torben
APPLICANT: HALKIER, Torben
TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
TITLE OF INVENTION: Activity
FILE REFERENCE: 22021 PC 1
CURRENT APPLICATION NUMBER: US/09/396,937
CURRENT FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Fusion OTHER INFORMATION: between murine OPGL, residues 158-316 with tetanus OTHER INFORMATION: toxoid P2 epitope introduced, and His tag
APPLICANT: HAANING, Jesper
TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
TITLE OF INVENTION: Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Fusion of OTHER INFORMATION: murine OPGL, residues 158-316 modified by OTHER INFORMATION: introduction of tetanus toxoid P30 epitope, and OTHER INFORMATION: His tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 - CWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 16.3%; Score 210; DB 4; Similarity 32.0%; Pred. No. 6.6e-14; 55; Conservative 31; Mismatches 56;
                                                                              FILE REFERENCE: 22021 PC 1
CURRENT APPLICATION NUMBER: US/09/396,937
UNRENT FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
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; Sequence 14, Application US/09396937
; Patent No. 6645500
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ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Sequence 16, Application US/09396937 Patent No. 6645500 GENERAL INFORMATION: APPLICANT: MÆE Biotech A/S

US-09-396-937-16

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86 AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYY 145
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Sequence 20, Application US/09396937

Parent No. 6645500

GENERAL INFORMATION

APPLICANT: MAERIER, Torben

APPLICANT: HANING, Jesper

TITLE OF INVENTION: Activity

FILE REFERENCE: 22021 FC. 1

CURRENT APPLICATION NUMBER: US/09/396,937

CURRENT FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 35

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
15.7%; Score 202.5; DB 4; Length 173;
Best Local Similarity 30.2%; Pred. No. 3.7e-13;
Matches 52; Conservative 28; Mismatches 53; Indels 39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: Fusion between
CTHER INFORMATION: murine OPGL, residues 158-316 with tetanus toxoid
CTHER INFORMATION: P30 epitope introduced, and His tag
189 RNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 242
                        191 SCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                      RESULT 15
US-09-396-937-20
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Search completed: March 23, 2004, 09:16:23 Job time : 24 secs

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March 23, 2004, 09:15:19; Search time 43 Seconds (without alignments) 1463.399 Million cell updates/sec
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1 TNELKQMQDKYSKSGIACFL.....NEHLIDMDHBASFFGAFLVG 243
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
GenCore version 5.1,6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1049977 seqs, 258955339 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                            - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                  US-10-662-429-2_COPY_39_281
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Maximum DB seq length: 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 10, Appl Sequence 29, Appl Sequence 7, Appl Sequence 11, Appl Sequence 16, Appl Sequence 16, Appl Sequence 17, Appl Sequence 17, Appl Sequence 13, Appl Sequence 2, Appli Sequence 15, Appl Sequence 10, Appl Sequence 20, App Sequence 9, Appli Description US-09-900-530A-10 US-09-779-050A-16 3 US-10-116-378-29 4 US-10-216-074-7 4 US-10-238-083-11 US-09-855-544A-16 US-09-779-050A-17 US-09-855-544A-15 US-09-855-544A-10 US-10-399-018-20 US-09-855-544A-9 US-10-286-696-13 US-10-338-785A-2 US-10-286-696-12 SUMMARIES Query Match Length DB 668.9 666.0 878 859 859 849 826 746.5 370 291 278 277 245.5 236 Score Result М М

Sequence 86, Appl	224,	Sequence 224, App	Sequence 10, Appl	Sequence 101, App	Sequence 84, Appl	Sequence 15, Appl	Sequence 103, App	۹,	Sequence 100, App		Sequence 320, App	Sequence 102, App	Sequence 76, Appl	8	Sequence 14, Appl	Sequence 99, Appl	'n	Sequence 3, Appli	Sequence 1, Appli	Sequence 17, Appl	Sequence 24, Appl	24,		Sequence 8, Appli	D,	Seguence 3, Appli	Sequence 30, Appl	č	Sequence 7, Appli	
12 US-10-289-456-86		14 US-10-050-898-224	14 US-10-338-083-10			9 US-09-779-050A-15			12 US-10-289-456-100		14 US-10-050-898-320	12 US-10-289-456-102		12 US-10-289-456-96	9 US-09-779-050A-14		14 US-10-185-425-2		14 US-10-185-425-1	9 US-09-934-465-17	14 US-10-272-411-24	14 US-10-272-328A-24	9 US-09-779-050A-8	14 US-10-170-812-8	14 US-10-216-074-5	14 US-10-338-083-3	13 US-10-116-378-30	9 US-09-877-156-22	9 US-09-779-050A-7	
199	199	199	151	158	159	160	165	178	180	185	185	187	170	193	160	170	213	213	159	149	34	34	143	152	138	138	140	141	143	
3.5 18.1	3.5 18.1	3.5 18.1	2.5 18.1	2.5 18.1	2.5 18.1	2.5 18.1	2.5 18.1	2.5 18.1	.5 18	2.5 18.1	2.5 18.1	232.5 18.1	0.5 17.9	0.5 17.9	228.5 17.8	228.5 17.8	190.5 14.8	4.5 14.3	177 13.8	175.5 13.6	13	175 13.6	13	175 13.6	H	13	=======================================	173 13.4	173 13.4	
16 23	17 23	18 233	19 232	20 23	21 232.	22 23	23 23;	24 232	25 232	26 232	27 23	28 23	29 230	30 23	31 22	32 22	33 19	34 184	35	36 17	37	38	39	40	41	42	43	44	45	

LIGNMENT

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APPLICANT: Seol, Dae-Wu
APPLICANT: Seol, Dae-Wu
APPLICANT: Seol, Dae-Wu
APPLICANT: Seol, Dae-Wu
APPLICANT: Seol, Dae-Wu
APPLICANT: Billiar, Timothy R.
TITLE OF INVENTION: DNA Cassette for the Production of
TITLE OF INVENTION: Secretable Recombinant Trimeric Trail Proteins, Tetracycline
TITLE OF INVENTION: Combination and Use in Gene Therapy
FILE REFERENCE: 5006-1-007
CURRENT APPLICATION NUMBER: US/09/900,530A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: KR 2000-38441
PRIOR FILING DATE: 2000-07-06
NUMBER OF SEO ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 LVIHEKGFYYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68.9%; Score 887; DB 9; Length 168; 100.0%; Pred. No. 4.2e-77;
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                  Sequence 10, Application US/09900530A Patent No. US20020128438A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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US-09-900-530A-10
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80 GPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIH 139
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Best Local Similarity
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US-10-216-074-7
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APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Marters, Scot A.
APPLICANT: Milliam
TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
TITLE OF INVENTION: NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P1206R1
CURRENT APPLICATION NUMBER: US/10/116,378
CURRENT FILING DATE: EARLIER APPLICATION NUMBER: 09/247,225
FRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US 60/074,087
FRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US 60/074,087
FRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
FRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
FRIOR FILING DATE: BARLIER FILING DATE: 1998-02-09
FRIOR FILING DATE: BARLIER FILING DATE: 1998-02-09
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     121 DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 EYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 68.2%; Score 878; DB 9; I
Best Local Similarity 100.0%; Pred. No. 3.1e-76;
Matches 166; Conservative 0; Mismatches 0;
                                                                                                             Sequence 16, Application US/09779050A
FAPLICANT: BOYLEA
APPLICANT: BOYLE, WILLIAM
APPLICANT: BOYLE, WILLIAM
TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
FILE REFRENCE: A-570B
CURRENT APPLICATION NUMBER: US/09/779,050A
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-12
PRIOR FILING DATE: 2000-02-13
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NO 16
TUMPER: OF DATE: 100 00 02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 29, Application US/10116378
Publication No. US/0020150993A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                               RESULT 2
US-09-779-050A-16
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US-10-116-378-29
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LENGTH: 164
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Sequence 7, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; TITLE OF INVENTION: WETHODS OF USE THEREOF
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT PILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR RILING DATE: 2000-05-05
; PRIOR FILING DATE: 2000-05-05
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NOS: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 FYYIYSQTYFRFQEEIKENTKNDKOMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 FYYIYSQIYFRFQEEIKENTKNDKQWVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 120
                                                                                                                               61 EKGFYYIYSQIYFRFQEEIXENTKNDKQWVQYIYKYTSYPDFILLMKSARNSCMSKDAEY 120
                                                                                             140 EKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEY 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
1 GPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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APPLICANT: Targer, Mail Lourdes G.
APPLICANT: Dahiyat, Bassil I.
TITLE OF INVENTION: Daminant Negative Proteins and Methods Thereof
FILE REFERENCE: A-71273-2
CURRENT APPLICATION NUMBER: US/10/338,083
CURRENT APPLICATION NUMBER: US 60/345,805
PRIOR PILING DATE: 2002-01-04
PRIOR PILING DATE: 2002-01-04
PRIOR FILING DATE: 2002-04-17
NUMBER: OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 66.0%; Score 850; DB 14; Length 161; Best Local Similarity 100.0%; Pred. No. 1.4e-73; Matches 161; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                  121 GLYSIYQCGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 164
                                                                                                                                                                                                                                200 GLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
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Sequence 11, Application US/10338083

Publication No. US20030166559A1

; GENERAL INFORMATION:
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                                                                                                                                                                                                            82 QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEK 141
                                                                                                                                                                                                                                                                                            142 GFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGL 201
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                                                                                                                                                                     ;
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                                                                                                                       Query Match
66.0%; Score 849; DB 14; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.8e-73;
Matches 161; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.2%; Score 826; DB 9; Length 208; 96.3%; Pred. No. 4.1e-71; tive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQKKKKTS 200
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                                                                                                                                                                                                                                                                                                                                                                            202 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 242
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Patent No. US20020061525A1

GENERAL INPORMATION:

APPLICANT: ROCATION YELIN et al.

TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS

CURRENT APPLICATION NUMBER: US/09/855,544A

CURRENT PILING DATE: 201-05-19

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin Ver. 2.1
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TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
FILE REPRENCE: 2786-0173P
CURRENT APPLICATION NUMBER: US/09/855,544A
CURRENT APPLICATION NUMBER: US/09/855,544A
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 188
TYPE: PRT
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SEQ ID NO 11
LENGTH: 161
TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
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LENGTH: 208
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126 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 185
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                                                                                                                                                                                                                                                                                                                          61 TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                              121 SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPD 180
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                                                                                                                                                                                                      1 TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEE
                                                                                                                                          Indels 93; Gaps
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                                                                                 Query Match 58.0%; Score 746.5; DB 9; Best Local Similarity 61.7%; Pred. No. 1.5e-63; Matches 150; Conservative 0; Mismatches 0;
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APPLICANT: BOYLE, WILLIAM
TITLE OF INVENTION: RECEPTOR FROM TWF FAMILY
FILE REFERENCE: A-570B
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR PAPLICATION NUMBER: 60/181,800
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE PATENTIN VERSION 3.0
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 17
LENGTH: 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 17, Application US/09779050A; Patent No. US20020160416A1; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-855-544A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Mus musculus
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DEPLOTED BY SECURIOR OF THE PRINCIPLE OF APPLICATION US/10399018

| Sequence 20, Application US/10399018
| Publication No. US20040002118A1
| GENERAL INFORMATION:
| APPLICANT: Smilansky, Zeev
| TITLE OF INVENTION: METHOD FOR DETERMINING MASS ALTERING MOIETY IN PEPTIDES
| PILE REFERENCE: 9124.137USMO
| CURRENT PEPLICATION NUMBER: US/10/399,018
| CURRENT PELING DATE: 2003-04-10
| PRIOR APPLICATION NUMBER: PILIO1/00944
| PRIOR PILING DATE: 2001-10-11
| PRIOR FILING DATE: 2000-10-11
| NUMBER OF SEQ ID NOS: 21
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 20
| LENGTH: 56
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                                                                                                                                                                                      1 INELKOMODKYSKSGIACFLKEDDSYMDPNDEESMNSPCWQVKWQLRQLVRK 52
                                                                                                                                                                                                                 39 TNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
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                                                                                        Length 98;
                                                                                           Query Match 22.6%; Score 291; DB 9; Length 98 Best Local Similarity 100.0%; Pred. No. 3.6e-20; Matches 52; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred, No. 6.9e-19;
Matches 49; Conservative 0; Mismatches 0;
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Sequence 9, Application US/09855544A

Patent No. US20020061525A1

GENERAL INFORMATION:

TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS

FILE REPREMENCE: 2786-0173P

CURRENT APPLICATION NUMBER: US/09/855,544A

CURRENT FILING DATE: 2001-05-19

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PATENTIN VET. 2.1

SEQ ID NO 9
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Best Local Similarity 100.0
Matches 56; Conservative
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ORGANISM: Homo sapiens
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  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-10
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US-09-855-544A-9
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78 ERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV 137
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34.7%; Score 446; DB 14; Length 85;
Best Local Similarity 100.0%; Pred. No. 3.8e-35;
Matches 85; Conservative 0; Mismatches 0; Indels
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Patent No. US20020061525A1
GENERAL INFORMATION:
APPLICANT: Rodrigo YELIN et al.
TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
FILE REPERENCE: 2786-0173P
CURRENT APPLICATION NUMBER: US/09/855,544A
CURRENT ELING DATE: 2010-05-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
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TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS; FILE REFERENCE: 2786-0173P
CURRENT APPLICATION NUMBER: US/09/855,544A
CURRENT FILING DATE: 2001-05-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
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; Patent No. US20020061525A1
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CORGANISM: Homo sapiens
US-09-855-544A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TISTVQEKQ 69
                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-10-286-696-12
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Best Local Similarity
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US-09-855-544A-15
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LENGTH: 113
                                                                                                                                                                                                                                                                     TYPE: PRT
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APPLICANT: Hailing
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APPLICANT: Hailing
APPLICANT: Wooden, Scott K
APPLICANT: Wooden, Scott K
APPLICANT: Wooden, Scott K
APPLICANT: Boyle, William J
TILE OF INVENTION: Fhm, A No. US20030129706Alel Member of the TNF Ligand Supergene F
FILE REPERENCE: 01017/35550A
CURRENT APPLICATION NUMBER: US/10/286,696
CURRENT APPLICATION NUMBER: US 60/147,294
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: contruct of human RANKL extracellular region with histidine tag
CTHER INFORMATION: and TEV protease cleavage site
US-10-338-785A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 PORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHE 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HUBERT, Ren S.
APPLICANT: E1 Yazal, Jamal
TITLE OF INVENTION: No. US20030219864A1e1 Variants of RANKL Protein
FILE REFERENCE: A-71486
CURRENT APPLICATION NUMBER: US/10/338,785A
CURRENT PILING DATE: 2003-01-06
PRIOR FILING DATE: 2002-01-04
PRIOR FILING DATE: 2002-01-04
PRIOR FILING DATE: US 60/345,805
PRIOR FILING DATE: US 60/345,805
PRIOR FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Version 3.2
SOFTWARE: Patentin Version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.1%; Score 245.5; DB 14; Length 87; 65.8%; Pred. No. 7.2e-16; ive 9; Mismatches 14; Indels 3.
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18.3%; Score 236; DB 15; Length 178;
Best Local Similarity 32.7%; Pred. No. 1.6e-14;
Matches 55; Conservative 35; Mismatches 64; Indels 14
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Publication No. US20030219864A1
GENERAL INFORMATION:
APPLICANT: Desjarlais, John R.
Sequence 13, Application US/10286696
Publication No. US20030129706A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 KGFYYIYSQTYFRFQE 156
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ORGANISM: Artificial sequence
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Best Local Similarity
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; ORGANISM: Mouse
US-10-286-696-13
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US-10-338-785A-2
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GenCore version 5.1.6
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OM protein - protein search, using sw model

March 23, 2004, 09:07:23; Search time 60 Seconds Run on:

(without alignments)
1144.317 Million cell updates/sec

US-10-662-429-2_COPY_39_281 1287 score: Title: Perfect

TNELKQMQDKYSKSGIACFL......NEHLIDMDHEASFFGAFLVG 243 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 243

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:* 1: geneseqp1980s:* Database :

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2004a:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AAY88630 Cell fact Ab576826 Human TRA Aau9896 Human TRA Aau99896 Human TRA Aab08274 Amino aci Ab71285 Partial h Ab608274 Amino aci Ab71985 C-termina Ab73985 TNF famil Ad03335 Tumour ne Aau99301 Human TRA Aau7959 Human TRA Aau7959 Human TRA Aau7959 Human TRA Aau7959 Human TRA Aau7959 Human TRA Aau7959 Human TRA Aau7959 Human TRA Aau17959 Human TRA Aau17959 Human TRA Aau17959 Human TRA Aau17959 Human TRA Aau17959 Human TRA Aau17959 Human TRA Aau17959 Human TRA Aau17959 Human TRA Aau17959 Human TRA Aau17959 Human TRA Aau17959 Human TRA Aau17959 Human TRA Aau17959 Human TRA Aau17959 Human TRA Abu08559 Human TRA Abu08659 Human TRA Ada50080 Human Will Abg94285 Mouse RAN
SUMMARIES	AAY88630 ABD76258 AABD6826 AABD72259 AAG72259 AAB08274 AAR89855 AAC03335 AAU79593 AAV01518 AAB08275 AAU7559 AAU75959 AAU75950 AAU75950 AAU75950 AAU75955 AAU75955 AAU75955 AAU75955 AAU7595
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Abg80597 Mouse rec	Aab67248 Human RAN	Aab08273 Amino aci	Human	Human	Human	Abg71827 Human RAN	Adb16998 Human RAN		Adb16999 Murine RA	Abr39854 RANK liga	Adc03334 Murine re	Aab08272 Amino aci	Aay84422 A murine	Aay84421 Amino aci	Aay84420 Amino aci	Aay91023 Mouse OBM	Aav84424 An osteop	Ā	An
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18.1	18.1	18.1	18.1	18.1	18.1	18.1	18.1	17.9	17.9	17.8	17.8	17.8	17.8	17.8	17.8	17.0	16.3	16.2	15.7
'n	32.5	232.5	232.5	232.5	232.5	232.5	232.5	230.5	230.5	228.5	228.5	228.5	228.5	228.5	228.5	219	210	208	202.5
233	~																		

ALIGNMENTS

Cell factor derivative TRAILD amino acid sequence. AAY88630 standard; protein; 220 AA. (first entry) kidney; leukaemia. 22-AUG-2000 AAY88630; RESULT 1 AAY88630

Cell factor derivative; TRAILD; anticancer; cancer; liver; breast;

Unidentified

CN1243748-A. 09-FEB-2000. 99CN-00111039. 28-JUL-1999; 99CN-00111039. 28-JUL-1999; (BASI-) INST BASIC MEDICAL SCI CHINESE ACAD MEDI. Zheng D, Liu Y, Ma Z;

WPI; 2000-351201/31.

New cell factor derivative causing cells to die, for anticancer therapy. Disclosure; Page 2; 10pp; Chinese. The present invention relates to a cell factor derivative (TRAILD) used as an anticancer derivative. The TRAIL protein can be expressed in soluble form in bacterial cytoplasm. The present sequence represents a TRAILD amino acid sequence. Recombinant TRAILD fusion proteins can be used in anti-cancer medicaments to treat cancer of the liver, breast, or kidney. It can also be used to treat leukaemia

Sequence 220 AA;

Gaps 1; Query Match 74,1%; Score 953.5; DB 3; Length 220; Best Local Similarity 97.9%; Pred. No. 7.4e-85; Matches 185; Conservative 1; Mismatches 2; Indels 1;

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56 RISEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINS 115

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The present invention relates to the isolation of cDNA encoding human tumour related apoptosis inducing ligand (Trail), and the Trail protein. The Trail full length cDNA is cloned, and is utilised to oreate a Trail prokaryotic expression system. The full length Trail cDNA is used to respectively clone cDNA of soluble ectocytic segment Trailing and Trail 114, and respectively create Trailing cDNA and Trailing and Trailing increase the expression and quantity of the Trail, Trailing, and arailing proteins, and may be useful in a new preparation for killing tumour calls. The present sequence represents the partial human Trail protein,
                                                                                                                                                                                                                                                   YTSYPDPILLMKSARNSLWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEA 211
                                                                 WESSRSGHSFLSNLHLRNGELVIH-EKGFYXIYSQTYFRFQEEIKENTKNDKQMVQYIYK 174
                                                                                                                    WESSRSGHSFLSNLHLRNGELVIHKEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK 151
                                                                                                                                                                                                       YTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEA 234
91
KTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSQTLSSPNSKNEKALGRKINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; tumour related apoptosis inducing ligand; Trail109;
Trail prokaryotic expression system; tumour cell death.
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71 NISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLH 130

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1; Indels

Score 907; DB 5; Pred. No. 1.9e-80; 0; Mismatches 1;

70.5%;

Matches 172; Conservative

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Similarity

Query Match Best Local S

Length 173;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSK 120
                                                                           61 LRNGELVIHEKGFYYIYSQTYFRFQEEIKENAKNDKQMVQYIYKYTSYPDPILLMKSARN 120
                 9
                                                                                                                                                                                                                                                                                                                                           Human, TRAIL, tumour necrosis factor, TNF, tumour necrosis factor related apoptosis inducing ligand, TRAIL, cancer, viral infection, cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a method for producing Tumour Necrosis Factor (TNF) Related Apoptosis Inducing Ligand (TRAIL) protein, and for crystallising the TRAIL protein and its three-dimensional structure, where the TRAIL protein has improved activity, which specifically kills cancer cells and cells infected by virus. The present sequence is human TRAIL, which was used in the invention
131 LRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 VRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Producing and crystallizing tumor necrosis factor related apoptosis inducing ligand protein, and its three-dimensional structure.
                                                                                                                                 121 SCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 173
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0
                                                                                                             SCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
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100.0%; Pred. No. 1.6e-78;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                   ABB76826 standard; protein; 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 14; 20pp; Korean.
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                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lee
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                 Human TRAIL.
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This invention relates to an expression vector containing the tumour necrosis factor related apoptosis inducing ligand (TRAID) protein receptor SDR5. The invention also comprises a method for producing the SDR5 protein from an E. coli transformed with the vector. The method of the invention is useful for crystalising the TRAIL-SDR5 complex. A TRAIL COMPLEX is useful for developing recombinant proteins i.e. proteins with improved stability or cytotoxic activity of a TRAIL protein which involves changing the amino acids of the AA loop to increase the warious interactions between amino acids or from the binding site of metal ions or the disulfide bonding, or changing the corresponding amino acids of the homotrimer interface or homodimer interface to increase the various interactions between amino acids or from the binding site of conferring specificity for the recognition between TNF family members and structure of the TRAIL-SDR5 complex is useful for the molecular strategy conferring specificity for the recognition between TNF family members and TNF receptor family members and for the development of TRAIL protein, which has a better stable, cycotoxic activity or an improved receptor homogeneous is factor receptor apoptosis including ligand (TRAIL) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel expression vector containing an sDR5 encoding gene transformed into Escherichia coli to produce sDR5 protein for crystallizing a tumor necrosis factor-related apoptosis-inducing ligand-sDR5 complex.
                                                                                                                                                                                        TRAIL; TNF receptor apoptosis including ligand; human; SDR5; tumour necrosis factor; crystal structure; TRAIL-SDR5 complex; apoptosis.
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                                                                                                                                                     Human TNF related apoptosis including ligand (TRAIL) protein.
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UNIV POHANG SCI & TECHNOLOGY.
                                    AAU99896 standard; protein; 168 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ryu JM, Hwang YH,
                                                                                                                                                                                                                                                                                                                                                                    10-JAN-2001; 2001WO-KR000034.
                                                                                                                                                                                                                                                                                                                                                                                                          29-DEC-2000; 2000KR-00085947.
                                                                                                               (first entry)
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                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                               21-OCT-2002
                                                                                                                                                                                                                                                                                                                               11-JUL-2002
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                                                                          AAU99896;
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RESULT 4
                    AAU99896
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The present invention relates to the isolation of cDNA encoding human the Trail full length cDNA is cloned, and (Trail), and the Trail protein. The Trail full length cDNA is cloned, and is utilised to create a Trail prokaryotic expression system. The full length Trail cDNA is used to respectively clone cDNA of soluble ectocytic segment Traill109 and Trail 114, and respectively create Traill109 cDNA and Traill109 and Traill expression systems. The prokaryotic expression systems created greatly increase the expression and quantity of the Trail, Traill09, and Traill14 proteins, and may be useful in a new preparation for killing tumour cells. The present sequence represents the partial human Trail protein, traill14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 LVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LVIHEKGFYYIYSQTYFRFQEEIKENAKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSK 120
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                                                                                                                                                                                       Human; tumour related apoptosis inducing ligand; Traill14; Trail prokaryotic expression system; tumour cell death.
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                                                                                                                                                                                                                                                                                                                       /note= "Encoded by CTT"
                                                                                                                                               Partial human Trail protein, Trail114.
                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                   ABG72259 standard; protein; 168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    30-NOV-2001; 2001CN-00132371.
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                                                                                                              (first entry)
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                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                            04-MAR-2003
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                                                                        ABG72259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB08265-83 represent tumour necrosis factor (TNF) ligands. The specification describes an AGP-3 polypeptide, which is TNF ligand family member. AGP-3 is a type II transmembrane protein, and is a potent B cell stimulatory factor. Expression of AGP-3 correlates to increases in the number of B cells and immunoglobulins produced. AGP-3 proteins, antibodies, and nucleic acids may be used to treat inflammatory and immune disorders, e.g. rheumatorid arthritis, Crohn's disease, lupus and graft versus host disease. The nucleic acids may be used to regulate the expression of an AGP-3 related protein. The AGP-3 proteins, antibodies and nucleic ands are also useful for the detection of AGP-3 agonists, antagonists and characterizing interactions with AGP-3 related proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 ERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polypeptides comprising tumor necrosis factor ligand family proteins, useful for treating inflammatory and immune disorders, e.g. rheumatoid arthritis.
                                                                                                                                    AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease; type II transmembrane protein; B cell stimulatory factor; inflammatory disorder; immune disorder; rheumatoid arthritis; lupus and graft versus host disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                               Amino acid sequence of a human TNF ligand TRAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Prec. ...
                                   AAB08274 standard; protein; 166 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; Fig 9; 71pp; English.
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99US-0166271P.
                                                                                                                                                                                                                                                                                11-FEB-2000; 2000WO-US003653
                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                              WO200047740-A2
                                                                                                                                                                                                                                                                                                       12-FEB-1999;
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Local St.
166;
                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                         Boyle WJ,
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                                                            AAB08274;
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The invention relates to a TNF-related apoptosis-inducing ligand encoding (TRAIL) cDNA and its encoded polypeptide. The gene of the invention is related to mutational human tumour necrosin. The polypeptide of the invention is useful for inducing the death of tumour cells. The current sequence represents the TRAIL amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Death induced ligand (TRAIL) cDNA and encoded polypeptide, useful for inducing the death of tumor cells, is related to mutational human tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 LVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MVRERG--RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
                                                                                                         TRAIL; INF-related apoptosis-inducing ligand; tumour; necrosin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDAEYGLYSIYQGGIFELKENDRIFVSVINEHLIDMDHEASFFGAFLVG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.3%; Score 866; DB 6; Length 16 ilarity 98.2%; Pred. No. 1.9e-76; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-terminal region of human TRAIL protein.
                                                                                                                                                                                                                                                                                                                                                                                                                            (CHEN-) CHENGDU DIAO PHARM GROUP CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY71985 standard; protein; 161 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Fig 2; 14pp; Chinese.
                                                                                                                                                                                                                                                                                                                     10-APR-2001; 2001CN-00105946.
                                                                                                                                                                                                                                                                                                                                                                       10-APR-2001; 2001CN-00105946
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(first entry)
                                                    TRAIL amino acid sequence
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es 166; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 167 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gao X,
                                                                                                                                                              Unidentified.
09-OCT-2003
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Matches
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118

ABR84402 standard; protein; 167 AA

ABR84402 ID ABR8 RESULT 7

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0; Indels

0; Mismatches

Conservative

Matches 161;

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post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                        Isolated TALL-1 protein is used to identify compounds that regulate lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders.
                                                                                                                                                                                                                                                                             (NAJE-) NAT JEWISH MEDICAL & RES CENT.
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'label= Beta_strand
                                                                                                                                                          18. .128 -
/label= Beta_strand
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/label= Beta_strand
                                                                Beta_strand
                                                                       42. .44
/label= Beta_strand
                                                                                    /label= Beta_strand
                                                                                                  53. .56
/label= Beta_strand
                                                                                                                61. .72
/label= Beta_strand
                                                                                                                                                                                       153. .160
/label= Beta_strand
                                   Location/Qualifiers
                                                                                                                                       Beta_strand
                                                                                                                                                     'label= Beta_strand
                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig 1b; 112pp; English.
                                                                                                                                                                                                                                          05-MAY-2000; 2000WO-US012266.
                                                                                                                                                                                                                                                         99US-0132892P
                                                                                                                                                                                                                                                               01-MAY-2000; 2000US-0201012P
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                                                                                                                                86. .91
/label= F
                                                          32. .34
/label= |
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                                                                                                                                                                                                             WO200068378-A1
                     Homo sapiens
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The present invention relates to Tumour necrosis factor (TNF) and Apolrelated Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules,
proteins (including homologues), and their antibodies. The invention in
particular relates to methods for regulating the interaction between TALL
land TALL-1 receptors (BCMA referred as B cell maturation factor) to
regulate monocyte, macrophage and B lymphocyte mediated immune responses.
TALL-1 protein is useful for identifying compounds that regulate B
C TALL-1 protein is useful for identifying compounds that regulate B
C TALL-1 protein is useful for identifying compounds that regulate B
C secont and all and a systemic lupus
erythematosus (SLE), insulin dependent diabetes mellitus, multiple
crythematosus (SLE), insulin dependent diabetes mellitus, multiple
cerythematosus (SLE), insulin dependent diabetes mellitus, multiple
collection and gravis, Grave's disease, autoimmune haemolytic
canaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,
c pemphigus vulgaris, acute rheumatic fever, post-streptococcal
corresponding nucleic acid sequence are also useful in diagnostic assays.
CC corresponding nucleic acid sequence are also thuman TRALL protein which
has 20-25% sequence identity with the C-terminal region of human TALL-1
corresponding nucleic protein TRALL protein is a TNF family member

The invention relates to a composition (I) comprising a protein complex in crystalline form, where the complex comprises an amino acid sequence of a Receptor Activator of Necrosis Factor RB (RANK) Ligand (RANKL) ectodomain. (I) is useful for identifying a compound with RANK modulating activity, and for identifying a RANK or OPG modulating compound. (I) is useful to intelligently design mutants that have altered biological properties and for identifying mutants that have altered biological properties and for identifying new therapeutic agents. (I) is also useful to computationally screen small molecule databases for chemical entities or compounds that can bind in whole, or in part, to RANK or RANKL. The present sequence represents a tumour necrosis factor (TNF) family member, TRALL (1d4v), used in a structural-based alignment study

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66.0%; Score 850; DB 4; Length 161; 100.0%; Pred. No. 6.5e-75;
                                     Query Match
Best Local Similarity
Sequence 161 AA;
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Length 161;

66.0%; Score 850; DB 6; I 100.0%; Pred. No. 6.5e-75; ilve 0; Mismatches 0;

Conservative

Local Similarity Les 161; Conserva

Matches

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Query Match

murine RANKL protein

Sequence 161 AA;

83 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 142

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142
                                                               61 FYXIXSQIYFRFQEEIKENTKNDKQWVQYIYKYTSYPDPILLIMKSARNSCWSKDAEYGLY 120
                                                143 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition for identifying a compound with Receptor Activator of Necrosis Factor kB, RANK modulating activity and for identifying RANK or osteoprotegerin modulating compound, has a protein complex in crystalline
              1 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 60
83 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                                                                                    RANK; receptor activator of necrosis factor kB; RANK ligand; RANKL; tumour necrosis factor; TNF; TRAIL; cytokine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fremont DH;
                                                                                                SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
                                                                                                              SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161
                                                                                                                                                                                                                                                             TNF family member, TRAIL (1d4v) protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ross FP, Teitelbaum SL, Nelson CA,
                                                                                                                                                                                     Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 3; 66pp; English.
                                                                                                                                                                                    ABR39855 standard; protein; 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BARN-) BARNES-JEWISH HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2002; 2002WO-US025287.
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22-MAR-2002; 2002US-00105057.
                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                 WO2003014077-A2.
                                                                                                                                                                                                                                      11-AUG-2003
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                                                                                                                                                                                                             ABR39855;
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The invention relates to a composition comprising a protein complex in crystalline form, where the complex comprises an amino acid sequence of a crystalline form, where the complex comprises an amino acid sequence of a creceptor activator of nuclear factor kappaB (NEKappaB) (RANKI) ligand (RANKI) ectodomain. The three-dimensional structural representation of a RANKI ectodomain crystal compound, and for identifying a RANK or costeoproteegerin (OPG) modulating compound, and for identifying a compound with RANK modulating activity. The crystals permit the determination of the three-dimensional X-ray diffraction structure of the crystal-line polypeptide to high resolution. The atomic structure coordinates are useful for identifying bone-forming compounds by methods which utilise the coordinates for solving the three-dimensional X-ray diffraction of the coordinates of other proteins, including mutant forms, to high resolution. The structural information may also be used in a variety of molecular modeling and computer-based screening applications to, for example design mutants of the crystallized RANKL, its receptors, or a portion or fragment of RANKL or its receptors. The coordinates of RANKL crystal, or subsets of such structural coordinates of the RANKL crystal, are useful for designing or identifying candidate compounds capable of modulating RANK biological activity, and for identifying compounds which
                                                                                FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLIMKSARNSCWSKDAEYGLY 202
Composition comprising crystalline receptor activator of NFkappaB (RANK) ligand ectodomain complex whose three-dimensional structural representation is useful for identifying RANK or osteoprotegrin modulating compound.
                                                                                                                                                                                                                                                                                                                                                                                                                        RANKL ectodomain crystal complex; RANK; osteoprotegerin; OPG; bone-forming compound; tumour necrosis factor; TNF family; cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nelson CA, Fremont DH;
                                                                                                                                  SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
                                                                                                                                                                   121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161
                                                                                                                                                                                                                                                                                                                                                                                        Tumour necrosis factor family cytokine, TRAIL.
                                                                                                                                                                                                                                                                     ADC03335 standard; protein; 161 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 3; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001; 2001US-0311163P.
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                                                                                                                                                                                                                                                                                                                                                (first entry)
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TEITELBAUM S I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2003050223-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAM J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-2003.
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                                                                                                                                                                                                                                                                                                            ADC03335;
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                                                                                                                                  203
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                                                                                                                                                                      9
the receptor. The present sequence represents the amino acid sequence of the tumour necrosis factor family cytokine, TRAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytostatic; neuroprotective; immunosuppressive; splice variant; tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand; TRAIL; apoptosis; programmed cell death; differentiation; development; cytokine; Apo-2 ligand; Apo-21; nuclear factor-B; NF-B; type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer; therapeutic; neurodegenerative disease; autoimmune disease; aging; chromosome 3q26; rpl-6-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New splice variants of tumor necrosis factor-related apoptosis inducing ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat diseases or disorders associated with low expression of the variants.
                                                                                                                                                                                                                 FYYIYSQIYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                           83 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                      RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                Gaps
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                                                                                    Length 161;
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                                                                                                                                                                                                                                                                       SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161
                                                                                                                                                                                                                                                       SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
                                                                                                                 ..
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                                                                                                   100.0%; Pred. No. 6.5e-75; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human TRAIL splice variant 8, rpl-6-6, protein.
                                                                                      66.0%; Score 850; DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    Ā
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                                                                                                                                                                                                                                                                                                                                                   AAU99301 standard; protein; 212
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                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                 Matches 161; Conservative
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YELIN R.
KHOSRAVI R.
SAVITZKY K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-479259/51.
                                                                                                   Local Similarity
                                                            Sequence 161 AA;
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                                                                                      Query Match
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Domain
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Homo sapiens.

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The invention discloses isolated, naturally occurring, polypeptide splice variants of human tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal cellular differentiation and development of multicellular organisms.

Apoptosis is induced by certain cytckines which include TNF and TRAIL (also referred to as Apo-2 ligand, Apo-21). TRAIL is a type II membrane protein which induces apoptosis and nuclear factor-B (NF-B) activation in containing receptors. DR4 and DR5, as well as two deach domain. CC and DCR2, lacking the intracellular signalling death domain. TRAIL, and DCR2, lacking the intracellular signalling death domain. TRAIL, and DCR2, lacking the intracellular signalling death domain. TRAIL, comman cells are relatively resistant without showing significant toxic side effects. Thus, TRAIL has the potential to be a very useful cormal cells are relatively resistant without showing significant toxic side effects. Thus, TRAIL has the potential to be a very useful continuour agent. The naturally occurring splice variants may differ in their cellular distribution, expression levels/timing and activity.

CC side effects. Thus, TRAIL products solls mechanisms for the induction of apoptosis of tumours cells. The splice variant polypeptides and polynucleotides can be used in gene therapy, to raise antibodies, to detect the levels, distribution and ratios of expression of TRAIL, and witch bind the variant TRAIL products and modulate its activity (agonists and antagonists). Pharmaceutical compositions, comprising an expression cytotoxic effect in cancer cells and for treatment of diseases which can cytotoxic effect in cancer cells and for treatment of diseases which can be ameliorated, cured or prevented by lowering or raising the level of the amino acid sequences are useful for causing the level of the amino acid sequences are useful for causing the lawing and expression of diseases that may be treated include cancer, neurodegenerative diseases a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases, autoimmune diseases, diseases involved in the non-normal development of tissues and aging. TRAIL's gene is located on chromosome 3Q26. The sequence presented is the human TNF-related apoptosis inducing ligand (TRAIL) splice variant 8, rp1-6-6, protein which has had an C-terminal section of the conserved TNF domain deleted
           Claim 4; Fig 8; 29pp; English.
\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\over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Sequence 212 AA;

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61 TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
                                                                                                                                               1 TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEE
                                   0; Gaps
                                                                                                                                                                                         SCHSFLSNLHLRNGBLVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY 173
                                                                                                                                                                                                          64.3%; Score 827; DB 5; Length 212; 91.3%; Pred. No. 1.7e-72;
                                 10; Indels
                               5; Mismatches
             Best Local Similarity 91.3
Matches 158; Conservative
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Query Match
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Human TRAIL splice variant 6, TRA-33-T7, protein.
         AAU79599 standard; protein; 188 AA
                                 (first entry)
                                24-SEP-2002
                     AAU79599;
RESULT 12
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Human; cytostatic; neuroprotective; immunosuppressive; splice variant; tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand; TRALL; apoptosis; programmed cell death; differentiation; development; cytokine; Apo-2 ligand; Apo-2L; nuclear factor B; NF-B; cype I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer; therapeutic; neurodegenerative disease; autoimmune disease; aging; chromosome 3q26; TRA-33-T7.

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The invention discloses isolated, naturally occurring, polypeptide splice variants of human tumour necrosis factor (TNF) related apoptobis inducing ligand (TRAAIL). Apoptosis, or programmed cell death, occurs during normal cellular differentiation and development of multicellular organisms.

Apoptosis is induced by certain cytokines which include TNF and TRAIL (also referred to as Apo-2 ligand, Apo-2L). TRAIL is a type IT membrane protein which induces apoptosis and nuclear factor-B (NF-B) activation in many tissues and cells. Receptors for TRAIL include two death domain containing receptors, DR4 and DR5, as well as two decoy receptors, DCR1 and DCR2, lacking the intracellular signalling death domain. TRAIL, induced by type I interferons, induces apoptosis in tumour cells, whereas normal cells are relatively resistant without showing significant toxic side effects. Thus, TRAIL has the potential to be a very useful antitumour agent. The naturally occurring splice variants may differ in their cellular distribution, expression levels/timing and activity. Containing these factors could provide possible mechanisms for the induction of apoptosis of tumours cells. The splice variant polypeptides and polymucleotides can be used in gene therapy, to raise antibodies, to contain the variants, in a biological sample and to identify compounds which bind the variant TRAIL products and modulate its activity (agonists and antagonists). Pharmaceutical compositions, comprising an expression vector or any of the amino acid sequences, are useful for causing a cytotoxic effect in cancer cells and for treatment of diseases which can be used in diseases that may be treated include cancer, neurodegenerative the amino acid sequences, are useful for causing a diseases that may be treated include cancer, neurodegenerative cutility in blocking or decreasing the activity of the minor of diseases intended and each of the ameliorment of diseases intended and each of the ameliorment of the amelior and aniver many of the amelior and aniver man
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New splice variants of tumor necrosis factor-related apoptosis inducing ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat diseases or disorders associated with low expression of the variants.
                                                                                                         17. .38 /note= "Transmembrane domain"
                                                                                                                                                     39. .188
/note= "Extracellular domain"
                                                                                  /note= "Cytoplasmic domain"
                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Savitzky K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Fig 9; 29pp; English.
                                                                                                                                                                                                                                                                                                          16-MAY-2001; 2001US-00855544.
                                                                                                                                                                                                                                                                                                                                                   16-MAY-2000; 2000IL-00136156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Khosravi R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-479259/51.
                                                                                                                                                                                                                                                                                                                                                                                          (YELI/) YELIN R.
(KHOS/) KHOSRAVI R.
(SAVI/) SAVITZKY K.
                                                                                                                                                                                                                     US2002061525-A1.
                                                                                                                                                                                                                                                              23-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yelin R,
                                                                  Domain
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Sequence 188 AA;

development of tissues and aging. TRAIL's gene is located on chromosome 326. The sequence presented is the human TNR-related apoptosis inducing ligand (TRAIL) splice variant (F, TRA-33-T7, protein which has had an N-terminal section of the conserved TNF domain deleted

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93;
58.0%; Score 746.5; DB 5; Length 188; 61.7%; Pred. No. 1.1e-64; ive 0; Mismatches 0; Indels 93.
                     Best_Local Similarity 61.73
Matches 150; Conservative
  Query Match
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181 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The specification describes the use a polypeptide corresponding to at least the primary sequence of part AAV01516-17 to produce a diagnostic, prophylateric or therapeutic composition useful in cases of degenerative, autoimmune and inflammatory diseases. The polypeptides can be used in treatment of neurodegenerative disease, lupus erythematosus, rhuematoid arthritis, and SEP. The polypeptides are apoptotic in central nervous system cells, antigenic and specifically recognise the surface receptor of the TRAIL protein. The polypeptide is a marker of disease and a therapeutic target, e.g. its apoptotic activity can be blocked with an anti-TRAIL antibody or a TRAIL equivalent that binds to specific receptors, inhibiting formation of natural complex. The present sequence represents a polypeptide of the invention
                                                TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
                                                                                                                                               -----ENTKNDKOMVQYIYKYTSYPD 125
TNELKQMQDXYSKSGIACFLKEDDSYMDPNDEESMNSPCWQVKWQLRQLVRKMLLRTSEE
                                                                                                                121 SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of polypeptide derived from TRAIL protein for diagnosis of degenerative disease - autoimmunity and inflammation, also useful in prevention or treatment, and similar use of corresponding ligand and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurodegenerative disease; autoimmune disease; inflammatory disease; lupus erythematosus; rhuematoid arthritis; SEP; apoptotic; surface receptor; TRAIL protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perron H;
                                                                                                                                                                                                                                                                                                                                                                 AAY01518 standard; peptide; 139 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 14; 21pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-156177/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 139 AA;
                                                                                                                                                                                                                                                241 LVG 243
                                                                                                                                                                                                                                                                                LVG 188
                                                                               TISTVO
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                                                                                                                                               105
                                                                                                                                                                                                               126
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                                                               116
                                                                                                                                                       61 ESSRSGHSFLENLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT 120
                                                                                                                                 117 ESSRSCHSFLSNIHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification describes an AGP-3 polypeptide, which is TNF ligand family member. AGP-3 is a type II transmembrane protein, and is a potent B cell stimulatory factor. Expression of AGP-3 correlates to increases in the number of B cells and immunoglobulins produced. AGP-3 proteins, antibodies, and nucleic acids may be used to treat inflammatory and immune disorders, e.g. rheumatoid arthritis, Crohn's disease, lupus and graft versus host disease. The nucleic acids may be used to regulate the expression of an AGP-3 related protein. The AGP-3 proteins, antibodies and nucleic ands are also useful for the detection of AGP-3 agonists, antagonists and characterizing interactions with AGP-3 related proteins
                                                                                               9
                                                                                1 TSETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW
                                                              57 TSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW
                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease; type II transmembrane protein; B cell stimulatory factor; inflammatory disorder; immune disorder; rheumatory districtis; lupus and graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polypeptides comprising tumor necrosis factor ligand family proteins, useful for treating inflammatory and immune disorders, erhoumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
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            Pred. No. 5.9e-63;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of a mouse TNF ligand TRAIL.
                                                                                                                                                                                                                                                                                                                            AAB08275 standard; protein; 172 AA.
100.08;
                                                                                                                                                                                                       177 SYPDPILLMKSARNSCWSK 195
                                                                                                                                                                                                                                      121 SYPDPILLMKSARNSCWSK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 14; Fig 9; 71pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                             139; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-558217/51.
              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boyle WJ, Hsu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 172 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200047740-A2.
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              Local
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              Best Loca
Matches
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81 PORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHE 140

8

56.5%; Score 727; DB 2; Length 139;

Query Match

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The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were by prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences draw the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                          141 KGFYYIYSQTYFRFQEE-----IKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWS 194
                                                                                                                                                      Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                                  33.0%; Score 425; DB 3; Length 121; 100.0%; Pred. No. 1.8e-33; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 13; SEQ ID NO 7833; 71pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein, SEQ ID NO: 7833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG03752 standard; protein; 121 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAC03758.
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61 TISTVQEKQQNISPLVRERG 80

0; Gaps

Similarity 100. 80; Conservative

Matches

ò Dp. 8

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completed: March 23, 2004, 09:13:49
99 TISTVQEKQQNISPLVRERG 118
                                                              Job time
                                                  Search
              g
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

(without alignments) 1168.727 Million cell updates/sec March 23, 2004, 09:11:39; Search time 20 Seconds

US-10-662-429-2_COPY_39_281 Title:

Perfect score:

1287 1 TNELKQMQDKYSKSGIACFL......NEHLIDMDHEASFFGAFLVG 243 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

125680 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 243

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

SS	Description	tumor necrosia fac	necrosis	necrosis	necrosis	Д	-18	tumor necrosis fac	lymphotoxin alpha	tumor necrosis fac	tumor necrosis fac	tumor necrosis fac	tumor necrosis fac	w	œ	tumor necrosis fac	tumor necrosis fac	tumor necrosis fac	tumor necrosis fac	tumor necrosis fac	hypothetical prote	conserved hypothet	hypothetical prote	peptide transport	dnaK suppressor pr	hypothetical prote		_	conserved hypothet	hypothetical prote
SUMMARIES	QI.	S17289	A25451	S12606	I54490	S24641	JQ1344	OWHUN	QWHUX	OMMSN	JU0029	S22052	JH0529	S06192	B27303	S52715	S24642	JN0869	JH0309	S11688	C89803	A82076	H71485	877753	B87569	E82910	B64396	B70438	AF0347	T26862
	DB	-	Н	Н	7	٦	Н	7	Н	Н	7	Н	Н	~	Н	7	Н	н	Н	7	7	~	~	N	7	7	~	7	7	7
	Length	204	234	232	235	204	234	233	202	235	235	233	234	193	202	185	233	202	197	233	203	202	223	195	142	201	223	227	112	123
ð	Query Match	10.5	10.2	10.	П	ο,		e,	ο,		o,	σ,	9.1	0.6	8.9	8.8	8.8	8.7	8.3	7.7	6.3	6.1	6.0	5.9	5.9	5.7	5.7	5.7	5.6	5.6
	Score	134.5	131.5	130	129.5	127.5	126	123	122	121	121	120	117.5	115.5	114	113.5	113	111.5	101	98.5	80.5	78	77	76.5	75.5		73	^	72.5	
	Result No.		63	m	4,	Ŋ	Q	7	ထ	o,	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	26	27	28	29

ALOSASA N.Alternate names: cachectin; TNF alpha C;Species: Oryctolagus cuniculus (domestic rabbit) C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 10-Sep-1959 #sequence revision 10-Sep-1999 #text_change 04-Feb-2000 C;Accession: A25454; A2541; JS0727 R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, E. DNA 5, 149-156, 1986 A;Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for re

probable secreted	hypothetical prote	sAM-dependent meth	conserved hypothet	formate dehydrogen	hypothetical prote	chitin synthase (E	hypothetical prote	conserved hypothet	lipoprotein [impor	hypothetical prote	OX40 ligand protei	chitin synthase (E	ABC transporter, A	hypothetical prote	ORF MSV139 hypothe
H71623	A99014	A99387	140422	H64336	T21543	D45188	T37839	C81749	D90593	H81292	JE0351	S53800	B90180	A81896	T28300
0	N	~	H	N	N	N	7	N	N	N	~	7	~	~	7
156	218	243	195	227	234	189	222	226	209	144	199	201	202	222	139
9	2.6	5.6	9.5	5.6	5.5	5.5	5.5	5.5	5.4	5.4	5.4	5.4	5.4	5.4	5.4
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72.5	72.5	72.5	71.5	71.5	71	70.5	70.5	70.	70	69	69.5	69	69.5	69.5	Ğ

ALIGNMENTS

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tumor necrosis factor beta precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S17289 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S17289 #sequence_revision 10-Sep-1999
C;Accession: S17289 #sequence rumor necrosis factor-encoding genes: sequence and comparative and A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative and A;Accession: S17289
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 STVQEKQQNISPLVRERGPQRVAAHITG-----TRGRSNTLSSPNSKNEKALGRKINS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.5%; Score 134.5; DB 1; Length 204;
Best Local Similarity 24.7%; Pred. No. 0.00037;
Matches 46; Conservative 31; Mismatches 76; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38638.1; PID:g2133 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage
F;l-33/Domain: signal sequence #status predicted <SIG>
F;34-204/Product: tumor necrosis factor beta #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-204 < KUH>
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42 SAAQPAHQH-PPKHLARGTLKPAAHLVGDPSTPDSLRWRANT-----DRAFLR----

176 TS-YPDPILLIMKSARNSCWSKDAEYGLYSIYOGGIFBLKENDRIFVSVTNEHLIDMDHEA 234

ò a RESULT 2

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A.Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138
K.Pauli, U.; Beutler, B.; Peterhans, E.
Gene 81, 185-191, 1989
A;Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reactio
A; Residues: 1-232 < KUH>
A; Residues: 1-232 < KUH>
A; Crose-references: BMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:g2134
A; Note: the authors translated the codon GAG for residue 202 as Gly
R; Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.
Submitted to the EMBL Data Library, January 1991
A; Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis A; Reference number: $18965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: 146659; MUID:90034181; PMID:2478420
A;Accession: 146559
A;Accession: 146559
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 44-232 <PAU>
A;Cross-references: GB:M29079; NID:gl64694; PIDN:AAA31128.1; PID:gl64695
C;Genetics:
                                                                                                                                                                                                                                                                  A; Accession: S18965
A; Molecule type: mRNA
A; Residues: 1-232 < CHO>
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A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-62, 'Q', 63-234 <SHA>
A; Residues: 1-62, 'Q', 63-234 <SHA>
A; Residues: 1-62, 'Q', 63-234 <SHA>
A; Residues: 1-62, 'Q', 63-234 <SHA>
A; Residues: 1-62, 'Q', 63-234 <SHA>
A; Residues: 1-62, 'Q', 63-234 <SHA>
A; Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756
C; Genetics: C; Superfeamily: tumor necrosis factor
C; Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
F; 181, pompeptide #statues predicted <MAT>
F; 82-234/Product: tumor necrosis factor #status predicted
F; 19, 20/Binding site: myristate (Lys) (covalent) #status predicted
F; 147-178/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-232 < CDRE>
A; Residues: 1-232 < CDRE>
A; Cross-references: EMBL: X54001; NID: 92135; PIDN: CAA37949.1; PID: 92136
B; Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A; Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal
A; Reference number: S17289; MUID: 91340150; PMID: 1874444
A; Accession: S17290
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-234 <IT2>
A; Residues: 1-234 <IT2>
A; Note: this sequence differs from that shown in having a Gln inserted between residues A; Note: this sequence differs from that shown in Dongeneel, C.V.; Nedospasov, S.A. Gene 95, 215-221, 1990
A; Itle: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-A; Reference number: JH0309; MUID:91065534; PMID:2249779
                                                                                                                                           A;Cross-references: GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
DNA S; 157-165, 1986
A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
A;Reference number: A25451; MUID:86219712; PMID:3519138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIY 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 VVA------NPQVEGQL----QWLSQRANAILLANGMKLTDNQLVVPADGLYLIY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 SQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDFILLMKSARNSCWSKDAEYG----L 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 SOVLFSGO-----GCRSYVLLTHTVSRFAVSYPNKVNLLSAIKSPCHRETPEEAEPMAWY 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93
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C;Species: Sus scrofa domestica (domestic pig)
C;Bate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: S12606; S17290; S18065; 146659
R;Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.
Nucleic Acids Res. 18, 5564, 1990
A;Title: Gene sequence of porcine tumor necrosis factor alpha.
A;Reference number: S12606; MUID:91016861; PMID:2216741
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A;Reference number: A25454; MUD:86219711; PMID:3519137
A;Accession: A25454
A;Molecule type: MRNA
A;Residues: 1-234 <ITO>
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                                                                                                                                                                                                                                                                                                                                             A; Accession: A2545:
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Matches
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Ajutrons: 62/3; 78/1; 93/1
C,Superfamily: tumor necrosis factor
C,Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myr
C;R-1-77/Domain: propeptide #status predicted <RRO>
F;1-77/Domain: propeptide #status predicted <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;19,10/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;144-176/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Crew, M.D.; Filipowsky, M.E.
fimunogenetics 35, 351-353, 193
A;Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leu
A;Reference number: 154490; MUID:92218012; PMID:1348497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 GPQRVAAHITGTRGRSNTLSSPNS---KNEKALGRKINSWESSRSGHSFLSNLHLRNGEL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 GPLSINPLAQGLRSSSQTSDKPVAHVVANVKAEGQL--QWQSGYANALLANGVKLKDNQL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 VIHEKGFYYIYSQTYFRFQEEIKEN---TKNDKQMVQYIYKYTSYPDFILLMKSARNSCW 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 VVPTDGLYLİYSQVLFRGQGCPSTNVFLTHTISRIA-----VSYQTKVNLLSAIKSPCQ 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumor necrosis factor alpha precursor - white-footed mouse
C;Species: Peromyscus leucopus (white-footed mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Gaps
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C;Genetics:
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C; Superfamily: tumor necrosis factor
C; Superfamily: tumor necrosis factor
C; Superfamily: tumor necrosis
F; Steywords: glycoprotein; lipoprotein; myristylation
F; 19, 20/Binding site: myristate [Lys] (covalent) #status predicted
F; 84/Binding site: carbohydrate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 SK-----DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG
                                                                                                                                                                                                                                                                                                                                                                                     0.0011; Length 232; 0.0011; Indels
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.1%; Score 130; DB Best Local Similarity 25.1%; Pred. No. 0.001 Matches 43; Conservative 30; Mismatches
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Gaps

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N'Alternate names: cachectin; TNFA
C;Specias: Homo Sapiens (man)
C;Date: 28-Aug-1985 #sequence revision 28-Aug-1985 #text change 08-Dec-2000
C;Accession: A93585; S36153; A93351; A44189; B61478; IS3311; S62610; IS4522; A01646; F
R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica,
Nucleic Acids Res. 13, 6361-6373, 1995
A;Tille: Human lymphotoxin and tumor necrosis factor genes: structure, homology and characterine number: A93585; MUID:86016093; PMID:2995927
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A, Rolecule type: DNA
A, Residues: 1-233 < RND
A, Cross-teferences: GB: X02910; GB: X02159; NID: G37209; PIDN: CAA26669.1; PID: G37210
A, Cross-references: GB: X02910; GB: X02159; NID: G37209; PIDN: CAA26669.1; PID: G37210
R, Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jun
Nature Genet. 3, 137-145, 1993
A; Title: Dense Alu clustering and a potential new member of the NFkappaB family within A, Reference number: S36152; MUID: 93272029; PMID: 8499947
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A:Title: Human tumour necrosis factor: precursor structure, expression and homology to
A:Reference number: A93351; MUID:85086244; PMID:6392892
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A; Residues: 1-233 <PEN>
A; Residues: 1-233 <PEN>
A; Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A; Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A; Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyt A; Mang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N. Science 228, 149-154, 1985
                                                                                                                                                                 A;Introns: 62/3; 79/1; 95/1

C;Superfamily: tumor necrosis factor

C;Superfamily: tumor necrosis factor

C;Reywords: cytckine; cytctoxin; glycoprotein; lipoprotein; lymphokine; macrophage;

F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>

F;78-205/Binding site: myristate (Lys) (covalent) #status predicted

F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;146-178/Disulfide bonds: #status predicted
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A;Accession: A44189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 ISTVOEKO-----QNISPLVR-----ERGP-QRVAAHITGTRGRSNTLSSPNSKNEKALG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 VLLTHTISRLAVSYPSKVNLLSAIKSPCHTESPEQAEAKPWYEPIYLGGVFQLEKGDQLS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---NPOAEG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 RKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQ 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---GCPSTH 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 YIYKYT-----SYPDPILLMKSARNSCWSKDAEYG----LYSIYQGGIFELKENDRIF 219
C,Comment: This protein is an important proximal mediator of endotoxemia. C,Genetics:
A,Gene: TNF-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48;
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0.0023;
thes 72; Indels
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; Pred. No. 0.00
35; Mismatches
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Best Local Similarity 22.5%;
watches 45; Conservative
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A;Residues: 1-62,'S',64-233 <WAN>
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C;Species: Equus cachectin; TNF alpha
C;Species: Equus cachectin; TNF alpha
C;Species: Equus cachectin; TNF alpha
C;Accession: 001344
R;Su, X; Morris, D.D.; McGraw, R.A.
R;Su, X; Morris, D.D.; McGraw, R.A.
R;Su, X; Morris, D.D.; McGraw, R.A.
R;Su, X; Morris, D.D.; McGraw, R.A.
R;Su, X; Morris, D.D.; McGraw, R.A.
R;Su, X; Morris, D.D.; McGraw, R.A.
R;Su, X; Morris, D.D.; McGraw, R.A.
R;Seference number: J01344; MJD:92084125; PMID:1748301
A;Reference number: J01344
A;Rocession: J01344
A;Residues: 1-234 <SUX>
A;Residues: 1-234 <SUX>
A;Cross-references: GB:MG4087; NID:g164244; PIDN:AAA30959.1; PID:g164245
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Cybate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
Cybate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
Cycosesion: 146046; 224641
RyCludts, I., Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, I.
Cytokine 5, 336-341, 1993
AyIttle: Cloning and characterization of the tandemly arranged bovine lymphotoxin and the AyReference number: 146046; MUID: 94083525; PMID: 8260599
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l Similarity 24.9%; Pred. No. 0.0015;
47; Conservative 29; Mismatches 78; Indels 35; Gaps
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AjReference number: I54522 MUID:94102809; PMID:7903959
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A;Accession: B61478
A;Molecule type: protein
A.Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738
F.Pkbudas, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An
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Eur. J. Biochem. 235, 431-437, 1996
A; Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
A; Reference number: S62610; MUID:96202967; PMID:8631363
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A,Map position: 6p21.3-6p21.3
A,Introns: 62/3; 78/1; 94/1
Complex: homotrimer
C,Superfamily: tumor necrosis factor
C,Keywords: cytokine; cytocoxin; 9lycoprotei
F:71-700main: propeptide #status predicted
F:77-233/product: tumor necrosis factor #sta
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A,Molecule type: protein
A,Residues: 77-99 TAK.
R,D'Alfonso, S.; Richiardi, P.M.
Immunogenetics 39, 150-154, 1994
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Best Local Similarity
Matches 43; Conserv
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A; Residues: 1-233 < MAR>
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A,Gene: GDB:TNF; TNFA
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A; Status: translation not shown; translated from GB/EMBL/DDBJ
A; Status: translation not shown; translated from GB/EMBL/DDBJ
A; Status: 1-124,'P',126-205 (RES)
A; Residues: 1-124,'P', 126-205 (RES)
A; Cross-references: GB-RIS5913, NID: 9339742; PIDN: AAB59455.1; PID: 9339743
A; Experimental source: ancestral haplotype 57.1
A; Note: 59-Asn was also found (ancestral haplotype 8.1)
B; Gray, P.W.; Aggarwal, B.B.; Benton, C.V.; Bringman, T.S.; Henzel, W.J.; Jarrett, J.A.
Nature 312, 721-724, 1984
A; Title: Cloning and expression of cDNA for human lymphotoxin, a lymphokine with tumou A; Reference number: A93350; MUID: 85086243; PMID: 6334807
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A;Cross-references: GB:X01393; NID:g34444; PIDN:CRA25649.1; PID:g34445
A;Experimental source: lymphoblastoid cell line RPMI-1788
R;Goeddel, D.V.; Aggarwal, B.B.; Gray, P.W.; Leung, D.W.; Nedwin, G.E.; Palladino, M.F.
Cold Spring Harb. Symp. Quant. Biol. 51, 597-609, 1986
A;Title: Tumor necrosis factors: gene structure and biological activities.
A;Reference number: A32877; MUID:87217059; PMID:3472740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lymphotoxin alpha precursor - human
N.Alternate names: lymphotoxin A; TNF beta; tumor necrosis factor beta (TNF beta)
N.Alternate names: lymphotoxin A; TNF beta; tumor necrosis factor beta (TNF beta)
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence revision 07-Jul-1995 #text change 16-Jun-2000
C;Accession: A92755; S56154; T54482; A93350; B32877; A91906; A61478; S26951; A01645; AZ
R;Nedwin, G.E.; Jarrett-Nedwin, J.; Smith, D.H.; Naylor, S.L.; Sakaguchi, A.Y.; Goeddel
A;Title: Structure and chromosomal localization of the human lymphotoxin gene.
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K.I.;
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A;Residues: 1-59, 'N',61-205 <NED>
R;Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurl
Nature Genet. 3, 137-145, 1993
A;Title: Dense Alu clustering and a potential new member of the NFkappaB family within
A;Reference number: S36152; MUID:93272029; PMID:8499947
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A;Residues: 35-205 <GOE>
R;Kobayashi, Y.; Miyamoto, D.; Asada, M.; Obinata, M.; Osawa, T.
A;Bicchem. 100, 727-733, 198
A;Title: Cloning and expression of human lymphotoxin mRNA derived from a human T cell
A;Reference number: A91906; MUID:87057135; PMID:3536896
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A;Rataus: mucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Robecule type: DNA
A;Rossidues: 1-12,'R',14-205 (IRI)
A;Cross-references: EMBL:215026; NID:g37211; PIDN:CAA78746.1; PID:g37213
A;Cross-references: EMBL:215026; NID:g37211; PIDN:CAA78746.1; PID:g37213
A;Note: the nucleocide sequence was submitted to the EMBL Data Library, August 1992
E;Abraham, L.J.; Du, D.C.; Zahedi, K.; Dawkins, R.L.; Whitehead, A.S.
Immunogenetics 33, 50-53, 1991
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A;Residues: 1-59, N',61-205 <KOB>
A;Cross-references: GB:D00102; NID:g219913; PIDN:BAA00064.1; PID:g219914
A;Cross-references: GB:D00102; NID:g219913; PIDN:BAA00064.1; PID:g219914
A;Note: the authors translated the codon TAT for residue 156 as Thr and ACC for R;Note: the authors Issand ACC for R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, Lymphokine Res. 7, 175-185, 1988
163 YQTKVNILISAIKSPCQRETPEGAEAKPWYEPIYLGGVFQLEKGDRLSAEINRPDYLDFAE 222
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A;Residues: 1-235 <SHA>
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R)Shakhov, A.N.; Nedospasov, S.A.
Bioorg, Khim. 13, 701-705, 1987.
A)Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucl
A;Reference number: S03791; MUID:87298639; PMID:3040015
A,Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
A,Reference number: A61478, MUID:88301617, PMID:2841543
                                                                                                                                                                                                                                     A;IILLe: Natural human tumor necrosis factor beta (lymphotoxin). Variable O-glycosylatid
                                                                                                                                                                                                                                                                                                                                                                                                                                                R.F. Fukushima, K.; Watanabe, H.; Takeo, K.; Nomura, M.; Asahi, T.; Yamashita, K. Arch. Bloofhem. BJophys. 304, 144-153, 1993
A;Title: N-linked augar chain structure of recombinant human lymphotoxin produced by CHC A;Reference number: S34742; MUID:93311995; PMID:8323280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        while having no detrimental effect on normal cells. It can also act synergistically wit C; Comment: This protein and TNF-alpha (tumor necrosis factor) are the products of differical activities but are produced by different cell types and have different induction ki
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A;Accession: A22908
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C; Comment: Secreted from mitogen-activated lymphocytes within 1-2 days after induction,
                                                                                              A,Molecule type: protein
A,Residues: 56-79;86-95, X', 97, 'X', 99;119-151, 'XX',154-162,'X',164,'X',166,'X',168,'X',
A,Residues: 56-79;86-95, X', 97, 'X', 99;119-151, 'XX',154-162,'X',164,'X',166,'X',168,'X',
R;Voigt, C.G., Maurer-Pogy, I.; Adolf, G.R.
REBS Lett. 314, 85-88, 1992
A,Title: Natural human tumor necrosis factor beta (lymphotoxin). Variable O-glycosylat:
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C;Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text change 04-Feb-2000
C;Accession: A22908; S03791; Ā27303; A25164; A23127; A34251; I59058; A36696
B;Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.
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A;Gross-references: GDB:120442; OMIM:153440
A;Map position: 6p21.3-6p21.3
A;Introns: 33/3; 69/1
A;Note: the first intron occurs before the initiator codon C;Superfamily: tumor necrosis factor
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A; Molecule type: protein
A; Residues: 35-59, N', 61-205 < VOI>A; Note: 60-Thr was also found
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A; Molecule type: DNA
                                                                 A; Accession: A61478
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A;Cross-references: GB:M13049; NID:g202082; PIDN:AAA40457.1; PID:g202083
R;Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.
Biochem. Blophys. Res. Commun. 173, 1072-1078, 1990
A;Title: Characterization of high molecular weight glycosylated forms of murine tumor r A;Reference number: A36696; MUID:91097531; PMID:2268312
A;Accession: A36696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A. Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
A;Title: Identification of a common nucleotide sequence in the 3'-untranslated region c A;Reference number: I59058; MUID:86149365; PMID:2419912
                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68530.1; PID:g54832
R;Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V.
Brc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985
A;Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necros A;Reference number: A25164; MUID:85298296; PMID:3898078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANote: the first intron occurs in the 5'-untranslated region G.Superfamily: tumor necrosis factor G.Superfamily: tumor necrosis factor G.Superfamily: tumor necrosis factor G.Superfamily: unwords: cytotoxin, glycoprotein; lipoprotein; lymphokine; macrophage; men F;80-235/Froduct: tumor necrosis factor #status experimental <MAT> F;20/Binding site: myristate (Lys) (covalent) #status predicted F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted F;148-179/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Cseh, K.; Beutler, B.
J. Biol. Chem. 264, 16256-16260, 1989
A;Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide results
A;Reference number: A34251; MUID:89380231; PMID:2777790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 17-235 ~PEN>
A;Cross-references: GB:M11731; NID:g202084; PIDN:AAA40458.1; PID:g202085
B;Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashima, Nucleic Acids Res. 13, 4417-4429, 1985
A;Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic exp. A;Reference number: A23127; MUID:85242112; PMID:2989794
                                                                                                                                                                        INF locus, including the TNF-alpha-(tumor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 EKFPNGLPLI-----SSMAQTLTLRSSSQNSSDKPVAHVVANHQVEEQL-----EWLSQR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRRQEEIKENTKUDKQMVQYIYKYT-SYP 179
                                                                                 R;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A. Nucleic Acids Res. 15, 9083-9084, 1387
Aprile: Nucleotide sequence of the murine TNF locus, including the TNF-alph A;Reference number: A93679; MUID:88067722; PMID:3684584
A;Cross-references: GB:M38296; NID:g202086; PIDN:AAA40459.1; PID:g202087
A;Note: article in Russian with English abstract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-235 <FRA>
A;Cross-references: GB:X02611; NID:g54844; PIDN:CAA26457.1; PID:g54845
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A,Residues: 80-85,'X',87-99 <SHE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein A; Residues: 70-87 < CSE>
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A;Residues: 1-235 <SEM>
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tumor necrosis factor alpha precursor - sheep
U;Alternate names: cachectin; TWF alpha
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: UH0529; S48118; S13114; S20661
R;Green, I.R.; Sargan, D.R.
A;Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with A;Reference number: JH0529; MUID:92112044; PMID:1765267
                                                                                                                                                                                                 R;Sanjanwala, M.; Edwards, A.
submitted to the EMBL Data Library, September 1991
A;Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
A;Reference number: S22052
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Immunol. Cell Biol. 69, 273-283, 1991
A.Title: Molecular cloning, expression and characterization of ovine TNF-alpha.
A, Reference number: S48118; MOLD:92155784; PMID:1786996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 SFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT----S 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 GPQR------VAAHITGTRGRSNTLSSPNSK-----NEKALGRKINSWESSRSGH 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 GPOREEFPKDPSLISPLAQAVRSSSRT---PSDKPVAHVVANPQAEGQL--QWLNRRANA 111
                        tumor necrosis factor alpha precursor - baboon
C;Species: Papio sp. (baboon)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: S2052
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R;Young, A.J.; Hay, J.B.; Chan, J.Y.C.
Nucleic Acids Res. 18, 6723, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160 C;Genetics:
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A;Residues: 1-214 <GRE>
A;Cross-references: BMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406
A;Experimental source: alveolar macrophage
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C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane
P;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;18/Binding site: carbohdrate (Ser) (covalent) #status predicted
F;145-177/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.3%; Score 120; DB 1; Length 233; Best Local Similarity 23.0%; Pred. No. 0.0076; Matches 43; Conservative 32; Mismatches 70; Indels 4
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                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: S22052
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <SAN>
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A;Molecule type: mRNA
A;Residues: 1-234 <NAS>
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Ajoure in Carry 1, 197/1

CjSuperfamily: tumor necrosis factor

CjSuperfamily: tumor necrosis factor #status predicted «MAT»

Fig. 205/Product: tumor necrosis factor #status predicted «MAT»

Fig. 207/Binding site: myristate (Lys) (covalent) #status predicted

Fig. 84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Fig. 86/Binding site: carbohydrate (Asn) (covalent) #status predicted

Fig. 86/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Residues: 1-38, P',40-162, T',164-201,'S',203-235 <BST>
A;Cross-references: GB:X66539; GB:S40199; NID:g395369; PIDN:CAA47146.1; PID:g395370
C;Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin and A;Gene:: TNF-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:L00981; NID:g205253; PIDN:AAA16275.1; PID:g205254
R;Estler, H.C.; Grewe, M.; Gaussling, R.; Pavlovic, M.; Decker, K.
Bail. Chem. Hoppe-Seyler 373, 271-281, 1992
A;Title: Ret tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in vitral A;Reference number: $21674; MUID:92329007; PMID:1627266
A,Accession: $21674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Molecule type: DNA
**Residues: 1-235 <SHID*
**Ricesidues: 1-235 <SHID*
**Ricesidues: 1-235 <SHID*
**Ricesidues: 1-235 <SHID*
**Ricesidues: 1-235 <INT*
**Ricesidues: 1.Y.; Benveniste, E.N.
**Gene 132, 227-236, 1993
**A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
**A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
**A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
**A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
**A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
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**A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
**A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
**A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
**A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
**A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
**A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
**A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
**A;Title: Cloning and Sequence analysis of the ratio and tumor necrosis factor-encoding genes.
**A;Title: Cloning and Sequence analysis of the ratio and tumor necrosis factor-encoding genes.
**A;Title: Cloning and Sequence analysis of the ratio and tumor necrosis factor-encoding genes.
**A;Title: Cloning and Sequence analysis of the ratio and tumor necrosis factor-encoding genes.
**A;Title: Cloning and Sequence analysis of the ratio analysis of the ratio and tumor necrosis of the ratio and tumor necrosis and tumor necrosis and tumor necrosis and tumor necrosis and tumor necrosis and tumor necrosis and tumor necrosis and tumor necrosis and tumor necros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NyAlternate names: cachettin, TNF alpha
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence revision 07-Jun-1990 #text_change 04-Feb-2000
C;Accession: JU0022; JN0868; Z21674
R;Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.
R;Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.
A;Title: Cloning and expression in Bscherichia coli of the gene for rat tumor necrosis
A;Reference number: JU0029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 QEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSP-----NSKNEXALGRKINSWESS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 EEKFPNGLPLI-----SSMAQTLTLRSSSQNSSDKPVAHVVANHQAEEQL----EWLSQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 RSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQWVQYIYKYT-SY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 RANALLANGMDLKDNQLVVPADGLYLIYSQVLFKGQ-----GCPDYVLLTHTVSRFAISY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 PDPILLMKSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDH 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 EKVNLLSAVKSPC-PKDTPEGAELKPWYEPIYLGGVFQLEKGDQLSAEVNLPKYLDFAES 225
---LYSIYOGGIFELKENDRIFVSVTNEHLIDMDHE 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30;
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180 DPILLMKSARNSCWSKDAEYG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumor necrosis factor alpha
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                                                                                                                                                                                   234 AS-FFG 238
                                                                                                                                                                                                                                                                          226 GQVYFG 231
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Matches 4
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A; Accession: S13114

11 RESULT

--- GCPSTHVLLTHTISRIAVS 162

42; Gaps

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A,Molecule type: DNA
A,Residues: 1-11;139-160,'CG',163-178 <NED>
A;Cross-references: BMBL:X06217
R;Weil, D.; Dautry, F.
Oncogene Res. 3, 409-414, 1988
A;Fitle: Induction of tumor necrosis factor-alpha and -beta and interferon-gamma mRNA L
A;Reference number: $10083; MUID:89144562; PMID:3147435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68529.1; PID:g54831
R;Nedospasov, S.A.; Hirt, B.; Shakhov, A.N.; Dobrynin, V.N.; Kawashima, E.; Accolla, R. Nucleic Acids Res. 14, 7713-7725, 1986
A;Title: The genes for tumor necrosis factor (TNF-alpha) and lymphotoxin (TNF-beta) are A;Reference number: S01342; MUID:87040736; PMID:3490653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Mouse lymphotoxin and tumor necrosis factor: Structural analysis of the cloned A;Reference number: I56004; MUID:87252204; PMID:2885372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N'Alternate names: lymphotoxin; TNF beta
C;Species: Mus musculus (house mouse)
Cjace: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 24-Sep-1999
C;Accession: B27303; S01342; S10083; I56004; I48853; I55980
R;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic, Acids Res. 15, 9083-9084; 11887
A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor A;Reference number: A93679; MUID:88067722; PMID:3684584
                                                        149 QTYFRFQEEIKENTKNDKQMVQYIYKYT----SYPDPILLMKSARNSCWSK---DAE 198
                                                                                                                            98 QVLFR------GHGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETPBAEAK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene sequence.
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R;Gardner, S.M.; Mock, B.A.; Hilgers, J.; Huppi, K.E.; Roeder, W.D.
J. Immunol. 139, 476-483, 1987
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-25, P',27-202 <RES>
A;Cross-references: GB:M17015; NID:g198880; PIDN:AAA39450.1; PID:g387407
R;Gray, P.W.; Chen, E.; Li, C.B.; Tang, W.L.; Ruddle, N.
Nucleic Acids Res. 15, 3937, 1987
A;Title: The murine tumor necrosis factor-beta (lymphotoxin) gene sequence
A;Reference number: 148853; MUID:87231097; PMID:3588316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB:M16819; NID:g202088; PIDN:AAA40460.1; PID:g202089 C; Comment: The first intron occurs in the 5'-untranslated region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:Y00137; NID:954842; PIDN:CAA68330.1; PID:954843
R;Li, C.
                                                                                                                                                                                                                                         149 PWYEPIYQGGVFQLEKGDRLSAEINQPEYLDYAESGQVYFG 189
                                                                                                                                                                                                   199 YGLYSIYQGGIFBLKENDRIFVSVTNEHLIDMDHEAS-FFG 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-202 <RE3>
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                tumor necrosis factor beta precursor - mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S10083
A; Molecule type: mRNA
A; Residues: 6-202 <WEI>
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A; Residues: 1-202 <SEM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 17
A; Introns: 32/3; 66/1
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-62,64-234 «YOU>
A;Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404
A;Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404
A;Note: comparison with the introns of homologous sequences suggest that this is probabl
A;Note: comparison with the introns of homologous sequences suggest that this is probabl
C;Superfamily; tumor necrosis factor
E;Te-234/Product: tumor necrosis factor alpha #status predicted
F;1-77/Domain: propeptide #status predicted
F;20/Binding site: myristate (Lys) (covalent) #status predicted
F;20/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;96/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;146-178/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Molecule type: mRNA
A;Residues: 36-38,'S',40-78,'A',80-88,'N',90-114,'Q',116-123,'D',125-144,'G',145-173,'L'
A;Residues: 36-38,'S',40-78,'A',80-88,'N',90-114,'Q',116-123,'D',125-144,'G',145-173,'L'
A;Cross-references: EMBL:X7731,'IND:9452607; PIDN:CAAB4523.1; PID:9452608
C;Superfamily: tumor necrosis factor
C;Reywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage; membrane protein
F;42/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;106-138/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 GPQRVAAHITG---TRGRSNTL-SSPNSKNEKALGRKINS------WESSRSGHSFLS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPÖREEQSPAGPSFNRPLVQTLRSSSQASNNRPVAHVVANISAPGQLRWGDSYANALMAN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 ILLMKSARNSCWSK----DAEYGLYSIYQGIFELKENDRIFVSVTNEHLIDMDHEAS- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 NIHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKOMVOYIYKYT----SYPDP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 TCTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYS .148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----NKPVAHV 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N'Alternate names: cachectin; TNF alpha
C; Species: Capra aegagrus hircus (domestic goat)
C; Accession: Sobly2; S41867.
C; Accession: Sobly2; S41867.
C; Accession: Sobly2; S41867.
C; Accession: Bobly2; S41867.
C; Accession: Sobly2; Salver, D.; Talhouk, A.
Submitted to the EMBL Data Library, March 1989
A; Reference number: Sobly2.
A; Accession: Socies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 117.5; DB 1; Length 234;
Pred. No. 0.013;
0; Mismatches 78; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.0%; Score 115.5; DB 2; Length 193; 10.4%; Pred. No. 0.014; ve 36; Mismatches 79; Indels 61.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 23.0%;
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Best Local Similarity 20.4%;
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A; Molecule type: mRNA
A; Residues: 1-193 <GOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 YFG 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FFG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S41867
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Union necrosis factor alpha precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: S52715
R;Mertens, B.; Gaidulis, L.
R;Mertens, B.; Gaidulis, L.
R;Mertens, B.; Gaidulis, L.
R;Mertens, B.; Gaidulis, L.
R;Mertens, B.; Gaidulis, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 TSGLYFVYSQVVFSGESCSPRAIPTPIYLAHEVQLFSSQYPFHVPLL-SAQKSVYPGLQG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 GPQRVAAHITGTRGRS---NTL-SSPNSKNEKALGR---KINS----WESSRSGHSFLS 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 KSARNSC-----WSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 238
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.8%; Score 113.5; DB 2; Length 185; Best Local Similarity 25.0%; Pred. No. 0.02; Matches 45; Conservative 29; Mismatches 79; Indels 27; Gaps
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage
                                                                                                                                                                                                                                                           18;
                                                                                                                                           Query Match 8.9%; Score 114; DB 1; Length 202; Best Local Similarity 23.5%; Pred. No. 0.02; Matches 38; Conservative 25; Mismatches 81; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 YGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

March 23, 2004, 09:07:59; Search time 17 Seconds Run on:

(without alignments)
744.297 Million cell updates/sec

US-10-662-429-2_COPY_39_281 Title:

1 TNELKQMQDKYSKSGIACFL...............NEHLIDMDHEASFFGAFLVG 243 Perfect score: Sequence:

BLOSUM62

Scoring table:

141681 segs, 52070155 residues Searched:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 243

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwiBsProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Match Length DB Result

				:	1 1 1 1 1 1
	174	Н	TN15 HUMAN	095150 homo	sapien
12.	240	н	TN14 HUMAN	043557 homo	
11.	239	Н	TN14_MOUSE	SUM 6	musculu
	235	н	TNFA RABIT		oryctolagus
10.	204	Н	TNFB_PIG		scrofa
10.	234	Н	TNFA_CAVPO	5 cavi	a porce
_	232	Н	TNFA PIG	Bus 8	ĕ
	235	Ч	TNFA PERLE		myscus
	204	н	TNFB BOVIN		taurus
6	234	н	TNFA HORSE		equus cabal
9	233	Н	TNFA_MARMO		marmota mon
9	233	ч	TNFA_HUMAN		homo sapien
9.	229	Н	TNFA_CEREL		us elap
9	205	Н	TNFB HUMAN		ă
9.	232	Н	TNFA_PANTR	pan	troglod
.6	235	Н	TNFA_MOUSE		mus musculu
. 9.	23	Н	TNFA RAT		rattus norv
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9.	23	н	TNFA_TURTR		iops tr
9.	8	Н	TNFB MACEU		opus eu
σ.	23	Н	TNFA_SHEEP		ovis aries
σ,	23	Н	TNFA_MACMU		ca mula
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	127.5 10.1 127.5 10.1 128 9.6 128 9.7 128 9.5 129 9.5 120 9.4 121 9.4 121 9.4 122 9.5 123 9.5 124 9.4 127 9.4 128 9.5 129 9.5 120 9.3 120 9.3 120 9.3 120 9.3 120 9.3 121 9.4 122 9.5 123 9.5 124 9.4 125 9.5 127 9.1 117 5 9.1 117 8 9.1 118 9.5 111 8.8 113.5 8.8 113.5 8.8 113.5 8.8 113.5 8.8		1001 1100	10.1 232 1 TNFA 10.1 235 1 TNFA 10.1 204 1 TNFA 10.1 204 1 TNFA 10.1 204 1 TNFA 10.1 204 1 TNFA 10.1 204 1 TNFA 10.1 204 1 TNFA 10.2 205 1 TNFA 10.3 203 1 TNFA 10.3 203 1 TNFA 10.4 203 1 TNFA 10.4 203 1 TNFA 10.5 203 1 TNFA 10.6 203 1 TNFA	10.1 232 TNRA_PIG P2563 BN P3693 P

P13296 capra hircu	Q86332 rattus norv	O9bdm7 macaca neme	P59695 papio anubi	077764 macropus eu	P10154 oryctolagus	Q9tsv8 sus scrofa	P19101 felis silve	P56783 arabidopsis	·	Q88wl7 lactobacill
TNFA CAPHI	INFB_RAT	TNF5_MACNE	TNFA_PAPAN	TNFA_MACEU	TNFB RABIT	TNFC_PIG	TNFA_FELCA	CEMA_ARATH	DKSA_CAUCR	KGUA_LACPL
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5.5	111.5	111	110	108	101	106.5	104.5	77.5	75.5	73.5
112	7									

ALIGNMENTS

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SEQUENCE FROM N.A.
TISSUE-BUDDILICAL vein;
MEDLINE-99091541 PubMed=9872942;
Zhai Y., Ni J., Jiang G.-W., Lu J., Xing L., Lincoln C., Carter K.C.,
Janat F., Kozak D., Xu S., Rojas L., Aggarwal B.B., Ruben S.,
Li L.-Y., Gentz R., Yu G.-L.;
"VEGI, a novel cytokine of the tumor necrosis factor family, is an angiogenesis inhibitor that suppresses the growth of colon carcinomas
                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 15 (Vascular endothelial cell growth inhibitor) (INF ligand-related molecule 1).
TWFSFIS OR VEGI OR TL1.
                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                       174 AA.
                       PRT;
                       STANDARD;
                                                                                                               Homo sapiens (Human)
                                                                                                                                                NCBI_TaxID=9606;
                      TN15 HUMAN
                                                                                                                                                                                                                                                              in vivo.";
RESULT 1
TN15_HUMAN
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FASEB J. 13:181-189(1999). -!- FUNCTION: Inhibits vascular endothelial growth and angiogenesis

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). -!- FUNCTION:

(in vitro).

-!- SUBGNATT: Homotrimer (Potential).

-!- SUBGNATT: Homotrimer (Potential).

-!- SUBGNATT: Homotrimer Specifically expressed in endothelial cells.

-!- TISSUE SPECIFICITY: Specifically expressed in endothelial cells.

-!- TISSUE SPECIFICITY: Specifically expressed in endothelial cells.

Detected in placenta, lung, tkiney, skeletal muscle, pancreas, spleen, prostate, small intestine and colon.

-!- SIMILARITY: Belongs to the tumor necrosis factor family.

-!- SIMILARITY: Belongs to the tumor necrosis factor family.

EMBL; AF039390; AAD08783.1; -. HSSP; P50591; 1D0G. Genew; HGNC:11931; TNFSF15. MIM; 604052; -.

GO; GO: 0005887; C: integral to plasma membrane; TAS. GO; GO: 0005102; F: receptor binding; TAS. GO; GO: 000014; P: resegulation of cell cycle; TAS. InterPro; IPR006053; TNF abc. InterPro; IPR006052; TNF family. InterPro; IPR008983; TNF family. InterPro; IPR008983; TNF subf. Ffam; PF00229; TNF; 1.

PRINTS; PR01234; INECROSISFCT. ProDom; PD002012; TNF_subf; 1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 TVVIIKVTDSYPEPTQLLMGTKSVC----EVGSNWFQPIYLGAMFSLQEGDKLMVNVSD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 VQYIYKYT-SYPDPILLMKSARNSCWSKDAEYG---LYSIYQGGIFELKENDRIFVSVTN 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=98122340; PubMed=9462508;
Mauri D.N., Ebner R., Montgomery R.I., Kochel K.D., Cheung T.C.,
Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.G.,
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ligands for herpesvirus entry mediator.";
Immunity 8:21-30(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TN14 HUMAN STANDARD; PRT; 240 AA.
043557; 075476; Q8WVF8; Q96LD2;
16-OCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor ligand superfamily member 14 (Herpesvirus entry
                                                                                                                         SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDITE=98438532; PubMed=9765287;
Harrop J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J., Tan K.B., Dede K., Spampanato J., Silverman C., Heneley P., Delprinzio R., Emery J.G., Deen K., Eichman C., Chabot-Fletcher M., Trunch A., Young P.R.;
"Herpesvirus entry mediator ligand (HVEM-L), a novel ligand for HVEM/TR2, stimulates proliferation of T cells and inhibits HT29 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21528948; PubMed=11673523; Granger S.W., Ware C.F., Granger S.W., Butrovich K.D., Houshmand P., Edwards W.R., Ware C.F., "Genomic Characterization of LIGHT reveals linkage to an immune response locus on chromosome 19p13.3 and distinct isoforms generated by alternate splicing or proteolysis."; Immunol. 167:5122-5128(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                        DOTENTIAL.
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                            48; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                          12.4%; Score 160; DB 1; Length 174; 35.3%; Pred. No. 2.5e-06; tive 24; Mismatches 48; Indels 1
                                                                                                                                                                                 174 EXTRACELLULAR (POTENTIAL).
125 POTENTIAL.
56 N-LINKED (GLCNAC. . . ) (PO 20131 MW; CCB83BA7EE673B98 CRC64;
                                                    Cytokine, Transmembrane, Glycoprotein, Signal-anchor. DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 2), AND PROCESSING.
                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 273:27548-27556(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 EHLIDMDHE-ASFEGAFLV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 ISLVDYTKEDKTFFGAFLL 174
                                PROSITE; PS50049; TNF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mediator-ligand) (HVEM-L).
TNFSF14 OR LIGHT OR HVEML.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                  12
25
SMART; SM00207; INF; 1.
                                                                                                                                                                                     26 1
85 1
56 1
152 1
                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42
                                                                                                                             TRANSMEM
                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local 8
                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                        DOMAIN
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TN14 HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                A Grausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Aleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Aleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heibh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,

A Broak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Wilalon D.K., Murny D.M., Sodergren E.J., Lu K., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A William M., Madan A., Young A.C., Shevchenko, V., Bouffard G.G.,

Blakesley R.W., Acteman J.W., Schenn E.D., Dickson M.C.,

Blakesley R.W., Krzywinski M.I., Skalska U., Smailus D.E.,

Chenerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Ronerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).

C FUNCTION: Cyclokine that binds to TNFRSF3/LTBR. Binding to the

decoy receptor TNFRSF6 modulates its effects. Activates NFKB,

c the adenocarcinoma HT-29. Acts as a receptor for Herpes simplex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=2; Synonyms=LIGHT delta-TM;
IsoId=043557-2; Sequence=VSP 006452;
TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE SPLEEN BUT ALSO
FOUND IN THE BRAIN, WEAKLY EXPRESSED IN PERIPHERAL LYMPHOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LUNG, APPENDIX, AND KIDNEY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- PTM: N-glycosylated.
-i- PTM: The soluble form of isoform 1 derives from the membrane form by proteolytic processing.
-i- SIMILARITY: Belongs to the timor necrosis factor family.
-i- CAUTION: Ref.4 sequence differs from that shown due to a frameshift in position 178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND KIL AND NO EXPRESSION SEEN IN FETAL TISSUES, ENDOCRINE GLANDS, OR NONHEMALOPOLETIC THROR LINES.
INDUCTION: UPREGULATED AFTER T-CELL ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (isoform 1); Cytoplasmic (isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0006917; P:induction of apoptosis; TAS. GO:0007165; P:signal transduction; TAS. InterPro; IPR006053; TNF abc. InterPro; IPR006052; TNF family. InterPro; IPR008983; TNF like. InterPro; IPR003836; TNF_subf. Fami, PF00229; TNF]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=043557-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005102; F:receptor binding; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AY028261; AAK26160.1; -. BC018058; AAH18058.1; ALT_FRAME.
                                         MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF036581; AAC39563.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF064090; AAC25169.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:11930; INFSF14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: Homotrimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP: P01375: 4TSV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     604520; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 SPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSOTYFRFQEBIK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 ENTKNDKOMVQY------IYKYT-SYPDPILLMKSARNSCWSKDAEYGLY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 GP-----LLWE-TQLGLAFLRGLSYHDGALVVTKAGYYYIYSK------ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVKWQLRQLVRKMILRTSEETISTVQEKQQN-ISPLVRERGPQRVAAHITGTRGRSNTLS 99
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                                                                                                                                                                                                               MEMBER 14, MEMBRANE FORM.
WHORN NECROSIS FACTOR LIGAND SUPERFAMILY
MEMBER 14, SOLUBLE FORM.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                   TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                   SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDITNE=20354998; PubMed=10894944; Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.; Mosawa K., nosaka T., Kojima T., Hirai M., Kitamura T.; "Molecular cloning and characterization of a mouse homolog of human TNFSF14, a member of the TNF superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 --SIYQGGIFELKENDRIFVSVTNEHLIDM-DHEASFFGAFLV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
CLEAVAGE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49D0BF67E1390B39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
N-LINKED (GLCNAC. .).
Missing (in isoform 2).
Frid=VSP 006452.
L -> V (IN REF. 4).
E -> K (IN REF. 2).
                   ProDom, PD002012; TNF subf; 1.
SMART, SM0207; TNF; 1.
PROSITE; PS50025; TNF; 1. FALSE NEG.
PROSITE; PS50049; TNF 2, 1.
CYtokine; Transmembrane; Glycoprotein; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Tumor necrosis factor ligand superfamily member 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Pred. No. 4.2e-06; 41; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.4%; Score 159.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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MEDLINE=20165223; Pubmed=10700230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26351 MW;
PRINTS; PR01234; INECROSISFCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.8%;
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                                                                                                                                                                                   240
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                                                                                                                                                                                                                                                                                                                                                                      240
83
187
102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                       Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
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                                                                                                                                                                                                                                                                                                           TRANSMEM
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DN 15-MAR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 YVXSKVQLS-GVGCPQGLANGLPITHGLYKRTSRYPKELELLVSRRSPCGRANSSRVWWD 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEMBER 14, MEMBRANE FORM.
TUMOR NECROSIS PACTOR LIGAND SUPERFAMILY
MEMBER 14, SOLUBLE FORM.
CYPOLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 AAHLTGANASLIGIGGP------LLWE-TRLGLAFLRGLTYHDGALVTMEPGYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTS-YPDPILLMKSARNSCWSKDABYGLY-
                                             TISSUE-Lymphoma;

Force W.R., Todd P.K., Mikayama T.;

Force W.R., Todd P.K., Mikayama T.;

"Mouse LIGHT; molecular genetics, ligand binding and expression.";

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: Cytokine that binds to INFRSF3/LTBR. Binding to the decoy receptor TNFRSF6B modulates its effects. Activates NFKB and stimulates the proliferation of T cells.

-! SUBUNIT: Homotrimer (By similarity).

-! SUBCELDILAR DOCATION: Type II membrane protein and secreted (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL,
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                  similarity).
-!- PIM: The soluble form derives from the membrane form by
proteclytic processing.
-!- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
CLEAVAGE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26338 MW; 217874AC71AD6BE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 SIYQGGIFELKENDRIFVSVTNEHLI-DMDHEASFFGAFLV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.8%; Score 152.5; DB 1 29.2%; Pred. No. 1.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
Cytogenet. Cell Genet. 89:89-91(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00251; TNF 1; FALSE NEG.
PROSITE; PS50049; TNF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR006053; TNF abc.
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF_like.
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AF123385; AAF76453.1; -. EMBL, AAD29152; BAA88559.1; -. EMBL, AF227533; AAF36722.1; -. HSSP; P01375; 4TSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nterPro; IPR003636; TNF subf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00229; TNF; 1.
PRINTS; PR01234; TNECROSISFCT.
ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1355317; Infsf14
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187
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58
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191
239 AA;
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Best Local Similarity
                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Cycokine that binds to TNFRSFIA/TNFRI and TNFRSFIB/TNFRI. Stockine that binds to TNFRSFIA/TNFRI and TNFRSFIB/TNFRE. It is mainly secreted by macrophages and can induce cell death of certain tumor cell lines. It is potent pyrogen causing fever by direct action or by stimulation of interleukin 1 secretion and is implicated in the induction of acchesia, Under certain conditions it can stimulate cell proliferation and induce cell differentiation.

SUBCELLUAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).

FTM: The soluble form derives from the membrane form by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISEASE: Cachexia accompanies a variety of diseases, including cancer and infection, and is characterized by general ill health
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=86219711; PubMed=3519137;
Ito H., Yamamoto S., Kuroda S., Sakamoto H., Kajihara J., Kiyota T.,
Hayashi H., Kato M., Seko M.;
                                                     13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-1987 (Rel. 05, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor piecursor)
Ilgand superfamily member 2) (TNF-a) (Cachectin).
TNF OR INFSF2 OR INFA.
                                                                                                                                                                                                                                                                                                                                                                      "Structural analysis of the rabbit TNF locus, containing the genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteolytic processing (By similarity).

PIN: The membrane form, but not the soluble form, is phosphorylated on serine residues. Dephosphorylation of the membrane form ocurrs by binding to soluble INFRSFIA/INFRI (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning and expression in Escherichia coli of the cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŚEĞUENCE FROM N.A.
MEDLINE=86219712; PubMed=3519138;
Ito H., Shirai T., Yamamoto S., Akira M., Kawahara S., Todd C.W.,
Wallace R.B.;
                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Lagomorpha, Leporidae, Oryctolagus.
NCBI TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning of the gene encoding rabbit tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                         encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and malnutrition.
SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                             Shakhov A.N., Kuprash D.V., Azizov M.M., Jongeneel C.V.,
                     235 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumor necrosis factor.";
                     PRT;
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=91065534; Pubmed=2249779;
                                                                                                                                                                                    Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M12845; AAA31486.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M12846; AAA31482.1; -. EMBL; M60340; AAA31484.1; -.
                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 95:215-221(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA 5:157-165(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coding for rabbit t
DNA 5:149-156(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  Nedospasov S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity)
                   INFA RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor."
                                          P04924;
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InterPro; IPR006053; INF_abc.

PIR; A25454; A25451. HSSP; P06804; 2TNF.

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----WESSRSG 122
                                                                                                                                                                                                                                                                                                                                                                                                                56 IGPQEEEQSPNNL--HLVNPVAQMVTLRSASRALSDKPLAHVVANPQVEGQLQWLSQRAN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                             123 HSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 ALLANGMKLTDNQLVVPADGLYLIYSQVLFSGQ-----GCRSYVLLTHTVSRFAVSYPNK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 ILLMKSARNSCWSKDAEYG----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-
                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
CLEAVAGE (BY ADAM17) (BY SIMILARITY).
PHOSPHORYLATION (BY CKI) (BY SIMILARITY)
                                                                                                                                                TUMOR NECROSIS FACTÓR, MEMBRANE FORM.
UMOR NECROSIS FACTÓR, SOLUBLE FORM.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                       23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Large white; TISSUE=Fibroblast;
MEDLINE=21108615; PubMed=11169259;
Chardon P., Rogel-Gaillard C., Cattolico L., Duprat S., Vaiman M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 42, Last annotation update)
Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis factor ligand superfamily member 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scroffa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE=91340150; PubMed=1874444;
Kuhnert P., Wuethrich C., Peterhans E., Pauli U.;
"The porcine tumor necrosis factor-encoding genes: sequence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Renard C.; "Sequence of the swine major histocompatibility complex region containing all non-classical class I genes.";
                                                                                                                                                                                                                                                                                                                          10.6%; Score 136.5; DB 1; Length 235; 23.0%; Pred. No. 0.00032; ive 37; Mismatches 81; Indels 23.
                                                                                                                                Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                   72 ISPLVRERGPQRVAAHITGTRGRSNTL-SSPNSKNEKALGRKINS--
                                                                                                                                                                                                                                                                                 MISSING (IN REF. 3).
610177D0BD2EF871 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 AA
                                                                                                                                                                                                                                                                   BY SIMILARITY
                                                                                                                                                                                                            (POTENTIAL
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF like.
InterPro; IPR003636; TNF like.
Pfam; PF00229; TNF; 1.
PRINTS; PR01234; TNFS subf.
ProDom; PD0021234; TNF subf.
PROSITE; PS00251; TNF il.
PROSITE; PS0049; TNF 1; 1.
                                                                                                                                                                                                                                                                                                25816 MW;
                                                                                                                                                                                                                                                                                                                                          23.0%;
                                                                                                                                                                                                                                                                                                                                      Local Similarity 23.0% nes 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comparative analysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 102:171-178(1991).
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235
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56
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179
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                                                                                                                                                                                                                                                                                                235 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 YFG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=9823;
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                                                                                                                                                                                                                                                                 148
                                                                                                                                                                             DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                     MOD RES
                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                  CHAIN
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                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 STVOEKOONISPLVRERGPORVAAHITG-----TRGRSNTLSSPNSKNEKALGRKINS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 WESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 -----HGFL----LSNNSLLVPTSGLYFVYSQVVFSGEGCFPKATPTPLYLAHEVQLF 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 TS-YPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 SŚQYPFHVPLLSAQKSVCPGPQGPW-VRSVYQGAVFLLTQGDQLSTHTDGTPHLLLSPSS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sue Antigens 57:55-65(2001).
FUNCTION: Cytokine that in its homotrimeric form binds to TNFRSFIA/TNFR, TNFRSFIB/TNFBR and TNFRSFI4/HVEM. In its heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is produced by lymphocytes and cytotoxic for a wide range of tumor cells in vitro and in vivo.
SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one LTB subunits or (less prevalent) two LTA and one LTB subunits (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor precursor)
Ilgand superfamily member 2) (TNF-a) (Cachectin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .) (POTENTIAL)
                                                                                                                                                          similarity).
-!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
associated (heterotrimers) (By similarity).
-!- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.5%; Score 134.5; DB 1; Length 204; 24.7%; Pred. No. 0.00039; ive 31; Mismatches 76; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 95 N-LINKED (GLCNAC. . .) (PC 204 AA; 21960 MW; 81263187435E56AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYMPHOTOXIN-ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; PO1374; TINR.

INTERFOR, IPROGOGOS; TNF_family.

INTERFOR, IPROGOGOS; TNF_family.

INTERFOR; IPROGOGOS; TNF_like.

PEAM; PEO0229; TNF; 1.

PRINTS; PR01234; TNECROSISFCT.

PRODM; PD00201; TNF; 1.

PROSITE; PS000207; TNF; 1.

PROSITE; PS000207; TNF; 1.

PROSITE; PS000207; TNF; 1.

PROSITE; PS000207; TNF; 1.

PROSITE; PS000207; TNF; 1.

PROSITE; PS000207; TNF; 1.

PROSITE; PS000207; TNF; 1.

PROSITE; PS000207; TNF_1; 1.

PROSITE; PS000207; TNF_2; 1.

PROSITE; PS000207; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ251914; CAB63853.1; -. PIR; S17289; S17289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cavia porcellus (Guinea pig)
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X54859; CAA38638.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 SFFGAF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 VFFGAF 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNFA CAVPO
P51435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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ID TNFA CAVPO

PC P51435;
DT 01-OCT-
DT 10-OCT-
DE TUMOF I
      Tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Б
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                                                                                                                                                                                                                                                                                                     Am. J. Physiol. 273:L524-L530(1997).

-I-FUNCTION: Cytokine that binds to TNFRSFIA/TNFR1 and TNFRSFIB/TNFRR.

-I-FUNCTION: Cytokine that binds to TNFRSFIA/TNFR1 and TNFRSFIB/TNFRR.

-I-FUNCTION: Cytokine that binds to TNFRSFIA/TNFR1 and can induce cell death of certain tumor cell lines. It is potent pyrogen causing fever by direct action or by stimulation of interleukin 1 secretion and is implicated in the induction of cachexia. Under certain conditions it can stimulate cell proliferation and induce cell differentiation.

-I-SUBGINIT: Homotrimex (By similarity).

-I-SUBCELULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).

-I-FTM: The soluble form derives from the membrane form by
                                                                                                                                                                                                           STRAIN=Dunkin-Hartley;
MEDINES-945215; Pubbed=9316485;
White A.M., Yoshimura T., Smith A.W., Westwick J., Watson M.L.;
"Airway inflammation induced by recombinant guinea pig tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLEAVAGE (BY ADAM17) (BY SIMILARITY).
PHOSPHORYLATION (BY CK1) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISEASE: Cachexia accompanies a variety of diseases, including cancer and infection, and is characterized by general ill health and malnutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteolytic processing (By similarity).
--- PTM: The membrane form, but not the soluble form, is phosphorylated on serine residues. Dephosphorylation of the membrane form ocurrs by binding to soluble TNFRSFIA/TNFRI (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal-anchor; Phosphorylation.
TUMOR NECROSIS FACTOR, MEMBRANE FORM.
TUMOR NECROSIS FACTOR, SOLUBLE FORM.
                                                                       SEQUENCE FROM N.A. STROUGHLUNG; STRANDSATHSFARTHER. STRANDSATHS TO STRANDSATH TO STRANDSATH TO STRANDSATH TO STRANDSATH TO STRANDSATH TO STRANDSATH TO STRANDSATH SUBMITTED (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 132.5; DB 1; Length 234; Pred. No. 0.00068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7272C940393E7E9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, P06804, 2TNF.
INTERPRO: IPRO06053; TNF abc.
INTERPRO: IPRO06052; TNF Family.
INTERPRO: IPRO08983; TNF Like.
InterPro: IPRO03636; TNF Subf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam, PF00229; TNF; 1. —
PRINTS; PR01234; TNECROSISPCT.
Probom; PD002012; TNF subf; 1.
SWART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25793 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U39839; AAB06492.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U77036; AAB19210.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00251; TNF 1; 1. PROSITE; PS50049; TNF 2; 1. Cytokine; Transmembrane; Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234
35
56
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178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD RES
DISÜLFID
SEQUENCE
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TRANSMEM
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80 GPQRVAAHITGT--RGRSNTL---SSPNSKNEKALGRKINS-----WESSRSGHSFL 126
                                                                            127 SNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDPILLM 185
                                                                                                      117 NGMGLSDNQLVVPSDGLYLIYSQVLFKGQ----GCPSYLLLTHTVSRLAVSYPEKVNLL 171
                                                                                                                                                186 KSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDM-DHEASFFG 238
 Gaps
                                                                                                                                                                                                                                                  01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Large white, TISSUB=Fibroblast, MEDLINE=21108615; PubMed=11169259; Chardon P., Rogel-Gaillard C., Cattolico L., Duprat S., Vaiman M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuhnert P., Wuethrich C., Peterhans E., Pauli U., "The porcine tumor necrosis factor-encoding genes: sequence and
25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Macrophage;
Choi C.S., Molitor T.W., Lin G.F., Murtaugh M.P.;
"Complete nuclectide sequence of a cDNA encoding porcine tumor
necrosis factor-alpha.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Renard C.; "Sequence of the swine major histocompatibility complex region containing all non-classical class I genes."; Tissue Antigens 57:55-65(2001).
77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91016861; PubMed=2216741;
Drews R.T., Coffee B.W., Prestwood A.K., McGraw R.A.;
"Gene sequence of porcine tumor necrosis factor alpha.";
Nucleic Acids Res. 18:5564-5564(1990).
                                                                                                                                                                                                                             232 AA
33; Mismatches
                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91340150; PubMed=1874444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anim. Biotechnol. 2:97-105(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 44-232 FROM N.A.
44; Conservative
                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comparative analysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 102:171-178(1991).
                                                                                                                                                                                                                                                                                                          ligand superfamily mem
TNF OR TNFSF2 OR TNFA.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Liver;
                                                                                                                                                                                                                             TNFA PIG
P23563;
Matches
                                                                                                                                                                                                   RESULT 7
                                                                                                                                                                                                               TNFA_PIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 GPQRVAAHITGTRGRSNTLSSPNS---KNEKALGRKINSWESSRSGHSFLSNLHLRNGEL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 WVPTDGLYLIYSQVLFRGQGCPSTNVFLTHISRIA-----VSYQTKVNLLSAIKSPCQ 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 GPLSINPLAQGLRSSSQTSDKPVAHVVANVKAEGQL--QWQSGYANALLANGVKLKDNQL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 VIHEKGFYXIYSQTYFRFQEEIKEN---TKNDKQMVQYIYKYTSYPDPILLMKSARNSCW 193
              -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).
-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
-!- PTM: The membrane form, but not the soluble form, is phosphorylated on serine residues. Dephosphorylation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLEAVAGE (BY ADAM17) (BY SIMILARITY).
PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
                                                                                                                                                   DISEASE: Cachexia accompanies a variety of diseases, including cancer and infection, and is characterized by general ill health and malnutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                        membrane form ocurrs by binding to soluble INFRSF1A/TNFR1 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
CLEAVAGE (BY ADAM17) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TUMOR NECROSIS FACTOR, MEMBRANE FORM TUMOR NECROSIS FACTOR, SOLUBLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 SK----DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 238

    -!- SIMILARITY: Belongs to the tumor necrosis factor family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.1%; Score 130; DB 1; Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY. 65B28F702D99C8BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30; Mismatches
 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IRR006053; INF abc.
InterPro; IRR006052; INF_family.
InterPro; IRR008983; TNF_like.
InterPro; IRR008983; TNF_like.
Pfam; PF00229; TNF; 1.
PRINTS; PRO1234; TNECROSISFCT.
ProDom; PD0022012; TNF subf.;
SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  X54859; CAA38639.1; -. X57321; CAA40591.1; -. AJ251914; CAB63852.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 B
25254 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNFA PERLE STANDARD;
P36939;
01-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X54001; CAA37949.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M29079; AAA31128.1; -. PIR; S12606; S12606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50049; TNF_1; 1. PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43; Conservative
 Homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232
232
35
56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P01375; 4TSV
                                                                                                                                          similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD RES
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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TNFA_PERLE
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                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
CLEAVAGE (BY ADAM17) (BY SIMILARITY).
PHOSPHORYLATION (BY CKI) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TUMOR NECROSIS FACTOR, MEMBRANE FORM.
HUMOR NECROSIS FACTOR, SOLUBLE FORM.
CYTOFLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISEASE: Cachexia accompanies a variety of diseases, including cancer and infection, and is characterized by general ill health
                                                                           Peromyscus leucopus (White-footed mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1umor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
1igand superfamily member 2) (TNF-a) (Cachectin).

INF OR TNFSF2 OR TNFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteolytic processing (By similarity).

FTM: The membrane form, but not the soluble form, is phosphorylated on serine residues. Dephosphorylation of the membrane form ocurrs by binding to soluble TNFRSFIA/TNFRI (By
                                                                                                                                                                                                          Crew M.D., Filipowsky M.E.; "Sequence of the tumor necrosis factor/cachectin (TNF) gene from "Sequence of the tumor necrosis factor/cachectin (TNF) gene from Percomyscus leucopus (family Cricetidae)."; Immunogenetics 35:315353(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, P06804, ZINF.
InterPro; IPR006053; TNF abc.
InterPro; IPR006053; TNF like.
InterPro; IPR0008983; TNF like.
InterPro; IPR003636; TNF like.
InterPro; IPR003636; TNF like.
InterPro; IPR003636; TNF like.
InterPro; IPR003636; TNF like.
IPR002039; TNF subf.
IPR002012; TNF subf; 1.
IPR0031E; PS00251; TNF like.
IPR0SITE; PS00251; TNF like.
IPR0SITE; PS00251; TNF like.
IPR0SITE; PS0049; TNF like.
IPR0SITE; PS0049; TNF like.
IPR0SITE; PS0049; TNF like.
IPR0SITE; PS0049; TNF like.
IPR0SITE; PS0049; TNF like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235A5CFC9F9AC624 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY
                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=92218012; PubMed=1348497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 N-
25822 MW;
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235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and malnutrition.
                                                                                                                              Peromyscus.
NCBI TaxID=10041;
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36
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10.1%; Score 129.5; DB 1; Length 235;

Query Match

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                                     σ.
                                                                   72 ISPLVRERGPORVAAHITGTRGRSNTL-SSPNSKNEKALGRKINSWE-----SSRSGH 123
                                                                                      124 SFLSN-LHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDP 181
                                                                                                                                                                                                               182 ILLMKSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS 235
                                                                                                                                                                                                                                      -i- FUNCTION: Cytokine that in its homotrimeric form binds to INFRSF1A/TWFR1, TWFRSF1B/TWFBR and TWFRSF14/HVEM. In its heterotrimeric form with LTB binds to TWFRSF3/LTBR. Lymphotoxin is produced by lymphocytes and cytotoxic for a wide range of tumor cells in vitro and in vivo.
-!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTA subunits or (less prevalent) two LTA and one LTB subunits (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 42, Last sequence update)
Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis factor ligand superfamily member 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arranged bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCRITUTAR LOCATION: Secreted (homotrimer) and membrane-associated (heterotrimers) (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cludts I., Cleuter Y., Kettmann R., Burny A., Droogmans L., "Cloning and characterization of the tandemly arranged bovilymphotoxin and tumour necrosis factor-alpha genes.";
                                     Indels
Pred, No. 0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                    204 AA.
         24.5%; Prec. ....
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INTERPRO; IPR006053; TNF abc.
INTERPRO; IPR006052; TNF family.
INTERPRO; IPR008983; TNF like.
INTERPRO; IPR00836; TNF aubf.
Pfam; PR00229; TNF; 1.
PRINTS; PR01234; TNECROSISFCT.
PRODOm; PD002012; TNF aubf; 1.
SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94083525; PubMed=8260599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z14137; CAA78510.1; -. PIR; I46046; S24641.
                                 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytokine 5:336-341 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine)
               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     236 -FFG 238
                                                                                                                                                                                                                                                                                                                       228 VYFG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
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                                                                                                                                                                                61 TISTVQEKQQNISPLVRERGPQRVAAHITG-----TRGRSNTLSSPNSKNEKALGRKI 113
                                                                                                                                                                                                                                      114 NSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY 173
                                                                                                                                                                                                                                                                  89 -----HGF----SLSNNSLLVPTSGLYFVYSOVVFSGRGCFPRATPTYLAHEVQ 135
                                                                                                                                                                                                                                                                                              174 KYT-SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTN-EHLIDMD 231
                                                                                                                                                                                                                                                                                                              :: || : |: :: || : 136 IFSPQYPFHVPLLSAQKSVCPGPPQGPW-VRSVYQGAVFLLTRGDQLSTHTDGISHLL-LS 193
                                                                                                                                                                                                            40 TPSAAQPAHQQL-PTPFTRGTLKPAAHLVGDPSTQDSLKWRANT------DRAFLK-- 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92084125; PubMed=1748301;
Su X., Morria D.D., McGraw R.B.;
"Cloning and characterization of gene TNF alpha encoding equine tumor
necrosis factor alpha.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       а'n
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pyrogen causing fever by direct action or by stimulation of interleukin 1 secretion and is implicated in the induction of cachexia, Under certain conditions it can stimulate cell proliferation and induce cell differentiation.
SUBGNIT: Homotrimer (By similarity).
SUBCELLUIAR LOCATION: Type II membrane protein. Also exists as extracellular soluble form (By similarity).
PIM: The soluble form derives from the membrane form by
                                                                                                                                                                                                                                                                                                                                                                                                                                                            P29553; Q9TTJ3;
D1-ARR-1993 (Rel. 25, Created)
01-ARR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annocation update)
Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor TNF-a) (TNF-a) (TNF-A) (TNF-A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteolytic processing (By similarity).

PTM: The membrane form, but not the soluble form, is phosphorylated on serine residues. Dephosphorylation of the membrane form ocurrs by binding to soluble TNFRSFIA/TNFRI (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Thoroughbred; TISSUE=Artery;
Ishida N., Sato F., Hasegawa T.;
Ishida N., Sato F., Hasegawa T.;
"Molecular cloning of equine tumor necrosis factor-alpha mRNA.";
Submitted (BC-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Cytokine that binds to TNFRSFIA/TNFB and
TNFRSFIB/TNFBR. It is mainly secreted by macrophages and can induce cell death of certain tumor cell lines. It is potent
                                                         1 33 BY SIMILARITY.
34 204 LYMPHOTOXIN-ALPHA.
95 N-LINKED (GLCNAC, . ) (POTENTIAL).
204 AA, 22098 MW; E2A9F0A2CEDB5425 CRC64;
                                                                                                                                                        35;
                                                                                                                          9.9%; Score 127.5; DB 1; Length 204; 24.9%; Pred. No. 0.0015; tive 29; Mismatches 78; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
SIMILARITY: Belongs to the tumor necrosis factor family.
PROSITE, PS00251; TNF 1; 1.
PROSITE, PS50049; TNF 2; 1.
Cytokine, Glycoprotein; Signal.
SIGNAL
33 BY SIMILARITY.
1204 LYMPHOTOXIN-ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                      47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 107:319-321(1991).
                                                                                                                                                                                                                                                                                                                                                    232 HEASFFGAF 240
                                                                                                                                                                                                                                                                                                                                                                              194 PSSVFFGAF 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Equus caballus (Horse)
                                                                                                                                          Best Local Similarity
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                                                                    CHAIN
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 VLLTHTISRLAVSYPSKVNLLSAIKSPCHTESPEQAEAKPWYEPIYLGGVFQLEKGDQLS 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
CLEAVAGE (BY ADAM17) (BY SIMILARITY).
PHOSPHORYLATION (BY CKI) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48; Gaps
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ligand superfamily member 2) (TNF-a) (Cachectin).
TNF OR INFSF2 OR INFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TUMOR NECROSIS FACTOR, MEMBRANE FORM TUMOR NECROSIS FACTOR, SOLUBLE FORM.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Sciuridae, Sciurinae,
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tive 35; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00251; TNF 1; 1.
PROSITE; PS0049; TNF 2; 1.
Cytokine; Transmembrane; Signal-anchor; Phosphorylation. CHAIN 1 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E79ACE91143DF373 CRC64;
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PCH -> LAN (IN REF. 2)
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15-UUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, PO1375, IA8M.
InterPro; IRRO06053; TWF abc.
InterPro; IPR006052; TWF family.
InterPro; IPR008983; TWF like.
InterPro; IPR003636; TWF Like.
Fram; PF00229; TWF; 1.
PRINTS; PR01234; TWF COSTSFCT.
PRODOM; PD002012; TWF; 1.
SWART; SM0207; TWF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                           ; AB035735; BAA88349.1; -. JQ1344; JQ1344.
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177 1
234 AA;
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035734;
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DISULFID
CONFLICT
SEQUENCE
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TRANSMEM
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                                                                                                                                                                                                                                                                 JEQUENCE FROM N.A.
TISSUE=Peripheral blood;
MEDLINE=20184748; PubWed=10721723;
Li D.H., Havell E.A., Brown C.L., Cullen J.M.;
Woodchuck lymphotoxin-alpha, -beta and tumor necrosis factor genes:
structure, characterization and biological activity.";
SEQUENCE FROM N.A.
TISSUE=Peripheral blood;
MEDLINE=98139533; PubMed=9472070;
MEDLINE=98139533; PubMed=9472070;
MEDLINE=98139533; PubMed=9472070;
"Molecular cloning of the woodchuck cytokines: INF-alpha, IFN-gamma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
DISEASE: Cachexia accompanies a variety of diseases, including cancer and infection, and is characterized by general ill health and malnutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                     Zhou H., Hu J., Seeger C.,
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR006053; TNF abc.
InterPro; IPR006052; TNF_family.
InterPro; IPR008983; TNF_like.
InterPro; IPR003636; TNF_aubf.
Pfam; PF00229; TNF; 1.
PRINTS; PR01234; TNF; 1.
PRINTS; PR01234; TNF; 1.
PROSITE; PS00207; TNF; 1.
PROSITE; PS0049; TNF; 1.
                                                                         mmunogenetics 47:332-335(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF082491; AA332615.1; --
EMBL; AF012910; AAF34863.1; --
EMBL; AF096268; AAF34867.1; --
EMBL; AF333967; AAK52718.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Y14137; CAA74569.1; -.
                                                                                             SEQUENCE FROM N.A.
TISSUE=Peripheral blood;
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                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                               II-6.";
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99 SSPNSKNEKALGRKINS------WESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQT 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 YFRRQEEIKENTKNDKQMVQYIYKY-TSYPDPILLMKSARNSCWSKDAEYGLYS----1 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: | : : : : | | | : | : | 194
140 LFKGQ-----GCPSYVLLTHTVSRFAVSYQDKVNLLSAIKSPCPKESLEGAEFKPWYEPI 194
                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
CLEAVAGE (BY ADAM17) (BY SIMILARITY).
PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
                              TUMOR NECROSIS FACTOR, MEMBRANE FORM.
TUMOR NECROSIS FACTOR, SOLUBLE FORM.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Gaps
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Nedospasov S.A., Shakhov A.N., Turetskaya R.L., Mett V.A.,
Azizov M.M., Georgiev G.P., Korobko V.G., Dobrynin V.N.,
Flippov S.A., Bystrov N.S., Boldyreva B.F., Chuvpilo S.A.,
Chumakov A.M., Shingarova L.N., Ovchinnikov Y.A.;
"Tandem arrangement of genes coding for tumor necrosis factor (TNF-alpha) and lymphotoxin (TNF-beta) in the human genome.";
Cold Spring Harb. Symp. Quant. Biol. 51:611-624(1986)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNFA HUMAN STANDARD; PRT; 233 AA.
P01375; 043647; Q9P1Q2; Q9U1V3;
21-UTU-1986 (Rel. 01, Created)
21-UTU-1986 (Rel. 01, Last squence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
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Pennica D., Nedwin G.E., Hayflick J.S., Seeburg P.H., Derynck R., Palladino M.A., Kohr W.J., Aggarwal B.B., Goeddel D.V.;
"Human tumour necrosis factor: precursor structure, expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shirai T., Yamaguchi H., Ito H., Todd C.W., Wallace R.B., "Cloning and expression in Escherichia coli of the gene for human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   69; Indels
   Transmembrane; Signal-anchor; Phosphorylation.
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MEDLINE=86016093; PubMed=2995927;
Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D.H.,
Jarrett-Nedwin J., Pennica D., Goeddel D.V., Gray P.W.;
                                                                                                                                                                                                                                                                                                                      34D3D1965DAAE0E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ligand superfamily member 2) (TNF-a) (Cachectin).
TNF OR TNFSF2 OR TNFA.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ||:|||::||:
195 YLGGVFELQKGDRLSAEVNLPSYLDFAESGQVYFG 229
                                                                                                                                                                                                                                                                                                                                                                            9.7%; Score 125; DB 1;
23.2%; Pred. No. 0.0028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                30; Mismatches
                                                                                                                                                                                                                                                                                 BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                   25764 MW;
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Nature 312:724-729(1984).
                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 23.2%
hes 36; Conservative
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Nature 313:803-806(1985)
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Cytokine;
                                                                                       DOMAIN
TRANSMEM
                                                                                                                                                                                                                                               MOD RES
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shiina S., Tamiya G., Oka A., Inoko H.; "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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and class I
                                                         [5] SEQUENCE FROM N.A.
MEDLINE=85142190; PubMed=3856324;
Wang A.M., Creasey A.A., Ladner M.B., Lin L.S., Strickler J.,
Wang A.M., Creasey A.A., Mark D.F.;
van Arsdell J.N., Yamamoto R., Mark D.F.;
"Molecular cloning of the complementary DNA for human tumor necrosis
                                                                                                                                                                                                                                                                MEDINE=86030296; PubMed=3932069;
Marmenout A., Fransen L., Tavernier J., van der Heyden J., Tizard R.,
Kawashima B., Shaw A., Johnson M.J., Semon D., Mueller R.,
Ruysschaert M.R., van Vliet A., Fiers W.;
"Molecular cloning and expression of human tumor necrosis factor and
comparison with mouse tumor necrosis factor.";
Eur. J. Blochem. 152:515-522(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Blood;
MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=93272029; PubMed=8499947;
Iris F.J.M., Bougueleret L., Prieur S., Caterina D., Primas G.,
Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-M., Dausset J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neville M.J., Milner C.M., Campbell R.D.; "A new member of the immunoglobulin superfamily and a V-ATPase G subunit are amongst the predicted products of novel genes close t
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'Human lymphotoxin and tumor necrosis factor genes: structure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shiina T., Ota M., Katsuyama Y., Hashimoto N., Inoko H., "Genome diversity in HLA: a new strategy for detection of polymorphisms in expressed genes within the HLA class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
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                   nomology and chromosomal localization.";
Nucleic Acids Res. 13:6361-6373(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   locus in the human MHC.";
                                                                                                                                                                                                         Science 228:149-154(1985).
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MEDLINE=96170872; PubMed=8597870;
Pocsik E., Duda E., Wallach D.;
"Phosphorylation of the 26 kDa TNF precursor in monocytic cells and in transfected HeLa cells.";
J. Inflamm. 45:152-160(1995).
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Moss M.L., Jin S.-L.C., Milla M.E., Burkhart W., Carter H.L.,
Moss M.L., Clay W.C., Didsbury J.R., Hassler D., Hoffman C.R.,
Kost T.A., Lambert M.H., Lesenitzer M.A., McCauley P., McGeehan G.,
Mitchell J., Moyer M., Pahel G., Rocque W., Overton L.K., Schoenen F.,
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                   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.S., Jones S.J., Marshys R.W., Green E.D., Dickson M.C., Schein J.S., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stevenson F.T., Bursten S.L., Locksley R.M., Lovett D.H.; "Myristyl acylation of the tumor necrosis factor alpha precursor on specific lysine residues.";
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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TISSUE=Prostatic carcinoma;
Shao C., Yan W., Zhu F., Yue W., Chai Y., Zhao Z., Wang (
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION BY CK1, AND DEPHOSPHORYLATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89159409; PubMed=2922050;
Jones E.Y., Stuart D.I., Walker N.P.,
"Structure of tumour necrosis factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (MEMBRANE FORM)
                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 77-233 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 385:733-736(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 LLANGVELRDNOLVVPSEGLYLIYSQVLFKGQ-----GCPSTHVLLTHTISRIAVS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 YPDPILLMKSARNSCWSK----DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDH 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).
-1- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
-1- PTM: The membrane form, but not the soluble form, is phosphorylated on serine residues. Dephosphorylation of the membrane form ocurrs by binding to soluble TNFRSFIA/TNFRI (By
                                                                                                                                                                                                                                                                                                                                                                   80 GPQR------VAAHITGTRGRSNTLSSPNSK------NEKALGRKINSWESSRSGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 SFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT----S
                                                                                                                                                                                                                                                                                                                               Gaps
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
Cervidae; Cervinae; Cervus.
                                                                                                   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDLINE=90008932; PubMed=2551905;
ECK M.J., Sprang S.R.;
"The structure of tumor necrosis factor-alpha at 2.6-A resolution. Implications for receptor binding.";
J. Biol. Chem. 264:17595-17605(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Last sequence update)
LoCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor Ingand superfamily member 2) (TNF-a) (Cachectin) (Fragment).
TNF OR TNFSF2 OR TNFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lockhart E.A.;

"Cloning and sequencing of cervine tumor necrosis factor.";

Submitted (SEP-1994) to the EMEL/GenBank/DDBJ databases.

-!- FUNCTION: Cytokine that binds to TNPRSF1A/TNFR1 and

TNPRSF1B/TNFBR. It is mainly secreted by macrophages and can induce cell death of certain tumor cell lines. It is potent

induce cell death of certain tumor cell lines. It is potent
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SUBUNIT: Homotrimer (By similarity).
                                                                                                                                                                                                                                                                                                                          42;
Jones E.Y., Stuart D.I., Walker N.P.; "The structure of tumour necrosis factor -- implications for
                                                                                                                                                                                                                                                                               Query Match 9.6%; Score 123; DB 1; Length 233; Best Local Similarity 23.0%; Pred. No. 0.0041; Matches 43; Conservative 32; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 AA.
                                        biological function.";
J. Cell Sci. Suppl. 13:11-18(1990),
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseaisebsib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 GPQREEQSPTGLSINSPLVQTLRSSSQASINKPVAHVVANINAQGQLLWLDSCANALMAN 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 KSARNSC-----WSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 GPQRVAAHITGTRGRSNTLSSPNSKNEKALGR-----KINS-----WESSRSGHSFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 NIHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK--YTSYPDPILLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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Nedospasov S.A., Shakhov A.N., Turetskaya R.L., Mett V.A.,
Nedospasov S.A., Edakhov A.N., Turetskaya R.L., Mett V.A.,
Edizov M.M., Georgiev G.P., Korobko V.G., Dobrynin V.N.,
Filippov S.A., Bystrov N.S., Boldyreva E.F., Chuvpilo S.A.,
Chumakov A.M., Shingarova L.N., Ovchinnikov Y.A.,
"Tandem arrangement of genes coding for tumor necrosis factor (TNF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
CLEAVAGE (BY ADAM17) (BY SIMILARITY).
BY SIMILARITY.
16BSF77AASA70B35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                TUMOR NECROSIS FACTOR, MEMBRANE FORM.
TUMOR NECROSIS FACTOR, SOLUBLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P01374; Q9UKS8;
2-1-UTL-1986 (Rel. 01, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-OCT-1014 precursor (LT-alpha) (TNF-beta) (Tumor necrosis factor ligand superfamily member 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 229;
SIMILARITY: Belongs to the tumor necrosis factor family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00251; TWF 1; 1.
PROSITE; PS50049; TNF 2; 1.
Cyrokine; Transmembrane; Signal-anchor.
1 1 1 1 1 1 TOMOR NECRG
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                                                                                                                                                                                                             InterPro; IPROGGOS3; TNF_abc.
InterPro; IPROGGOS2; TNF family.
InterPro; IPROGGOS3; TNF_like.
InterPro; IPROGGGG6; TNF_Bubf.
Pfam; PFOG229; TNF; TNF_gubf.
                                                                                                                                                                                                                                                                                                    PRINTS; PR01234; TNECROSISECT.
ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 AA; 24987 MW;
                                                                                                                                                                           EMBL; U14683; AAA50759.1; -.
HSSP; P01375; 4TSV.
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229
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SEQUENCE FROM N.A.
Neville M.J., Milner C.M., Campbell R.D.;
"A new member of the immunoglobulin superfamily and a V-ATPase G
"A new member of the predicted products of novel genes close to the
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Shiina S., Tamiya G., Oka A., Inoko H.;
"Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Palladino M.A., Nedwin G.E., "Cloning and expression of cDNA for human lymphotoxin, a lymphokine with tumour necrosis activity.";
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"Nuclectide sequence of a cDNA encoding human tumor necrosis factor
beta from B lymphoblastoid cell RPMI 1788.";
FEBS Lett. 302:141-144(1992).
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Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-M., Dausset J.,
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Nat. Genet. 3:137-145(1993).
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"Sequence of the human major histocompatibility complex class III
                                                                                                                                        "Structure and chromosomal localization of the human lymphotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chung M.-W., Lee K.L.,
                                                                                                                                                                                                                                                             Kobayashi Y., Miyamoto D., Agada M., Obinata M., Ogawa T.; "Cloning and expression of human lymphocoxin mRNA derived from human T cell hybridama.";
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alpha) and lymphotoxin (TNF-beta) in the human genome."; Cold Spring Harb. Symp. Quant. Biol. 51:611-624(1986).
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Sakaguchi A.Y., Goeddel D.V., Gray P.W.;
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                                                                                                                                                                              Cell. Biochem. 29:171-181(1985)
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MEDLINE=93272029; Pubmed=8499947;
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MEDLINE=87057135; PubMed=3536896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT PRO-125.

WADDIANE-91139175; PubMed=1671667;

Abraham L.J., Du D.C., Zahedi K., Dawkins R.L., Whitehead A.S.;

Abraham L.J., Du D.C., Zahedi K., Dawkins R.L., Whitehead A.S.;

"Haplotypic polymorphisms of the TNFB gene.";

Immunogeneetics 33:50-53(1991).

-!- FUNCTION: Cytokine that in its homotrimeric form binds to

TNFRSF1A/TNFR1, TNFRSF1B/TNFBR and TNFRSF14/HVEM. In its

heterotrimeric form with LTB binds to TNFRSF14/HVEM. In its

produced by lymphocytes and cytotoxic for a wide range of tumor

cells in vitro and in vivo.
                                                                                                                                                                                                                    MEDILNE=93258809; PubMed=8387891;
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Broger C., Loetscher H., Lesslauer W.;

Crystal structure of the soluble human 55 kd TNF receptor-human TNF
Deta complex: implications for TNF receptor activation.";

Cell 73:431-445(1993).
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J. Exp. Med. 173:209-219(1991).
                                                                       MEDLINE=92129275; PubMed=1733919;
Eck M.J., Ultsch M., Rinderknecht E., de Vos A.M., Sprang S.R.;
"The structure of human lymphotoxin (tumor necrosis factor-beta) at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one LTA subunits or (less prevalent) two LTA and one LTB subunits.-!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
                                                                                                                                                                                       K-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 61-205 OF COMPLEX WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the tumor necrosis factor family.
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MIM. 153440; -
GO; GO:000510; F:receptor binding; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
                                                     X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
                                                                                                                                                 J. Biol. Chem. 267:2119-2122(1992)
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91086846; PubMed=1670638;
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D12614; BAA01139.1;
MS5913; AABS9455.1;
Z15026; CAA78746.1;
Y14768; CAA75071.1;
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               FEBS Lett. 314:85-88(1992).
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GlycoSuiteDB; P01374; -.
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variation.";
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85 AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T -> N (in allele TNFB*2; dbSNP:1041981).
FYTId=VAR 007511.
T -> P (in allele 8.1).
/FYTId=VAR 007512.
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110-0CT-2003 (Rel. 42, Last sequence update)
110-0CT-2004 (Rel. 43, Last annotation update)
110-0CT-2004 (Rel. 43, Last annotation update)
110-0CT-2004 (Rel. 43, Last annotation update)
110-0CT-2004 (Rel. 43, Last annotation update)
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R GO; GO:0006917; P:induction of apoptosis; TAS.

R GO; GO:0007165; P:signal transduction; TAS.

GO; GO:0007165; P:signal transduction; TAS.

R InterPro; IPR006053; TNF abc.

R InterPro; IPR0080983; TNF_like.

R InterPro; IPR0080983; TNF_like.

R Pfan; PF00229; TNF; TNF_subf.

R PROMOST; PR01234; TNFRCROSISPCT.

R PRODON; P0002012; TNF subf; 1.

R PROSTIE; PS00249; TNF 1: 1.

R PROSTIE; PS00249; TNF 1: 1.

R Cytokine; Glycoprotein; Signal; Polymorphism; 3D-structure.
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N-LINKED (GLCNAC. .).
/FTIG=CAR_000048.
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tive 29; Mismatches
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O'Huigin C., Tichy H., Klein J.,

O'Huigin C., Tichy H., Klein J.,

O'Huigin C., Tichy H., Klein J.,

"Molecular evolution in higher primates; gene specific and organism
"Molecular evolution in higher primates; gene specific and organism
"Molecular evolution in higher primates; gene specific and organism
"The Towarton Cyckine that binds to TWRESFLATMEN and
"The TOWARTON: Cyckine that binds to TWRESFLATMEN and
"THERFIP INTER. It is mainly secreted by macrophages and can
induce cell death of certain tumor cell lines. It is potent
pyrogen causing fever by direct action or by stimulation of
interleukin secretion and is implicated in the induction of
cachexia, Under certain conditions it can stimulate cell
proliferation and induce cell differentiation (By similarity).

CH. SUBGELLULAR MOLOCATION: Type II membrane protein. Also exists as an
extracellular soluble form (By similarity).

CH. PTM: The soluble form derives from the membrane form by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-aib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Anzai T., Shilna T., Kimura N., Yanagiya K., Kohara S., Shigenari A., Yamagata T., Shilna T., Naruse T.K., Fujimori Y., Fukuzumi Y., Yamazaki M., Tashiro H., Iwamoto C., Umehara Y., Imanishi T., Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H., Meyer A., Ikeo K., Gojobori T., Bahrama S., Inoko H., Comparative sequencing of human and chimpanzee WHC class I regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLEAVAGE (BY ADAM17) (BY SIMILARITY).
PHOSPHORYLATION (BY CK1) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TUMOR NECROSIS FACTOR, MEMBRANE FORM (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TUMOR NECROSIS FACTOR, SOLUBLE FORM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteclytic processing (By similarity).

-!- PTM: The membrane form, but not the soluble form, is phosphorylated on serine residues. Dephosphorylation of the membrane form course by binding to soluble TNRRSFIA/TNRRI (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.5%; Score 122; DB 1; Length 232; Best Local Similarity 22.3%; Pred. No. 0.0049; Matches 41; Conservative 31; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal-anchor; Phosphorylation
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E4D71B19C6AE0D03 CRC64;
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                                                                                                                                                                divergence.";
Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713(2003).
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EMBL; AB100082; BAC78157.1; --
EMBL; AV091964; AAM76582.1; --
INTERPRO; IPR006053; TNF abc.
INTERPRO; IPR006053; TNF family.
INTERPRO; IPR008983; TNF like.
INTERPRO; IPR008983; TNF Subf.
PEAM; PP00229; TNF 1.
PRODOM; PD002012; TNF ubf; 1.
PRODOM; PD002012; TNF 1.
PROSTE; PS00201; TNF 1.
PROSTE; PS00201; TNF 1.
PROSTE; PS00201; TNF 1.
PROSTE; PS00201; TNF 2; 1.
CYtokine; Transmembrane; Signal-anc
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7:

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        Qy
        72 ISPLVRERGPORV----AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFL 126

        Db
        70 ISPLVRERGPORV-----AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFL 126

        Cy
        127 SNLHLBAGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT------GYPD 180

        Cy
        114 NGVELRDNGLVVPSEGLYLIYSQVLFKQQ-------GCPSTHVLLTHTISRIAVSYQT 164

        Cy
        181 PILLMKSARNSCWSK----DAEYGLYSIYQGGIFELKENDRIFVSTHNHLIDMDHEAS 235

        Db
        165 KVNLLSAIKSPCQRETPEGAEAKFWYEPIYLGGVFGLEKGDRLSAEINRPDYLDFAESGQ 224

        Qy
        236 -FFG 238

        Search completed: March 23, 2004, 09:14:18

        Scarch completed: March 23, 2004, 09:14:18
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

March 23, 2004, 09:11:14; Search time 45 Seconds Run on:

(without alignments)
1703.798 Million cell updates/sec

US-10-662-429-2_COPY_39_281 1287 Title: Perfect score:

1 INELKQMQDKYSKSGIACFL.......NEHLIDMDHEASFFGAFLVG 243

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

1017041 segs, 315518202 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 243

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SPIREMBL 25;*

sp_archea.*
sp_bacteria.*
sp_fungl:*
sp_human.*
sp_invertebrate.*
sp_mammal:*
sp_mcs.*
sp_organelle.* vertebrate:* _unclassified:* sp rodent:* sp_plant:* sp_virus:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_bacteriap:* sp_archeap:*

rvirus:*

	Description	Q9ddz5 brachydanio	O9wv90 marmota mon	OBmil9 macaca mula	O7t2q3 cyprinus ca	070332 mesocricetu	OBaw02 cyprinus ca	O80xa4 peromyscus	O91z14 sigmodon hi	Ogbee8 erinaceus e	O9erg6 peromyscus	O7tlu4 pagrus majo	OBid37 ictalums p	09ib42 paralichthy	099ndl tamiasciuru	Ogbec4 talpa europ	Q9bec9 ochotona pr
SUMMARIES	ΩI	Q9DDZ5	06VW60	Q8MJ19	Q7T2Q3	070332	QBAW02	Q80XA4	Q91ZL4	O9BEE8	Q9ERG6	Q7T1U4	Q8JG37	Q9IB42	Q99ND1	O9BEC4	бэвесэ
	DB	13	11	9	13	11	13	11	11	9	11	13	13	13	11	9	ø
	Query Match Length DB	214	169	154	227	216	231	232	156	215	217	222	230	225	215	216	216
øķo	Query	23.7	13.6	12.2	11.8	11.2	11.0	10.7	10.5	10.5	10.5	10.1	6.6	9.6	9.7	9.6	9.6
	Score	305.5	175.5	157	151.5	144.5	141	137.5	135	135	135	130.5	128	126.5	125	124	123.5
	Result No.	7	64	æ	4,	ហ	φ	7	σ	σ	10	11	12	13	14	15	16

3,

Gaps

Query Match 23.7%; Score 305.5; DB 13; Length 214; Best Local Similarity 37.6%; Pred. No. 1.1e-17; Matches 62; Conservative 37; Mismatches 59; Indels 7;

Q8n4c3 homo sapien Q9lb41 paralichthy Q8awc9 cyprinus ca Q80we7 percomyscus	യവമ		Q864y7 tupaia tana Q9beg1 bradypus tr O9be£4 cabassous u			Q80205 dipodomys m Q80204 anomalurus		Q80z02 trichys fas		Q9r136 meriones un O8izi4 homo sapien	Q80z03 castor cana	ᅼ	closti
Q8N4C3 Q9IB41 Q8AWC9 Q8OWE7	097543 Q9BEG0 Q9TTJ2	097538 Q9TTG8 Q9BEF3	Q864Y7 Q9BEG1 Q9BEF4	Q80206 Q9TTG7	Q9BEES Q9BECS	Q80Z05 Q80Z04	Q81Z15 Q81Z16	Q80Z02 O7ZZX5	Q864Z0	Q9R136 OBIZ14	Q80Z03	Q800J1	Q8XLG9
4 13 13 13 14 14 15 15 15 15 15 15 15 15 15 15 15 15 15	669	999	و و و	11 6	φφ	11	4 4	11	9		11	13	16
205 225 237 202	149 217 93	149 149 214	103 217 217	102	216 217	102	174	102	103	101	102	240	163
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122 121.5 120 119	115.5 110.5 110	109.5 109.5 108.5	108 108 107	106.5	103 99	98.5	97	93.5 92.5	92	90.5	88.5	85.5	83
11 118 20	21 22 23	2 2 2 4 4 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	2 2 2 2 2 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4	30 31	32 33	34 35	36 37	38 39	40	4T 42	43	44	45

ALIGNMENTS

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TNFSF10L.
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii; Teleostei; Ostarlophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                         214 AA; 24093 MW; 98C002474FF691AA CRC64;
                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
magnitude protein.
                  214 AA.
                PRT;
                                                                                                                                                                                                                                                Pfan, PF00229; TNF; 1.
ProDom; PD002012; TNF; 1.
SMART; SM00207; TNF; 1.
SROSTE; PS50049; TNF; 1.
SROUSNCE 214 AA; 24093 MW;
                 PRELIMINARY;
                Q9DDZ5
RESULT 1
         29DDZ
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136
                     47 QRPSAHLTLSSASDNSRPQSDMHQPQFDLHQSCRHPVHTW-ANKSFGAHLYNMTLTNGRL 105
                                                                      137 VIHEKGFYYIYSQTYFRF-QEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSK 195
                                                                                                         106 RVPQDGRÝYLÝSQVÝFRYPSPSDSDQSSVSHQLVQCIYKKTSÝLNPÍQLLKGVGTKCWAP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 QLRQLVRKMILRISEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSK 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 DKQMVQYIY-KYTSYPDPILLMK-SARNSC-----WSKDAEYGLYSIYQGGIFELKENDR 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 NQPLSHKVYVKNSKYPQDLVLMEGKMMNYCTTGQMWAR-----SSYLGAVFNFTSNDH 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 ELRESINQ---RNTEPSL----EKQIGHPSSPSDKKALRRAAHLT---GKDNSRSSP--- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 13.6%; Score 175.5; DB 11; Length 169;
1 Similarity 27.8%; Pred. No. 5.9e-07;
54; Conservative 39; Mismatches 58; Indels 43; Gaps
ORVAAHIIGIRGRSNT----LSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R GO; GO:0005576 C:extracellular; IEA.

R GO; GO:0005567 C:extracellular; IEA.

R GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.

R GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.

R GO; GO:0005155; P:apoptosis; IEA.

GO; GO:0007155; P:apignal transduction; IEA.

R InterPro; IPR006055; TIVE family.

R InterPro; IPR006052; TIVE family.

R InterPro; IPR008033; TIVE family.

R PRINTS; PR01681; FASLIGAND.

R PRODOM; PD002012; TIVE subf.

R PRODOM; PD002012; TIVE subf. 1.

R PROSITE; PS00251; TIVE 1; 1.

R PROSITE; PS00251; TIVE 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Sciuridae, Sciurinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILINE=20010026; PubMed=10540161;
Hodgson P.D., Grant M.D., Michalak T.I.;
Hodson P.D., Grant M.D., Michalak T.I.;
"Perforin and Fas/Fas ligand-mediated cytotoxicity in acute and chronic woodchuck viral hepatitis.";
Clin. Exp. Immunol. 118:63-70(1999).
EMBL; AF122368; AAD38387.1; -.
                                                                                                                                            196 DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
                                                                                                                                                                   166 DAEYALHSVYQGGLFELRAGDEVFVSVSSPTWVYGEDSSSYFGAF 210
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                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Fas ligand (Fragment).
Marmota monax (Woodchuck).
                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9995;
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                                                                                                                                                                                                                                       RESULT 2
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117 ESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY-KY 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 TSOKHTASSLEKÖLGHPSPPPEKKEÖRKVÁHLTG------KPNSRSMPL-----EW 52
                                                                                                                                                                                                                                                                                                                                                                             "Caspase-dependent and -independent cell death pathways characterize pathogenic Simian Immunodeficiency Virus infection. Relationship with disease evolution.";
                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

R GD1, ARM95636.1; --

R GO1 GO:0005576; C:extracellular; IEA.

GO2 GO:0005576; C:extracellular; IEA.

GO3 GO:0005164; F:tumor necrosis factor receptor binding; IEA.

R GO3 GO:0006915; P:apoptosis; IEA.

R GO3 GO:0006915; P:apoptosis; IEA.

R GO3 GO:0007165; P:immune response; IEA.

R GO4 GO:0007165; P:immune response; IEA.

R InterPro; IPR008064; Fas ligand.

R InterPro; IPR0080635; TNF-family.

R InterPro; IPR008083; TNF-like.

R InterPro; IPR008083; TNF-like.
                                                                                                                                                                                                                                                                                                                             Petit F., Arnoult D., Lelievre J.-D., Lecossier D., Hance A.J., Monceaux V., Ho Tsong Fang R., Hurtrel B., Ameisen J.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 TSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 SKYPQDLVMMEGKMMS-YCTTGQMWAHSSYLGAVFNLTSADHLYVNVS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 AA; 17410 MW; 971A43779E029449 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-07-2003 (TrEMBLrel. 25, Created)
01-07-2003 (TrEMBLrel. 25, Last sequence update)
01-07-2003 (TrEMBLrel. 25, Last annotation update)
Tumor necrosis factor-3 alpha.
                                                                                                                                                 01-0CT-2002 (TrEMBLrel. 22, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
12.2%; Score 157; DB 6;
Best Local Similarity 27.4%; Pred. No. 1.9e-05;
Matches 46; Conservative 33; Mismatches 65.
                                                                                                   154 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 AA.
                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, Created)
                                                                                                 PRT;
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                                                                                                                                                                                    Fas ligand CD178 (Fragment).
Macaca mulatta (Rhesus macaque).
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PROSITE; PS50049; TNF_1; 1.
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                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                               Estaquier J.;
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NON TER
SEQUENCE
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                                                                                                   QBMJ19
                                                                RESULT 3
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                                                                                    Q8MJ19
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75 LVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 ELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD-----PILLMKSA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 EIIIPNDGIYFIYSQVSFHI--SCKNDMTEDQEVMHVSHAVFHYSDFFGIYKP--LIRAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 RNSCW----SKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHL--IDMDHEASFFGAF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Spleen;
MEDLINE=98234044; PubMed=9573100;
Melby P.C., Tryon V.V., Chandraeekar B., Freeman G.L.;
"Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and analysis of cytokine mRNA expression in experimental visceral leishmaniasis.";
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                               ^ Match 11.8%; Score 151.5; DB 13; Length 227; Local Similarity 25.3%; Pred. No. 8.7e-05; Los 45; Conservative 34; Mismatches 68; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO, GO:0016020; Cimembrane; IEA.
GO; GO:0016020; Cimembrane; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0006955; F:tumor response; IEA.
INTERPRO; IPR006052; TNF_abc.
InterPro; IPR006052; TNF_IME.
InterPro; IPR008983; TNF_IME.
InterPro; IPR008088; TNF_IME.
PF00229; TNF; 1.
                                                                                                                                                                                                                                                Savan R., Sakai M.;
Savan R., Sakai M.;
"Cloning of tumor necrosis factor 3 alpha in carp.";
"Loning of tumor necrosis to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB112424; BAC77690.1; -
SEQUENCE 227 AA; 25226 MW; 010BC2B1E8D7265E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23793 MW; BADAE3F83F45B533 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor necrosis factor-alpha (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mesocricetus auratus (Golden hamster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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EMBL; AF046215; AAC40100.1; -.
HSSP; P06804; 2TNF.
Cyprinus carpio (Common carp).
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ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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216 AA;
                                                                                                                                                                                                                            TISSUE=Head kidney;
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11.2%; Score 144.5; DB 11; Length 216;

Query Match

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                                                           80 GPQRVAAH---ITGTRGRSNTL-SSPNSKNEKALGRKINS-----WESSRSGHSFLS 127
                                                                                                 49 GPQREEKFPNPIIGSMGQTLTLRSSSQNSNDKPVGHVVANHQVEEQLEWLSHRANALLAN 108
                                                                                                                                         128 NIHIRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK-----YTSYPD 180
                                                                                                                                                                               109 GMSLKDNQLVIPADGLYLVYSQVLFRGQ-----GCPSYVLLTHTVSRIAVSYED 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 GRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 -----YDPDVCKDNL-----DWKQNQDQAFVSGGLELVDREIIIPNDGIYFVYSQVSF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 RFQEEIKENTKNDKQMV-----QYIYKYTSYPDPILLMKSARNSC-WSKDAEYGLY-S 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 HI--SCKHDMTEDQDVVHMSHAVLRYSESYGSYKP---LFSAIRSACVHASDSEDLWYNT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 WRVCGVLLAVALCAAAAVCFTLNKSQNNQEGGNALRITLRDHLSKENVTSKVAIHLTGA- 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 WOLROLVRKMILRISEETISTVOEKOON-----ISPLVRERGPORVAAHITGTR
                   37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus.
NCBI_TaxID=7962;
                                                                                                                                                                                                                       181 PILLMKSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLID 229
                                                                                                                                                                                                                                               158 NVNLLSAIKSPC-PKETPEGEELKPWYEPIYLGGVFQLEKGDRLSAEVNLPKYLD 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNF polymorphism with trypanotolerance.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, AJ311801; CAC64642.2; -...
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
InterPro; IPR006053; TNF abc.
InterPro; IPR006053; TNF family.
InterPro; IPR008983; TNF like.
InterPro; IPR0080366; TNF subf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.0%; Score 141; DB 13; Length 231; 23.3%; Pred. No. 0.00068; tive 38; Mismatches 90; Indels 46
26.9%; Pred. No. 0.00032;
ive 28; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Head kidney;
Saeij J.P., Stet R.J., de Vries B., van Muiswinkel W.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      550049; TNF 2; 1.
231 AA; 25927 MW; 2AD8871D0B1A82F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 IYQGGIFELKENDRIFVSVTNEHL--IDMDHEASFFGAF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 IYLGAAFNLRARDRLRTETTKELLPRVESENGKTFFGVF 229
                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                 231 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Putative tumour necrosis factor alpha two.
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01-MAR-2003 (TrEMBLrel. 23, Last seq
                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyprinus carpio (Common carp).
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PRINTS; PR01234; TNECROSISFCT.
ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
PROSITE; PSS0049; TNF, 2; 1.
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Matches 51; Conservative
Best Local Similarity 26.9
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                       RESULT 6
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HSSP; P01375; 4TSV.
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Matches 43; Conserv
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OGT-2003 (TrEMBLrel. 25, Last annotation update)
Tumor necrosis factor alpha (Fragment).
Sigmodon hispida (Hispid cotton rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AY249143; AAP3078.15.

R GO; GO:0016020; C:membrane; IRA.

GO; GO:0016020; C:membrane; IRA.

GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.

GO; GO:0006164; F:tumor necrosis factor receptor binding; IEA.

GO; GO:0006164; F:tumor necrosis factor receptor binding; IEA.

GO; GO:0006164; F:tumor necrosis factor receptor binding; IEA.

GO; GO:0006164; F:tumor necrosis factor receptor binding; IEA.

R InterPro; IPR006053; TNF abc.

R InterPro; IPR008083; TNF lamiy.

R PRIMYS; PR00229; TNF, 1.

R PRIMYS; PR00229; TNF; 1.

R PRODOM; PR00207; TNF; 1.

R PROSITE; PS50049; TNF_1; 1.

R PROSITE; PS50049; TNF_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Green R.M., Herbst M.M., Schountz T.; "Cloning of the deer mouse tumor necrosis factor gene."; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 20 Potential.
80 >232 tumor necrosis factor.
232 232 AA, 25704 MW, E48A9379DB4F216D CRC64;
                                                                                                                                                         01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Tumor necrosis factor precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                           Peromyscus maniculatus (Deer mouse).
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                                                                                    PRELIMINARY;
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Best Local Similarity
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SEQUENCE
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291ZL4
1D 291Z
AC 291Z
DT 01-D
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65 VQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHS 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 LLMKSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 LANGMDLRNNOLVIPADGLYLVYSQVLF-----KGLGRSNCELLTHTVSRIAVSYEDKV 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LRSSSQNLS------DKPVAHVVA------NQQAEEQL-----EWLSQRANAL 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brinaceus europaeus (Western European hedgehog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceus.
NCBI_TaxID=9365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              van Dijk M.A.M., de Jong W.W.;
"Indels indicate that rodents are monophyletic and lagomorphs are
"Indels indicate that rodents are monophyletic and lagomorphs are
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ286830; CAC28522.1; --
                                                                                                                                                 R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0016164; F:tumor necrosis factor receptor binding; IEA.

R GO; GO:0006955; P:immune response; IEA.

R InterPro; IPR006053; TNF abc.

R InterPro; IPR006053; TNF abc.

R InterPro; IPR006053; TNF abc.

R InterPro; IPR008983; TNF like.

R PEAM: PF00229; TNF; I.

R PRINTS; PR01214; TNECROSISFCT.

R PRODON; PR00203; TNF | 1.

R PROSITE; PS00251; TNF | 1.

R PROSITE; PS00251; TNF | 1.

R PROSITE; PS0049; TNF | 2; 1.
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GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:00005164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0000695; P:tumor response; IEA.
InterPro; IPR006052; TNF_family.
InterPro; IPR008983; TNF_like.
InterPro; IPR008983; TNF_like.
FinterPro; IPR00856; TNF_subf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.5%; Score 135; DB 11; Length 156; 23.5%; Pred. No. 0.0013;
Blanco J.C., Pletneva L.M., Prince G.A.; "Sigmodon hispidus cytokines, chemokines and interferons."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF421388; AAL18818.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43; Conservative 33; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON TER 1 Ī SEQUENCE 156 AA, 17303 MW, DC565F3BC3C826E4 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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106 ALLANGMDLKDNQLVIPADGLYLVYSQVLFKGQ-----GCSNYVLLTHTVSRFAVSYEDK 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 WESSRSGHSFL-SNLHLRNGELVIHEKGFYYIYSQTYFRFQ----EEIKENTKNDKQMVQ 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 WKSGQ-GQAFAQGGFRLVDNKIVIPQTGLYFVYSQASFRVSCSDGEEEGAGGHHTPLSHR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 OTEALTKTDTAEKTDPHSTLRRISSKAKAAIHLEGSYDEDE-----GSKDQV-----G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 YIYKYTSYPDPILLMKSARNSC--WSKDAEY----GLY-SIYQGGIFELKENDRIFVSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pagrus major (Red sea bream) (Chrysophrys major).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Perciformes, Percoidei,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cai Z., Song L., Gao C., Qiu L., Xiang J.;
"Cloning and expression of TNFa from Red Seabream (Pagrus major).";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY314010; AAP76392.1; -.
SEQUENCE 222 AA; 24382 MW; 8D8496F855AAF552 CRC64;
                                                                                                                                       182 ILLMKSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLID 229
                                                                                                                                                                             Ictalurus punctatus (Channel catfish).
Bukaryota, Metazoa, Chordata, Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Zou J., Chinchar G., Long S., Miller N., Secombes C.J.;

Zou J., Chinchar G., Long S., Miller N., Secombes C.J.;

"Cloning and expression of a tumor necrosis factor homologue in catfish, Ictalurus punctatus.";

Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ417565; CAD10389.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 10.1%; Score 130.5; DB 13; Length 222; Local Similarity 24.4%; Pred. No. 0.0049; les 48; Conservative 33; Mismatches 91; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                       222 AA.
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                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 NEHLIDMDHEASFFGAF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 QLSELETEEGKTFFGVF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor necrosis factor a.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=143350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pagrus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sparidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      07T1U4;
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                                                                                                                                                                                                                                                                                                                                                                                                                             80 GPQR--VAAHITGTRGRSNTLSSPNSKNEKALGRKINS-----WESSRSGHSFLSNL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 HLRNGELVIHEKGFYYIYSQTYFRFQEEIKEN---TKNDKOMVQYIYKYTSYPDFILLMK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 KLIDNQLVVPLDGLYLIYSQVLFKGQGCPSTHVFLITHNIKRYA------VSYQKDVNLLS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISPLVRERGPORVAAHITGTRGRSNTL-SSPNSKNEKALGRKINS------WESSRSG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 IGPQREEKFPNNLP--IGSMAQTLTLRSSSQNSSDKPVAHVVANHQVDEQLEWLSRRAN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 GPQRDEFPDNIQLNNALAQTLRSSRTQSDKPVAHVVASIKSEGQLLWESEVANALLANGM 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herbet M.M., Schountz T.;
"Cloning of the deer mouse interferon gamma, interleukin-10 and tumor necrosis factor genes.";
Submitted (SRP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF307013; AGG30264.1; -.
                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-00T-2003 (TrEMBLrel. 25, Last annotation update)
Tumor necrosis factor alpha (Fragment).
Peromyscus maniculatus (Deer mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 SARNSCWSK-----DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMD 231
                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moser of coords and control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of co
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                                                                                                                                                                                                                                                                                                DB 6; Length 215;
                                                                                                                                                                                                                                                                                         Query Match 10.5%; Score 135; DB 6; Length 219
Best Local Similarity 25.3%; Pred. No. 0.002;
Matches 43; Conservative 31; Mismatches 72; Indels
                                                                                                                                                                                                                                   3E337E7E65F074EA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 AA.
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                           ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF 1; 1.
PROSITE; PS50049; TNF 2; 1.
                                                                                                                                                                                                                            23696 MW;
PRINTS; PR01234; INECROSISFCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 16,
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                                                                                                                                                                                                                               215 AA;
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01-MAR-2001
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Q9ERG6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----LMKSARNSCWSKDAEYGLY---SIYQGGIFELKENDRIFVSVTNEHLIDMDHEA-- 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
9.9%; Score 128; DB 13; Length 230;
Best Local Similarity 29.1%; Pred. No. 0.0082;
Matches 37; Conservative 25; Mismatches 53; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDILINE=26491932; PubMed=11035080;
Hirono I., Nam B., Kurobe T., Aoki T.,
Molecular Clonins, Kurobe T., Aoki T.,
Molecular Clonins, Characterization, and Expression of TNF cDNA and
Gene from Japanese Flounder Paralychthys olivaceus.";
J. Immunol. 165:4423-4427(2000).
EMBL; AB040448; BAA94969.1; --
HSSP; P01375; 4TSV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinopterygii, Neopterygii, Teleostei, Miteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Pleuronectiformes; Pleuronectoidei, Paralichthyidae, Paralichthys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 9.8%; Score 126.5; DB 13; Length 225; l Similarity 22.0%; Pred. No. 0.011; 42; Conservative 40; Mismatches 78; Indels 31;
                     GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA. GO; GO:006955; P:immune response; IEA. InterPro; IPR006053; TNF _amily. InterPro; IPR008053; TNF _family. InterPro; IPR008083; TNF _like. InterPro; IPR008083; TNF _like. Pro; IPR0080893; TNF _like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0016020; C:membrane; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR006053; TNF abc.
InterPro; IPR006052; TNF Tamily.
InterPro; IPR008983; TNF Tamily.
InterPro; IPR008983; TNF Tamily.
                                                                                                                                                                                                                                                                               IF 2; 1.
25598 MW; 3A40D391F75DB019 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
Tumor necrosis factor.
Paralichthys olivaceus (Flounder).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
GO; GO:0016020; C:membrane; IEA. GO; GO:0005164; F:tumor necrosis GO; GO:0006955; P:immune response
                                                                                                                                                                                               PRINTS; PRO1234; TARECROSISFCT.
ProDom; PD002012; TNF subf; 1.
SMART; SM0207; TNF; 1.
PROSITE; PSS0049; TNF 2; 1.
SEQUENCE 230 AA; 25598 MW;
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ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS50049; TNF 2; 1.
SEQUENCE 225 AA; 24965 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Best Local Similarity
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091B42
AC 091B44
AC 091B4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 ESLGTQVSLMSAVRSACQKSQEDAYRDGQGWYNAIYLGAVFQLNEGDKLWTETNMLSELE 212
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47 EXTEPHNTLRQISSRAKAAIHLEG-RDEEDESTSENKL/VWKNDEGLA-----FTQGGF 98
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Submitted (FBE-2000) to the EMBL/GenBank/DDBJ databases.

R MEL, AJ266804; 2TNF.

R HSSP, P06804; 2TNF.

R GO; GO:0016162; Fitumor necrosis factor receptor binding; IEA.

GO; GO:001655; Fitumor necrosis factor receptor binding; IEA.

GO; GO:0005165; Fitumor necrosis factor receptor binding; IEA.

R InterPro; IPR006053; TNF abc;

R InterPro; IPR008093; TNF like.

R InterPro; IPR008993; TNF like.

R RINTS; PR01234; TNF: 1.

R PRINTS; PR01234; TNF: 1.

R PRODITS; PR01234; TNF: 1.

R PRODITS; PS00251; TNF: 1.

R PROSITE; PS0049; TNF: 1.

T NON TER 215

C SEQÜENCE 215 AA; 23739 MW; 36441309CA5E9898 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tamiasciurus hudsonicus (American red squirrel).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria, Rodentia; Sciurognathi, Sciuridae, Sciurinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Tumor necrosis factor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 AA.
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RESULT 15

67 EKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNS---KNEKALGRKINSWESSRSGH 123

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125 FLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY----TSYPD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 QEKQONISPLVRERGPO-RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHS 124
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1 Similarity 21.8%; Pred. No. 0.016;
38; Conservative 37; Mismatches 75; Indels 24; Gaps
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SEQUENCE FROM N.A.
Van Dijk M.A.M., de Jong W.W.;
Indels indicate that rodents are monophyletic and lagomorphs are their sister group.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ286831; CAC28539.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R GO; GO:0016620; C:membrane; IEA.
R GO; GO:0016620; C:membrane; IEA.
R GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
R GO; GO:0005164; F:tumor response; IEA.
R InterPro; IPR006053; TNF_family.
R InterPro; IPR006053; TNF_family.
R InterPro; IPR008381; TNF_family.
R Pfam; PF00229; TNF; 1.
R PR01234; TNECROSISFCT.
R Probom; PD002012; TNF subf; 1.
R PROSITE; PS002012; TNF subf; 1.
R PROSITE; PS002051; TNF 1; 1.
R PROSITE; PS0021; TNF 1; 1.
R PROSITE; PS0049; TNF 1; 1.
R PROSITE; PS0049; TNF 2; 1.
                                                                                                                                                                                                                                                                       Talpa europaea (European mole).
Bukaryota: Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Insectivora; Talpidae; Talpa.
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SEQUENCE 216 AA; 23542 MW; FFFEFE8DBBD27836 CRC64;
                                                                 01-UUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Tumor necrosis factor (Fragment).
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PRELIMINARY;
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INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 281 amino acide TYPE: amino acid TYPE: amino acid MOLECULE TYPE: protein US-08-670-354-2
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1: /cgn2_6/ptcdata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/2/iaa/pcarus_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-384-031-1
US-08-383-086-1
US-09-320-424-2
US-09-157-864-12
US-09-157-864-12
US-09-157-864-12
US-09-157-864-12
US-09-167-825-63-2
US-09-072-993C-3
US-09-825-563-11
US-09-825-563-11
US-09-825-563-11
US-09-825-563-13
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Steven R. Wiley and
APPLICANT: Steven R. Wiley and
APPLICANT: Raymond G. Goodwin.
TITLE OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                             US-09-577-780-11
US-09-46-480-11
US-09-477-800-11
US-09-871-856-11
US-09-871-291-11
US-09-871-650-11
US-08-842-842-7
US-08-989-362-2
US-09-671-658A-2
US-09-671-658A-2
                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWAREN Microsoft Word, Version 6.0.1
SOFTWAREN TAPPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-JUN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
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US-09-215-649A-13
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                                                                                                                                           US-09-396-937-6
                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REGISTRATION NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFRAK: (206) 233-0644
                                                                                                                                                                                                                                                         ; Sequence 2, Application US/08670354; Patent No. 5763223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
USA
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ZIP: 98101
                                                                                                                                                                                                                                    RESULT 1
US-08-670-354-2
 STATE:
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DB 1; Length 281;

100.0%; Score 1478;

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61 DDSYWDPNDEESWASPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                              1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
                          Indels
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  11 Similarity 100.0%; Pred. No. 2.7e-149; 281; Conservative 0; Mismatches 0;
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Patent No. 6030945
GENERAL INFORMATION:
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22US03
CURRENT APPLICATION WUMBER: US/08/584,031A
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 281; Conserv
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LENGTH: 281
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61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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Patent No. 6171787
GENERAL INFORMATION:
APPLICANT: WILEY, STEVEN
TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Abbott Laboratories
STREET: 100 Abbott Park Road
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100.0%; Pred. No. 2.7e-149;
ative 0; Mismatches 0;
                                                                                                                                                                                                                          MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CUREBNT APPLICATION DATA: APPLICATION NUMBER: US/08/780,496
FILING DATE: 08-Jan-1997
                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
Apo-2 Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Marechang, Diane L.
REGISTRATION NUMBER: 35,600
REFRENCE/DOCKET NUMBER: P097
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/925-5416
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 08-Jan-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 100.
Matches 281, Conservative
                                                                                                                                                                                 ZIP: 94080
COMPUTER READABLE FORM:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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COUNTRY:

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EARLIER FILING DATE: 1995-11-01
BARLIER APPLICATION NUBER: 08/496,632
EARLIER FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
LENGTH: 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DEEN, KEITH C.
APPLICANT: YOUNG, PETER R.
APPLICANT: MARSHALL, LISA A.
                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 281; Conservative
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Best Local Similarity 100.0
Matches 281; Conservative
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                                                                                                                                          TYPE: PRT
ORGANISM: human
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100.0%; Pred. No. 2.7e-149;
.ive 0; Mismatches 0; Indels 0
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| Sequence 2, Application US/09320424
| Patent No. 6284236|
| Patent No. 6284236|
| GENERAL INFORMATION:
| APPLICANT: Wiley, Steven R.
| APPLICANT: Goodwin, Raymond G.
| TITLE OF INVENTION: Cytokine that Induces Apoptosis FILE REFERENCE: 2835-E
| CURRENT APPLICATION NUMBER: US/09/320,424
| CURRENT APPLICATION NUMBER: 09/190,046
| EARLIER FILING DATE: 1998-11-10
| EARLIER FILING DATE: 1998-03-26
| EARLIER FILING DATE: 1996-03-26
| EARLIER FILING DATE: 1996-06-25
| EARLIER FILING DATE: 1996-06-25
| EARLIER FILING DATE: 1996-06-25
| EARLIER APPLICATION NUMBER: 08/670,354
                                                                                                                                                                                                                                                                                                                        6134.US.01
                                                                       OPERATING SYSTEM: DOS
SOPTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,086
                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 61
TELECOMMUNICATION:
TELEPHONE: 847-937-0378
                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: No. 6171787e
                                   E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 281 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 281; Conservative
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                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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Best Local Similarity
                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                         121 RVAAHIIGIRGESNILSSPNSKNEKALGRKINSWESSRSGHSFLSNLHIRNGELVIHEKG 180
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                                                                                                                                                                 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
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                                                                                                                             1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                     0; Gaps
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APPLICANT: TAN KONG B.
APPLICANT: TAN KONG B.
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR, TITLE OF INVENTION: TR6
FILE REPERENCE: GH-50008-2
CURRENT FALLING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR APPLICATION NUMBER: 08/853,684
PRIOR APPLICATION NUMBER: 08/853,684
PRIOR PILING DATE: 1997-05-09
PRIOR PILING DATE: 1997-05-09
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
TENNOTH: 201
100.0%; Score 1478; DB 3; Length 281; 100.0%; Pred. No. 2.7e-149; ive 0; Mismatches 0; Indels 0
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100.0%; Pred. No. 2.7e-149;
ive 0; Mismatches 0;
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181 FYYIYSQTYPRFQEEIKENTKNDKQNVQYIYKYTSYPDPILLMKSARNSCWSKDABYGLY 240
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                                      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                   181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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   121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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GENERAL INFORMATION:
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: CYTOKine that Induces Apoptosis
FILE REPRENCE: 2835-E
CURRENT PELING. 2001-04-02
FILE REPRENCE: 2001-04-02
CURRENT FILING DATE: 2001-04-02
PRIOR FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: 09/120,046
PRIOR APPLICATION NUMBER: 09/120,046
PRIOR APPLICATION NUMBER: 09/046,641
PRIOR APPLICATION NUMBER: 09/046,641
PRIOR APPLICATION NUMBER: 08/10,354
PRIOR FILING DATE: 1996-06-25
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100.0%; Pred. No. 2.7e-149;
iive 0; Mismatches 0;
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US-10-039-785-66
; Sequence 66, Application US/10039785
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Patent No. 6521228
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Best Local Similarity 100.8
Matches 281; Conservative
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ORGANISM: human
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DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
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; Patent No. 6440694
; GENERAL INFORMATION:
    APPLICANT: Mills, Cynthia J
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MEDIUM TYPE: 3.5 Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/157,864
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ATTORNEY/ACENT INFORMATION:
NAME: KETECT, LOT'L.
REGISTRATION NUMBER: 41,113
REFERENCE/DOCKET NUMBER: 6111.
TELEPHONE: 616/833-0974
TELEPHONE: 616/833-8997
TELEFAX: 616/833-8997
TELEFAX: 224401
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
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Best Local Similarity 100./
Matches 281, Conservative
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STRANDEDNESS: si
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CITY: Kalamazoo
STATE: MI
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61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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GAPELICANT: Salcedo et al.

APPLICANT: Salcedo et al.

TITLE OF INVENTION: Receptors
FILE PERSONE: PF550
CURRENT PILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-04-06
PRIOR FILING DATE: 2002-12-20
PRIOR FILING DATE: 2001-12-20
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-07
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GENERAL INFORMATION:
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
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FWGTH: 281
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PCT-US96-10895-2
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GENERAL INFORMATION:
APPLICANT: Michael R. Brigham-Burke
APPLICANT: Peter R. Young
APPLICANT: Peter R. Young
IITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
TITLE OF INVENTION: ANTAGONIST FOR TUMOR NECROSIS RELATED RECEPTORS TRI AND TR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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            MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
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CURRENT APPLICATION NUMBER: US/09/072,993C
CURRENT FILING DATE: 1998-05-06
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 60/055,513
PRIOR APPLICATION NUMBER: 60/056,980
                                                                                                                                                                                                                                                                                                 PRICR APPLICATION:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECHONIS. (206) 587-0430
TELEPHONE: (206) 233-0644
                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
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INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
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amino acid
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Matches 281; Conservative
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COMPUTER READABLE FORM:
                                                                                                                                                              FILING DATE: 2 CLASSIFICATION:
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US-09-072-993C-3
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128 SSRSGHSFLSNLHIRNGELVIHEKGFYXIXSQTYFRFQEEIKENTKNDKQMVQXIXKYTS 187
            SEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 155
                                                    68 SEETISTVÕEKOONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 127
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                                                                                                      156 SSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTS
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APPLICANT: Wiley, Steven R.
APPLICANT: Wiley, Steven R.
APPLICANT: Goodwin, Raymond G.
TITLE OF INFORMATION: Cytchine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/825,563
CURRENT FILING DATE: 2001-04-02
PRIOR PILING DATE: 1999-05-26
PRIOR PILING DATE: 1999-06-26
PRIOR APPLICATION NUMBER: 09/10,046
PRIOR APPLICATION NUMBER: 09/10,046
PRIOR APPLICATION NUMBER: 09/10,046
PRIOR APPLICATION NUMBER: 09/640,354
PRIOR FILING DATE: 1996-06-25
PRIOR FILING DATE: 1996-06-25
PRIOR FILING DATE: 1996-06-25
PRIOR FILING DATE: 1996-06-25
PRIOR PRILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PACENTIN VUMBER: 08/496,632
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PACENTIN VUMBER: 253
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Best Local Similarity 78.99
Matches 194; Conservative
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US-09-825-563-11
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TITLE OF INVENTION: CYtokine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION: CYtokine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT APPLICATION NUMBER: 09/190,046
EARLIER APPLICATION NUMBER: 09/048,641
EARLIER PILING DATE: 1998-03-26
EARLIER PELING DATE: 1998-03-26
EARLIER PELING DATE: 1996-06-25
EARLIER PELING DATE: 1996-06-25
EARLIER PELING DATE: 1995-11-01
EARLIER PELING DATE: 1995-06-25
EARLIER PELING DATE: 1995-06-25
EARLIER PELING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOSTWARE: PRICENTIN NUMBER: 08/496,632
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PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/057,550
PRIOR FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 279
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Matches 279; Conservative
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; ORGANISM: synthetic fusion
US-09-320-424-11
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                                                                                                                                                                    TYPE: PRT
ORGANISM: HOMO SAPIENS
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US-09-320-424-11
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Best Local S
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Search completed: March 23, 2004, 09:07:54 Job time : 24 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 66.8%; Score 988; DB 3; Length 256;
Best Local Similarity 78.9%; Pred. No. 4.4e-97;
Matches 194; Conservative 15; Mismatches 13; Indels 24; Gaps
                                                                                                    GENERAL INFORMATION:
APPLICANT: Woodwin, Steven R.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT FILING DATE: 1999-05-26
EARLIER APPLICATION NUMBER: 09/190,046
EARLIER APPLICATION NUMBER: 09/190,046
EARLIER APPLICATION NUMBER: 09/048,641
EARLIER APPLICATION NUMBER: 08/640
EARLIER PILING DATE: 1998-03-26
EARLIER PILING DATE: 1996-06-25
EARLIER FILING DATE: 1995-10-01
EARLIER FILING DATE: 1995-10-01
EARLIER FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 13
LENGTH: 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/0982563
Fatent No. 652128
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
MILEY, Steven R.
TILE OF INVENTION: CYTCKINE that Induces Apoptosis
FILE REPERENCE: 2835-E
CURRENT APPLICATION UNMBER: US/09/825,563
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 09/120,424
PRIOR APPLICATION NUMBER: 09/190,046
PRIOR PLING DATE: 1999-10-10
PRIOR PLING DATE: 1999-01-26
PRIOR PLING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 09/190,046
PRIOR PLING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 09/190,046
PRIOR PLING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 09/190,046
PRIOR APPLICATION NUMBER: 09/190,046
PRIOR PLING DATE: 1998-03-26
PRIOR FILING DATE: 1996-03-26
                                          ; Sequence 13, Application US/09320424; Patent No. 6284236; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-320-424-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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US-09-320-424-13
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                                                                                                                                                                                                                                                                                                                       Query Match 66.8%; Score 988; DB 4; Length 256;
Best Local Similarity 78.9%; Pred. No. 4.4e-97;
Matches 194; Conservative 15; Mismatches 13; Indels 24; Gaps
PRIOR APPLICATION NUMBER: 08/548,368
PRIOR FILING DATE: 1995-11-01
PRIOR APPLICATION NUMBER: 08/496,632
PRIOR FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 256
                                                                                                                                                                                                                TYPE: PRT; ORGANISM: synthetic fusion US-09-825-563-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 GAFLVG 281
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March 23, 2004, 09:06:53; Search time 46 Seconds (without alignments) 1581.879 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAMMEVQGGPSLGQTCVLIV......NEHLIDMDHEASFFGAFLVG 281
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_pep:*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1049977 segs, 258955339 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                      OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
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	Description		3B-6 Sequence 6, Appli	Segmence 8.	Sequence 17,	Sequence 8,	-	Sequence 11		Sequence 2,	Sequence 2,	Sequence 2, 1	Seguence 66,	Sequence 4, 7	Sequence 54,	Seguence 54.	
	ΙD	2	US-08-916-625B-6	US-08-971-317	US-09-813-329-17	US-09-193-663	US-09-934-465-1	US-09-919-039-118	US-10-202-06	US-10-662-429-2	US-10-662-430-2	US-10-662-431-2	US-10-039-78	US-10-011-125-4	US-10-001-05	US-10-093-766-54	** *** ***
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	Query Match Length DB		281	281	281	281	281	281	281	281	281	281	281	281	281	281	6
de	Query Match		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	0
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Sequence 41, Appl Sequence 20, Appl Sequence 72, Appl Sequence 14, Appl Sequence 1, Appl Sequence 1, Appl Sequence 13, Appl Sequence 13, Appl Sequence 14, Appl Sequence 2, Appl Sequence 2, Appl Sequence 14, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 20, Appli Sequence 20, Appli	11
14 US-10-151-882-14 US-10-218-547-14 US-10-218-547-14 US-10-218-547-15 US-10-310-793-15 US-10-313-718-547-19 US-10-319-2238-12 US-10-319-2238-12 US-10-319-2238-12 US-10-319-2238-12 US-10-319-2238-12 US-10-319-2238-12 US-10-319-2238-12 US-10-319-2238-12 US-10-319-2238-12 US-10-319-2238-12 US-10-319-2238-12 US-10-319-2238-12 US-10-318-083-12 US-10-318-083-12 US-10-318-083-12 US-10-318-083-12 US-10-318-083-12 US-10-318-083-12 US-10-318-083-12 US-10-318-083-12 US-10-318-083-12 US-10-318-083-12 US-10-318-083-12 US-10-318-083-12 US-10-318-083-12 US-10-318-083-12 US-10-318-083-12 US-10-318-083-12 US-10-318-038-12 US-10-318-12 US-10-3	-60-SD 6
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ALIGNMENTS

US-08-916-625B-6

Jequence 6, Application US/08916625B

Publication No. US20010010924A1

GENERAL INFORMATION:

APPLICANT: DEEN, KEITH C.

APPLICANT: VOUNG, PETER R.

TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED

TITLE OF INVENTION: RECEPTOR, TR6

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: RAINER & PRESTIA

STREET:

P.O. BOX 980

CITY: VALLEY FORGE
STREET:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OFFUTATION NUMBER: US/08/916,625B

FILING DATE: 22-AUG-1997

ATTORNEY AGENT INFORMATION:

NAME: PRESTIA, PAUL F

REFERENCE/DOCKET NUMBER: GH-50008-1

TELEPHONE APPLICATION NUMBER: GH-50008-1

TELEPHONE: 610-407-0700

Page

us-10-662-429-2.rapb

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                                                                                                                                                                                                                                                                                                                                      61 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                      100.0%; Score 1478; DB 8; Length 281; 100.0%; Pred. No. 1.8e-133;
                                                                                                                                                                                                                          0; Indels
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Publication No. US20010010925A1

GENERAL INPORMATION:

APPLICANT: Willey, Steven R.

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES:

CORRESPONDENCE Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park Road

CITY: Abbott Park Road

STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,317A
FILING DATE: 17-NOV-1997
                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 6255.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 935-7550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39,046
TELEX: 846169
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
STPEANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (847) 938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          Matches 281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Goller, Mimi C
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 17-NOV-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                         MOLECULE TYPE: protein
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ZIP: 60064-3500
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US-08-916-625B-6
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US-08-971-317A-8
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Sequence 17, Application US/09813329
Patent No. US20020012968A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20020012966A1e1 Drosophila Tumor Necrosis Factor Class Mol
TITLE OF INVENTION: Variants Thereof
FILE OF INVENTION: Waiants Thereof
FILE REPERENCE: D0016.mp
CURRENT PILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                                                                      100.0%; Score 1478; DB 8;
100.0%; Pred. No. 1.8e-133;
tive 0; Mismatches 0;
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100.0%; Pred. No. 1.8e-133;
tive 0; Mismatches 0;
                                                                                     TOPOLOGY: linear MoLECULE TYPE: No. US20010010925A1e
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SOFTWARE: Patentin version 3.0
SEQ ID NO 17
LENCTH: 281
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.(
Matches 281; Conservative
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Best Local Similarity
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US-10-202-062-20
: Sequence 20, Application US/10202062
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Best Local Similarity 100.0°
Matches 281; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                        Sequence 8, Application US/09193663
; Patent No. US20020055624A1
; GENERAL INFORMATION:
    TITLE OF INVENTION: TNP-DELTA LIGAND AND USES THEREOF
; FILE REFERENCE: 6255.US.02
; CURRENT APPLICATION WUMBER: US/09/193,663
; CURRENT FILING DATE: 1998-11-17
; EARLIER FILING DATE: 1997-11-17
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ. ID NOS: 10
; SOFTWARE: FaetSEQ for Windows Version 3.0
                 241 SIYQGGIFELKENDRIFVSVTWEHLIDMDHEASFFGAFLVG 281
 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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Patent No. US20020102233A1
GENERAL INPORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REPERENCE: 1166-2.2US03
CURRENT APPLICATION NUMBER: US/09/934,465
CURRENT APPLICATION NUMBER: 08/584,031
PRIOR APPLICATION NUMBER: 08/584,031
PRIOR APPLICATION NUMBER: 08/584,031
PRIOR FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver: 2.0
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Matches 281; Conservative
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US-09-193-663-8
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US-09-934-465-1
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LENGTH: 281
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APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR PAPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
SOFTWARE: PERL PROGRAM
SOCTION 0118
LENGTH: 281
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                                              1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVVYFTNELKQMQDKYSKSGIACFLKE
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US-09-919-039-118
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100.0%; Pred. No. 1.8e-133;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 118, Application US/09919039; Publication No. US20030108871A1; GENERAL INFORMATION;
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CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/10/662,430
FILING DATE: 16-Sep-2003
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PF261
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kimball, Paul, C. REGISTRATION NUMBER: 34,610
                   TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10662430 Publication No. US20040048340A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELEFAX: (301) 309-8512
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COUNTRY: US
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             GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT; Human Genome Sciences, Inc.,

TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members

FILE REFERENCE: PF59

CURRENT APPLICATION NUMBER: 2010-07-25

PRIOR APPLICATION NUMBER: 60/307, 838

PRIOR FILING DATE: 2001-07-27

NUMBER OF SEQ ID NOS: 42

SOFTWARE: Patentin version 3.0
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; Publication No. US20040038347A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Apoptosis Inducing Molecule I
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1478; DB 12; 100.0%; Pred. No. 1.8e-133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/662,429
FILING DATE: 16-Sep-2003
CLASSIFICATION: 530
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APPLICATION NUMBER: US/08/816,981
FILING DATE: 13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PF261
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REGISTRATION NUMBER: 34,610
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US20040038349A1
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                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: human
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                                                                   .;
Query Match

Query Match

Best Local Similarity 100.0%; Pred. No. 1.8e-133;

Matches 281; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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APPLICANT: Ruben, Steven M
TITLE OF INFORMINEAPOPHOSIS Inducing Molecule I
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/816,981
FILING DATE: 13-MAR-1997
ATTORNEY/AGENT INPORMATION:
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US-10-662-431-2

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Gaps ó

Length 281;

Sequence 2, Application US/10662431

Publication No. US20040047864A1

GENERAL INFORMATION:

APPLICANT Ruben, Steven M

TITLE OF INVENTION: Apoptosis Inducing Molecule I

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: MD MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/662,431
FILING DATE: 16-Sep-2003
CLASSIFICATION: 530 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/816,981
FILING DATE: 13-MAR-1997
ATTORNEY/AGENT INFORMATION: NAME: Kimball, Paul, C. REGISTRATION NUMBER: 34,610 REFERENCE/DOCKET NUMBER: PF261 TELEPHONE: (301) 309-8504 TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 2: TELECOMMUNICATION INFORMATION: COUNTRY: US ZIP: 20850 COMPUTER READABLE FORM: RESULT 10 US-10-662-431-2

61 DDSYWDPNDEESMNSPCWQVXWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120 61 DDSYMDFNDEESMNSPCWQVKWQLKQLVRKMILKTSEETISTVQEKQQNISPLVRERGPQ 120 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180 181 FYXIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDABYGLY 240 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60 Sequence 66, Application US/10039785
Publication No. US20020067646A1
GENERAL INFORMATION:
APPLICANT: Salcede et al.
TITLE OF INVENTION: Receptors
FILE OF INVENTION: Receptors
FILE OF INVENTION: Receptors
FILE OF INVENTION: Receptors
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FILE OF INVENTION: Receptors
FILE OF INVENTION: RECEPTOR
FILE OF INVENTION: DATE: 2002-04-05
FRIOR PELING DATE: 2001-12-07
FRIOR FILING DATE: 2001-11-14
FRIOR FILING DATE: 2001-11-04
FRIOR FILING DATE: 2001-11-07
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FRIOR FILING DATE: 2001-06-05 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 181 FYYIYSQTYFRFQEEIKENTKNDKOMVOYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE Gaps ö DB 12; Length 281; Query Match
100.0%; Score 1478; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; 0; Indels 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281 Query Match 100.0%; Score 1478; DB 12; Best Local Similarity 100.0%; Pred. No. 1.8e-133; Matches 281; Conservative 0; Mismatches 0; NUMBER OF SEQ ID NOS: 66 SOFTWARE: Patentin Ver. 2 TYPE: PRT ORGANISM: Homo sapiens US-10-039-785-66 US-10-039-785-66 윤 ਨੇ ద ö d 임 a à à à ò 9 9

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TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:

SEQUENCE CHARACTERISTICS: LENGTH: 281 amino acids TYPE: amino acid

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APPLICANT: Wood, William
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
TITLE OF INVENTION: CELL GROWTH
FILE REFERENCE: P3034R1PCT
CURRENT APPLICATION NUMBER: US/10/001,054
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                      PRIOR PELING DATE: 1998-03-27
PRIOR PELING DATE: 1998-03-27
PRIOR PELING DATE: 1998-03-27
PRIOR PELING DATE: 1998-03-27
PRIOR PELING DATE: 1998-03-29
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PRIOR PELING DATE: 1998-04-24
PRIOR PELING DATE: 1998-04-29
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                                  Watanabe, Colin
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DDSYMDPNDEESMNSPCWQVKWQLKQLVRKMILRTSEETISTVQEKQQNISPLVREKGPQ 120
                                                                                 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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                                                                                                                                                                                                                                                                                                                                                       241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4.7

Sequence 4.7

Publication No. US200201423881

GENERAL INFORMATION:

APPLICANT: Chen, Christina Yu-Ching

TITLE OF INVENTION: BACTERIAL HOST STRAINS

FILE REPERENCE: PIGGARI

CURRENT APPLICATION NUMBER: US/10/011,125

CURRENT FILING DATE: 2001-12-07

PRIOR PAPLICATION NUMBER: US 60/256,162

PRIOR FILING DATE: 2000-12-14

NUMBER: OF SEQ ID NOS: 10
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APPLICANT: Baker, Kevin
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Hebert, Carolyn
APPLICANT: Henzel, William
APPLICANT: Kabakoff, Rhona
APPLICANT: Shelton, David
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LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-001-054-54
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OR FILING DATE: 2001...

OR APPLICATION NUMBER: 09/92796

OR APPLICATION NUMBER: 09/929404

OR FILING DATE: 2001.08-06

OR APPLICATION NUMBER: 09/929404

OR FILING DATE: 2001.08-28

OR APPLICATION NUMBER: 09/946374

OR APPLICATION NUMBER: 09/946374

OR APPLICATION NUMBER: 09/946374

OR APPLICATION NUMBER: 07/US99/00106

OR FILING DATE: 1998-00-10

OR APPLICATION NUMBER: PCT/US99/00106

OR FILING DATE: 1999-01-05

OR FILING DATE: 1999-01-05

OR FILING DATE: 1999-03-08

OR FILING DATE: 1999-03-08

OR FILING DATE: 1999-03-08

OR FILING DATE: 1999-03-08

OR FILING DATE: 1999-12-02

OR APPLICATION NUMBER: PCT/US99/28133

OR FILING DATE: 1999-12-02

OR APPLICATION NUMBER: PCT/US99/28133

OR FILING DATE: 1999-12-02

OR APPLICATION NUMBER: PCT/US99/28634

OR FILING DATE: 1999-12-02

OR APPLICATION NUMBER: PCT/US99/30095

OR FILING DATE: 1999-12-02

OR APPLICATION NUMBER: PCT/US99/30095

OR FILING DATE: 1999-12-02

OR APPLICATION NUMBER: PCT/US99/30095

OR FILING DATE: 1999-12-02

OR APPLICATION NUMBER: PCT/US99/30095

OR FILING DATE: 1999-12-03

OR APPLICATION NUMBER: PCT/US99/3099

OR FILING DATE: 1999-12-06

OR APPLICATION NUMBER: PCT/US99/3099

OR FILING DATE: 2000-02-18

OR APPLICATION NUMBER: PCT/US00/04342

OR APPLICATION NUMBER: PCT/US00/04342

OR APPLICATION NUMBER: PCT/US00/04342

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FILING DATE: 2000-03-02
APPLICATION NUMBER: PCT/USO0/06884
FILING DATE: 2000-03-15
                                                                                                                                       R APPLICATION NUMBER: 09/380138
R FILING DATE: 1999-08-25
R APPLICATION NUMBER: 09/380913
R FILING DATE: 1999-09-09
R APPLICATION NUMBER: 09/403297
R APPLICATION NUMBER: 09/423741
R FILING DATE: 1999-10-18
R FILING DATE: 1999-11-10
R APPLICATION NUMBER: 09/709238
R FILING DATE: 2000-11-08
R APPLICATION NUMBER: 09/709238
                   R APPLICATION NUMBER: 09/218517
R FILING DATE: 1998-12-22
R APPLICATION NUMBER: 09/284291
R FILING DATE: 1999-04-12
R APPLICATION NUMBER: 09/380137
R FILING DATE: 1999-08-25
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R APPLICATION NUMBER: 09/882636
R FILING DATE: 2001-06-14
A APPLICATION NUMBER: 09/918585
R FILING DATE: 2001-07-30
R APPLICATION NUMBER: 09/924419
                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2001-03-09
APPLICATION NUMBER: 09/866034
FILING DATE: 2001-05-25
APPLICATION NUMBER: 09/872035
FILING DATE: 1998-11-19
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100.0%; Score 1478; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0;
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                                              PRIOR APPLICATION NUMBER: PCT/USO0/13705
PRIOR APPLICATION NUMBER: PCT/USO0/14042
PRIOR FILING DATE: 2000-05-27
PRIOR PFLING DATE: 2000-05-27
PRIOR PILING DATE: 2000-05-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-02
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                              FILING DATE: 2000-03-30
APPLICATION NUMBER: PCT/US00/13705
PCT/US00/08439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; APPLICANT: Lasek, Amy W. ; APPLICANT: Jones, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo Sapien
US-10-001-054-54
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61 DDSYMDPNDEBSMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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APPLICANT: Karpf, Adam R.

TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
FILE REPERENCE: PA-0047 US
CURRENT APPLICATION NUMBER: US/10/093,766
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PERL PROGRAM
SEQ ID NO 54
LENGTH: 281
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Legal Services
                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030013099A1 059509CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: 15.5 Diskette
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/174,654
FILING DATE: 19-Jun-2002
CLASSIFICATION: <u >cutemain</u>
CLASSIFICATION: <u >cutemain</u>
CLASSIFICATION: <u >cutemain</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIXQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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Publication No. US20030044937A1
GENERAL INFORMATION:
MILLS OF WALLE OF WALLE OF USENIOR APPLICANT: Bienkeyski, Michael J
Jones, David A
TITLE OF INFORMION: TNF-Related Death Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Kerber, Lori L.
REGISTRATION NUMBER: 41,113
REFERENCE/DOCKET NUMBER: 6111.N CN1
TELECOMMUNICATION INFORMATION:
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CITY: Kalamazoo
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COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 281; Conservative
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                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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US-10-174-654-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0;
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                                                                                               | LENGTH: 281 amino acids | LENGTH: 281 amino acids | TYPE: amino acid | STRANDEDNESS: single | TOPOLOGY: linear | MOLECTLE TYPE: protein | SEQUENCE DESCRIPTION: SEQ ID NO: 11: US-10-174-654-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: March 23, 2004, 09:12:35
TELEPHONE: 616/833-0974
                        TELEFAX: 616/833-8897
                                                 TELEX: 224401
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Job time : 47 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

March 23, 2004, 09:04:03; Search time 21 Seconds (without alignments) 1287.134 Million cell updates/sec

US-10-662-429-2 Title: Perfect score:

1 MAMMEVQGGPSLGQTCVLIV.....NEHLIDMDHEASFFGAFLVG 281 Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table: Sequence:

283366 segs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

283366

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

COLUMNIES		DB ID Description	A53062 Fas	138707 Fas ligand -	A49266 fas ligand -	S53090 CD40 ligand -	153476 CD40 ligand -	A25451 tumor necrosis	CD40]	S17289	S12606 tumor necrosis	\$22052 tumor necrosis	1 JQ1344 tumor necrosis fac	S24642 tumor necrosis	IS4490 tumor necrosis	S24641 lymphotoxin - b	OWHUN	QWMSN tumor necrosis		lymphotoxin alp	JH0529	S06192		S52715 tumor necrosis	2 I49139 lymphotoxin-beta -	QQBY2M	1 JN0869 tac	I48083 amphotropic mur	JH0309	A46066 lymphotoxin bet	
		Length D	279	281	278	261	261	234	260	204	232	233	234	233	235	204	233	235	235	205	234	193	202	185	306	638	202	652	197	244	
de	Query	Match	12.8	12.6	12.0	11.1	10.0	9.5	9.5	9.1	9.0	8.9	9.0	8.8	8.8	9.8	8.5	8.4	8.4	8.3	8.2	7.8	٠		7.7	7.6	•	٠	7.2		
		Score	189.5	186	177.5	164	147.5	141	141	134.5	133	131.5	131	130.5	129.5	127.5	125.5	123.5	123.5	122	121	115.5	_	113.5	113.5	112.5	111.5	109	107	102	
	Result	No	н	71	m	4	Ŋ	9	7	c c	σ	10	11	12	13	14	15	16	17	18	19	70	21	22	23	24	25	56	27	28	

tumor necrosis fac	protein kinase, pr	DNA ligase homolog	hypothetical prote	hypothetical prote	hypothetical prote	chromodomain helic	heat shock transcr	cardiac muscle fac	myosin-light-chain	activin receptor-1	serine/threonine k	hypothetical prote	hypothetical prote	NBS-LRR type resis	alpha-N-arabinofur
S11688	F95122	T14707	T15010	G95104	T18489	T23056	A31593	T29095	JN0583	A53444	JC2491	T40578	E96636	T03031	B59296
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233	448	345	365	455	4981	1465	833	1538	1176	502	502	1284	907	313	328
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ALIGNMENTS

RESULT 1
A53062
Fas ligand - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 05-Nov-1999
C;Accession: A53062
R; Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Na
Cell 76, 969-976, 1994
A, Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in
A;Reference number: A53062; MUID:94185175; PMID:7511063
A;Accession: A53062
A:Status: preliminary
A; Molecule type: mRNA
A;Residues: 1-279 <tak></tak>
A; Cross-references: GB: U06948; NID: g473564; PIDN: AAA17800.1; PID: g473565
Chorac Match

33; Gaps Length 279; Indels 64; DB 2; Query Match
12.8%; Score 189.5; DB 2
Best Local Similarity 25.8%; Pred. No. 1.5e-08;
Matches 51; Conservative 50; Mismatches 64

9 111 ELREFTNOSL-----KVSSFEKQIANPSTPSEKKEPRSV-AHLTG------NPHSR 154 83 QLRQLVRKMILRISEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSK 142 143 NEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKN 202 203 DKOMVQYIY-KYTSYPDPILLMKSAR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSV 260 202 NQPLNHKYYMRNSKYPEDLVLMEEKRLNYCTT--GQIWAHSSYLGAVFNLTSADHLYVNI 259 ò d à g g ò

261 TNEHLIDMDHEASFFGAF 278 : ||: : :|| : 260 SQLSLINFEESKTFFGLY 277 à 셤

RESULT 2

Fas ligand - human

C.Species: Homosapiens (man)
C.Species: Homosapiens (man)
C.Joace: 29-May-1998 #sequence revision 29-May-1998 #text_change 21-Jul-2000
C.Joacesion: 13870; JC2340; S25565; I38554
R.Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
Int. Immunol. 6, 1567-1574, 1994
Int. Immunol. 6, 1567-1577, MUD:95127560; PMID:7826947
A.Faterence number: 138707
A.Accession: 138707
A.Accession: I38707
A.Accession: Lype: mRNA
A.Faterence number: REMEL:Ull821; NID:9595430; PIDN:AAC50124.1; PID:9595431
A.Accessione: 1-281 cRES>

Length 278;

DB 2;

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A4926
Cis Ligand - rat
Cis Ligand - rat
Cis Species: Rattus norvegicus (Norway rat)
Cibate: 13-0an-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
Ciscusion: A49266
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                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: S57565
A;Accus: preliminary
A;Molecule type: mRNA
A;Residues: 1-281 «SCH>
A;Cresidues: 1-282 «SCH>
A;Cresidues: 1-281 «SCH>
A;Crosis = references: EMBL:X89102; NID:9887455; PID:9887456
A;Crosis = references: EMBL:X89102; NID:9887455; PID:9887456
A;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; G. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death in human I lymphocytes.
            T.; Hijioka, T.; Kasahara, A.; Fusamoto,
R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusam Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A;Title: Role of Fas ligand in apoptocsis induced by hepatitis C virus infection. A;Reference number: JC2340; MUID:95071350; PMID:7980502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Introns: 151/1; 116/3
C;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <TMM>
F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :::| | | | |::| | |::
71 LKKRGNHSTG-LCLLVMFFMVLVALVGLGLGMFQLFHLQKELAELRESTSQMHTASSLEK 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: 13854; MUID:95105731; PMID:7528780
A; Accession: 13854
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-281 <RE2>
A; Residues: 1-281 <RE2>
A; Cross_references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 DAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 QIGHPSPPE-----KKELRKV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S57565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 63; Conserva
                                                                                                                                                           A, Accession: JC2340
A, Molecule type: DNA
A, Residues: 1-281 <MIT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Genetics:
A,Gene: FasL
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CD40 ligand - human
NyAlternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: O2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2001
C;Accession: S28017; JH0793; S36694; S28852; I53476; S25684; S30593
R;Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.;
EMBO J. 11, 4313-4321, 1992
A;Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                             100 ISTVQEKQQNISPLVRERGPQRVAAHITGT-RGRSNTLSSPNSKNEKALGRKINSWESSR 158
                                                                                                                                                                                                     ----EWEDT- 162
                                                                                                                                                                                                                                                           159 SGHSFLSNIHLRNGELVIHEKGFYYIYSQTYFRPQEEIKENTKNDKQMVQYIY-KYTSYP 217
                                                                                                                                                                                                                                                                                                                                                                                         218 DPILLMKSAR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276
                                                                                                                                                                                                                                                                                                                                                                                                                              217 GDLVLMEEKKLNYCTT--GQIWAHSSYLGAVFNLTVADHLYVNISQLSLINFEESKTFFG 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 IQRCNKGEGSLSLLNCEBIRSRFEDLV-KDIMQNKE-----VKKKEKNFEMHKGDQBPQ- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 YWDPNDEESMNS--PCWQVKWQLRQLVRKMILRISEETISTVQEKQQNISPLVRERGPQR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 VAAHIIGIRGRSNTLSSPNSKNEKALGRKINSWESSRSCHSFLSN--LHLRNG-ELVIHE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 IAAHV-----ISEASSKTTSVL----QW--APKGYYTLSNNLVTLENGKQLAVKR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 KGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,ACCESSION: S53090
R;Mertens, B.E.L.C.; Muriuki, M.
submitted to the EMBL Data Library, February 1895
A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
A;Reference number: S53090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Species: Bos primigenius taurus (cattle)
C,Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-261 <MER>
A;Cross-references: EMBL:Z48469; NID:g732569; PIDN:CAA88363.1; PID:g732570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 VQGGPSLGQTCVLIVIFTVLL -- QSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40; Gaps
                                                                          Gaps
                                                                       29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
11.1%; Score 164; DB 2; Length 26;
Best Local Similarity 25.9%; Pred. No. 2.1e-06;
Matches 72; Conservative 52; Mismatches 114; Indels
                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276
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                                                                                                                                                                                          121 VSSFEKQIANPSTPSETKKPRSV-AHLTGNPRSRSIPL-
Query Match
12.0%; Score 177.5; DB 3
Best Local Similarity 27.5%; Pred. No. 1.6e-07,
Matches 50; Conservative 39; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-261 <MER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277 AF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 LY 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD40 ligand - bovine
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A; Cross-references: EMBL:215017; NID:938483; PIDN:CAA78737.1; PID:938484
S.Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T. J. Exp. Med. 176, 1543-1550, 1992
A; Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobuli A; Reference number: JH0793; MUID:93094757; PMID:1281209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Kesiduca: 1-261 cGRA-
A;Cross-references: EMBL:X68550; NID:g37269; PIDN:CAA48554.1; PID:g37270
B;Gauchat, J.F.; Aubry, J.P.; Mazzel, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J.
A;Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of A;Reference number: S28852; MUID:93138085; PMID:7678552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-261 <GAU>
A;Cross-references: EMBL:L07414; NID:g180123; PIDN:AAA35662.1; PID:g180124
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 EESMN-SPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 TRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSN--LHLRNG-ELVIHEKGFYYIY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQTYFRRQEEIKENT-----KNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEY 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 AQVIFCSNREASSQAPFIASLCLKSPGRFER-------ILLRAANTHSSAKPC-- 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 VLIVIFTVLL--QSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDSYWDP-----ND
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                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-261 <SPR>
A; Cross-references: GB: X67878; NID: 938411; PIDN: CAA48077.1; PID: 938412
A; Cross-references: GB: X67878; NID: 938411; PIDN: CAA48077.1; PID: 938412
A; Experimental source: peripheral blood T-cell
R; Graf. D.; Korthaeuer, U.; Mages, H.W.; Senger, G.; Kroczek, R.A.
Eur. J. Immunol. 22, 3191-3194, 1992
A; Title: Cloning of TRAP, a ligand for CD40 on human T cells.
A; Reference number: S26694; MUID: 93076854; PMID: 1280226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Map position: Xq26-Xq26
C;Keywords: glycoprotein; transmembrane protein
F;13-4/Domain: transmembrane #status predicted <TMM>
F;45-261/Domain: extracellular #status predicted <EXT>
F;6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
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A;Reference number: S28017; MUID:93049181; PMID:1385114
A;Accession: S28017
A;Molecule Lype: mRNA
A;Residues: 1-261 <HOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.0%; Score 147.5; DB 2 23.7%; Pred. No. 5.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: GDB:CD40LG; HIGM1; IMD3
A:Cross-references: GDB:120632; OMIM:308230
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                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: S26694
                                                                                                                                                                                                                                                                                                A;Accession: JH0793
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tumor necrosis factor alpha precursor - rabbit
NiAlternate names: cachectin; TNF alpha
CiSpecies: Oryctolagus cuniculus (domestic rabbit)
CiDate: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 04-Feb-2000
CiAccession: A25454; A25451; JS0727

```
R,Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, F. Mns. 5, 149-156, 1986
A; Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for reA; Reference number: A25454; MUID:86219711; PMID:3519137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA

**Residues: 1-234 <-IT2.

A; Note: this sequence differs from that shown in having a Gln inserted between residues

R; Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.

R; Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.

A; Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF

A; Reference number: JH0309; MUID: 91065534; PMID: 2249779
                                                                                                                                                                                                                                             A;Cross-references: GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B. DNA 5, 157-165, 1986
A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
A;Reference number: A25451; WUID:86219712; PMID:3519138
A;Accession: A25451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Introns: 62/3; 80/1; 96/1
(Superfamily: fumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; mem
F;1-81/Domain: propeptide #status predicted <PRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RjArmitage, R.J.; Fanslow, W.C.; Strockbine, L.; Sato, T.A.; Clifford, K.N.; Macduff, Cosman, D.; Spriggs, M.K.
Nature 357, 80-82, 1992
A;Title: Molecular and biological characterization of a murine ligand for CD40.
A;Reference number: S21738; MUID:92244364; PMID:1374165
A;Accession: S21738
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: JS0727
A;Status: nucleic acid sequence not shown; translation not shown
A;Nolecule type: DNA
A;Residues: 1-62,'Q',63-234 <SHA>
A;Residues: 1-62,'Q', GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 NDEESMNSPCWQVKWQLRQLVRKMI-LRTSEETISTVQEKQQNISPLVRERGPQRVAAHI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 VA------NPQVEGQL-----QMLSQRANALLANGMKLTDNQLVVPADGLYLIYS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 QTYFRFQEEIKENTKNDKQMVQXIYKY-TSYPDPILLMKSARNSCWSKDAEYG----LY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 TGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYY1YS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 QERESPIN-----LHLVNPVAQMYTLRSASRALSD-----KPL-----AHV 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 GGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDSYWDP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F:82-234/Product: tumor necrosis factor #status predicted <MAT>
F:91,20/Bainding site: myristate (Lyg) (covalent) #status predicted
F:83/Bainding site: carbohydrate (Ser) (covalent) #status predicted
F:147-178/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.5%; Score 141; DB 1; 22.4%; Pred. No. 0.00016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 GGPOGSKRCLCLSLFSFLL----VAGATTLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 22.4%
Matches 62; Conservative
                                                                                                                                                                                                               A; Residues: 1-234 <ITO>
                                                                                                                                                                                    A; Molecule type: mRNA
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C; Superfamily: tumor necrosis factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Introns: 62/3; 78/1; 93/1
                                                                                                                                                                                                                                                                                                        A;Accession: S17290
A;Molecule type: DNA
A;Residues: 1-232 <KUH>
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLLNCEEMRRQFEDLVXDITLNK-----BEKKENSFEMQRGDEDPQIAAHV---- 125
                                                                                                                                                                                                                                                                                                                                                                                      177 CSNRE----PSSQRPFIVGLWLKPSIGSERILLKAANTHSSSQLCEQ--QSVHLGGGVFEL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----HGFL-----LSNNSLLVPTSGLYFVYSQVVFSGEGCFPKATPTPLYLAHEVQLF 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S--PCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGR 132
                                                                                                                                                                                                                                                                                                     SNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNL-HLRNG-ELVIHEKGFYYIYSQTYF 190
                                                                                                                                                                                                                                                                                                                                   ---VSEANSNAASVL----QW-AKKGYYTMKSNLVMLENGKQLTVKREGLYYVYTQVTF 176
                                                                                                                                                                                                                                                                                                                                                                191 RFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFEL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 STVQEKQONISPLVRERGPQRVAAHITG-----TRGRSNTLSSPNSKNEKALGRKINS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 WESSRSGHSFLSNIHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 TS-YPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEA 272
                                                                                                                                                                          17 VLIVIFTVLL--QSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMN 74
                                                                                                                                                                                              SAAQPAHQH-PPKHLARGTLKPAAHLVGDPSTPDSLRWRANT-----DRAFLR----
                                                                                                                                              Gaps
A,Residues: 1-260 cARM>
A,Cross-references: EMBL:X65453; NID:g50351; PIDN:CAA46448.1; PID:g50352
C,Keywords: glycoprotein; transmembrane protein
F;23-46/Domain: transmembrane fatuus predicted <TWM>
F;47-260/Domain: extracellular #status predicted <EXT>
F;239/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                              38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 204;
                                                                                                             Score 141; DB 2; Length 260; Pred. No. 0.00019;
                                                                                                      9.5%; Score 11.,
23.5%; Pred. No. 0.00019;
tive 50; Mismatches 104; Indels
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Pred. No. 0.00048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31; Mismatches
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                                                                                                                                            59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               251 KENDRIFVSVT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 QAGASVĖVNYT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 VFFGAF 202
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A; Molecule type: mRNA
A; Residues: 1-232 <CHO.
A; Cross-references: 18. Peterhans, E.
R; Pauli, U.; Beutler, B.; Peterhans, E.
Gene 81, 185-191, 1989
A; Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reactic
A; Reference number: 146659; MUID:90034181; PMID:2478420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:g2134
A;Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:g2134
A;Note: the authors translated the codon GAG for residue 202 as Gly
R;Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.
submitted to the EMBL Data Library, January 1991
A;Poscription: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis f
A;Accession: S18965
                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-232 < CRES.
A; Cross-references: EMBL: X54001; NID: 92135; PIDN: CAA37949.1; PID: 92136
R; Kuhmert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.
A; Kullert, P.; 171-176, 1991
A; Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative ana
A; Reference number: S17289; MUID: 91340150; PMID: 1874444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 VAAHITGTRGRSNTLSSPNS---KNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 -----GLRSSSQTSDKFVAHVVANVKAEGQL--QMQSGYANALLANGVKLKDNQLVVPT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 KGFYYIYSQTYFRFQEEIKEN---TKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSK-- 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 DGLYLIXSQVLFRGQGCPSTNVFLTHTISRIA-----VSYQTKVNLLSAIKSPCQRETP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: Sus Sofo (strong to the sequence revision 10-Sep-1999 #text_change 04-Feb-2000
Cispecession: Sla606; Sl799; Sl9955; I46659
Ribrews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.
Nucleic Acids Res. 18, 5564, 1990
A;Title: Gene sequence of porcine tumor necrosis factor alpha.
A;Reference number: Sl2606; MUID:91016861; PMID:2216741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKED
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A)Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695 C;Genetics:
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61; Conservative 40; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.0%; Score 133; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
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8.9%;
                                                                                                        Query Match
Best Local Similarity 20.8*
Matches 60; Conservative
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C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AD3144

JQ1344

Lumor necrosis factor alpha precursor - horse

N;Alternate names: cachectin; TNF alpha

C;Species: Equus caballus (domestic horse)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C;Date: 10-Sep-1991 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

R;Su, X.; Morris, D.D.; McGraw, R.A.

Gene 107, 319-321, 1991

A;Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis

A;Reference number: JQ1344; MUID:92084125; PMID:1748301
                                                                                                                                                  C.Species: Papio sp. (baboon)
C.Bate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C.Accession: $22052
C.Accession: $22052
S.Bate: 10-Sep-1999 #text_change 04-Feb-2000
C.Accession: $20052
S.Bate: 10-Sep-1999 #text_change 04-Feb-2000
C.Accession: A.Bate: A.Bate: A.Bate: A.Bate: 1991
A.Bescription: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 DSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 YYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-----SYPDPILLMKSARNSCWSK-- 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 PVAHVVA------NPQAEGQL--QWLNRRANALLANGVELRDNQLVVPSEGL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 ALPKKTGGPQGSRRCLFLSLFSFLLVAGATTLFCLLHFGVIGPQREEFPK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----DP----SLISPLAQA-----VRSSSRTPS-----DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 VAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGF
                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule From 1.233 < SAN>
A; Residues: 1-233 < SAN>
A; Residues: 1-233 < SAN>
A; Residues: 1-233 < SAN>
A; Crosa-references: EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160
C; Genetics: 62/3; 78/1; 94/1
C; Superfamily: tumor necrosis factor
C; Superfamily: tumor necrosis factor
C; Keywords: glycoprotein; lipoprotein; myristylation; transmembrane prote
F; 19, 20/Ainding site: myristate (Lys) (covalent) #status predicted
F; 19, 20/Ainding site: carbohydrate (Ser) (covalent) #status predicted
F; 145-177/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB: M64087; NID: g164244; PIDN: AAA30959.1; PID: g164245 C; Comment: This protein is an important proximal mediator of endotoxemia. C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 233;
182 EGAEAKPWYEPIYLGGVPQLEKDDRLSAEINLPDYLDFAESGQVYFG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 EGAEAKPWYEPIYLGGVFQLEKGDRLSAEINLPDYLDFAESGQVYFG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 --- DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 131.5; DB Pred. No. 0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49; Mismatches
                                                                                                                                 factor alpha precursor - baboon o sp. (baboon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55; Conservative
                                                                                                                                                                                                                                                                                                          A;Reference number: S22052
A;Accession: S22052
A;Status: preliminary
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A, Molecule type: DNA
A, Residues: 1-234 <SUX>
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                                                                                                                                 necrosis
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Ricludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A;Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and A;Reference number: 146046; MUID:94083525; PMID:8260599
A;Accession: 146047
                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 EDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 ORVAAHITGTRGRSWTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 DKPVÄHVVA-------NPQAEGQL--QWLSGRANALLANGVKLITDNQLVVPLD 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 GFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT----SYPDPILLMKSARNSCWSK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 ---KEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 IHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK--YTSYPDPILLMKSARNSC--- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 VPADGLYLIYSQVLFRGQ-----GCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aintrons: 62/3; 78/1; 94/1
C;Superfamily: tumor necrosis factor
C;Superfamily: tumor necrosis factor
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
C;Keywords: glycoprotein; lipoprotein; myristatus (covalent) #status predicted
F;20/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;145-177/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumor necrosis factor alpha precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: 146047; S24642
                                                                                                                                                                                                                                                                    8 GGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFL-----K
                                                                                                                                                                                                                                                                                                                                            ------CLLHFGVIGPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 ERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 ----NKPVAHVVA-----DINSPGOLR------WMDSYANALMANGVKLEDNOLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 MMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFL---
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A;Residues: 1-233 <CL2>
A;Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798
C;Genetics:
                                                                                                                                                                                                         Indels 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 DAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;19,20/Binding site: myristate (Lys) (covalent) #status predicted F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted F;146-178/Disulfide bonds: #status predicted
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                                                                                                                                   Score 131; DB 1; Length 234;
Pred. No. 0.0011;
0; Mismatches 89; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 EEQL---PNAFQSIN-PLAQT------LRSSSRTPS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95;
                                                                                                                                                                                                                                                                                                                                  22 GGPQGSRRCLCLSLFSFLL----VAGATTLF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDBJ
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A;Molecule type: mRNA
A;Residues: 1-62, S', 64-233 <WAN>
A;Cross-references: GB:M1098B; NID:g339737; PIDN:AAAG1198.1; PID:g339738
R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; A
R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; A
R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; A
A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta an
A;Reference number: A61478; MUID:88301617; PMID:2841543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NyAlternate names: cachectin; TNFA
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence revision 28-Aug-1985 #text_change 08-Dec-2000
C;Accession: A93585; S36153; A943189; B64478; I53311; S65610; I54522; A01646; B2
R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, Nicleic Acids Res 13, 6361-6373; 1985
A;Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chr
A;Reference number: A93585; MUID:86016093; PMID:2995927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-233 <PEN.
A; Residues: 1-233 <PEN.
A; Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A; Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyel
R; Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.;
Science 228, 149-154, 1985
A; Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
A; Reference number: A44189; MUID:85142190; PMID:3856324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AjCross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
Kilis, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurk
Nature Genet. 3, 137-145, 1993
AjTitle: Dense Alu clustering and a potential new member of the NFkappaB family within
A,Reference number: S36152; MUID:93272029; PMID:8499947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Regidueg: 1-233 <IRI>
A;Crose-references: EMBL:215026, NID:g37211; PIDN:CAA78745.1; PID:g37212
A;Crose-references: EMBL:215026, NID:g37211; PIDN:CAA78745.1; PID:g37212
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R;Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A Rature 312, 724-729, 1884
A;Title: Human tunmour necrosis factor: precursor structure, expression and homology to A;Reference number: A93351; MUID:85086244; PMID:6392892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;18
A; Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;18
Finarmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,
Eur. J. Biochem. 152, 515-522, 1985
A; Fitle: Molecular cloning and expression of human tumor necrosis factor and comparison
A; Reference number: 153311; MUID:86030296; PMID:3932069
                                                                                                                                                     89 ------HGF----SLSNNSLLVPTSGLYFVXSQVVFSGRGCFPRATPTPLYLAHEVQ 135
                                                                                                                                                                                                                                                                                                               212 KYT-SYPDPILLMKSARNSCWSKDAEYGLYSIYOGGIFELKENDRIFVSVTN-EHLIDMD 269
                                                                                                          152 NSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY 211
                               40 TPSAAQPAHQQL-PTPFTRGTLKPAAHLVGDPSTQDSLRWRANT------DRAFLR-- 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumor necrosis factor alpha precursor [validated] - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-233 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                              270 HEASFFGAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 PSSVFFGAF 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-233 <NED>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S36153
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R;Crew, M.D.; Filipowsky, M.E.
Imunogenetics 35, 351-353, 192
A;Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leuc A;Reference number: I54490; MUID:92218012; PMID:1348497
A;Accession: I54490
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Cybecies: Bos primigenius taurus (cattle)
Cybecies: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
Cybecies: 146046; 234641
Cytokine 5, 336-341, 1993
AyTitle: Cloning and characterization of the tandemly arranged bovine lymphotoxin and AyReference number: 146046; MUID:94083525; PMID:8260599
AyAccession: 146046
AyStatus: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 ISPLVRERGPQRVAAHITGTRGRSNTL-SSPNSKNEKALGRKINSWE-----SSRSGH 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 IGPOREEKFPNNLP--IIGSMAQTLTLRSSSQNSSDKPVAHVVANHQVDEQLEWLSRGAN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFLSN-LHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDP 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220 ILLMKSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS 273
                                                                                                                                                                                                                                                    tumor necrosis factor alpha precursor - white-footed mouse
C;Species: Peromyscus leucopus (white-footed mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-235 <RES>
A;Cesserzeferences: GB:MS9233; NID:g202506; PIDN:AAA40596.1; PID:g202507
C;Genetics:
A;Gene: PITNF
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A,Cross-references: EMBL:214137; NID:g796; PIDN:CAA78510.1; PID:g797 C.Genetics: 32/3; 68/1
                                   ---WSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 62/3; 81/1; 97/1
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 235;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 129.5; DB 2; Pred. No. 0.0015; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78; Indels
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tive 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.8%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lymphotoxin - bovine
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99 TISTVQEKQQNISPLVRERGPQRVAAHITG-----TRGRSNTLSSPNSKNEKALGRKI 151

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A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Residues: 1-8 cABL.
A, Residues: 1-8 cABL.
A, Torses-references: GB:S68530; NID:g544751
R, Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A, Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lys A, Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lys A, Contents: annotation; identification of myristylated lysines
A, Contents: annotation; identification of myristylated lysines
A, Title: Human tumor necrosis factor. Production, purification, and characterization.
A, Reference number: A92511; MUD:85130974; PMID:3871770
                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 77-99 <TAK>
A;Residues: 77-99 <TAK>
R;D'Alfonso, S.; Richiardi, P.M.
Immunogenetics 39, 150-154, 1994
A;Title: A polymorphic variation in a putative regulation box of the TNFA promoter regic
A;Reference number: IS4522; MUID:94102809; PMID:7903959
A;Accession: IS4522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; macr F;1-76(Domain: propeptide #status predicted <PRO> F;7-23.4) Froduct: tumor necrosis factor #status experimental <NAT> F;19,20/Binding site: myristate (Lys) (covalent) #status experimental F;19,20/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental F;145-177/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction out detriment to normal cells. It can also act synergistically with interferon gamma to C;Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes closely user are produced by different cell types and have different induction kinetics.

A;Gene: GDB:TNF; TNFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 PVAHVVA-------NPQAEGQL--QWLNRRANALLANGVELRDNQLVVPSEGL 131
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Eur. J. Biochem. 235, 431-437, 1996
A;Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
A;Reference number: S62610; MUID:96202967; PMID:8631363
A;Accession: S62610
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A;Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764
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8.5%; Score 125.5; DB 1; Length 233;
Best Local Similarity 17.8%; Pred. No. 0.0033;
Matches 51; Conservative 52; Mismatches 99; Indels 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 ALPKKTGGPQGSRRCLFLSLFSFLIVAGATTLFCLLHFGVIGPQREEFPR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GDB:120441; OMIM:191160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: tumor necrosis factor
                                           A; Experimental source: U-937 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Map position: 6p21.3-6p21.3
A;Introns: 62/3; 78/1; 94/1
C:Complex: homotrimer
C:Superfamily: tumor necrosis
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Search completed: March 23, 2004, 09:07:19

Job time : 22 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

March 23, 2004, 09:04:03; Search time 17 Seconds (without alignments) 860.689 Million cell updates/sec Run on:

US-10-662-429-2 1478 1 MAMMEVQGGPSLGQTCVLIV.....NBHLIDMDHBASFFGAFLVG 281

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 141681 seqs, 52070155 residues Searched:

141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Query	Length	DB	ID	Descri
1478	100.0	281	-	TN10 HUMAN	P50591
. 930	62.9	291	Н	TN10 MOUSE	P50592
267.5	18.1	318	Н	TN11_RAT	09ese2
258.5	17.5	316	Н	TN11 MOUSE	035235
251.5	17.0	317	٦	TN11 HUMAN	014788
				1	

	Description	P50591 homo sanien			035235 m tumor nec	д	P41047 mus musculu	Q9bdn1 cercocebus	P48023 homo sapien	-	O9i8d8 gallus gall		P36940 rattus norv	P51749 bos taurus			_	Q9bdn3 callithrix		O97605 felis silve	Q9bdc7 macaca mula	O97626 canis famil				P04924 oryctolagus			воф	ratt		cavi	I hishali	TOUTH A
	ID	TN10 HUMAN	TINI 0 MOUSE	TN11 RAT	TN11 MOUSE	TN11 HUMAN	TWF6 MOUSE	TNF6 CERTO	TNF6 HUMAN	TNF6 MACMU	TNF5 CHICK	TNF6_PIG	TNF6 RAT		TN15 HUMAN	TN14 HUMAN	TN14 MOUSE	TNF5_CALJA	TNF5_AOTTR	TNFS FELCA	TNFS MACMU	TNF5 CANFA	TNFS HUMAN	TNF5_PIG	TWF5 MOUSE	TNFA RABIT	TNFA CEREL	TNFB PIG	TNFA BOSIN	TNF5 RAT	TNFA PIG	TNFA CAVPO	TNFA BUBBU	
	DB	: ⊣	ч	Н	н	٦	Н	П	ч	ч	Н	П	Н	Н	Н	Н	Н	Н	Н	н	Н	H	٦	-	Н	Н	Н	-	Н	-	ч	Н	Н	
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9	Match	100.0	62.9	18.1		7	12.8	2	S		•	12.3	N	11.1	0	10.8	0	10.3	0	10.1	10.0			•	•	9.5		9.1			9.0			
	Score	1478	. 930	267.5	258.5	251.5	189.5	187	186	185	184	182	177.5	164	160	159.5	152.5	152		149.5	148	147.5	147.5	143	140	136.5	135	134.5	134	133.5	133	133	131.5	
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P29553 equus cabal	Q8jfg3 sparus aura	Q06599 bos taurus	P36939 peromyscus	Q06600 bos taurus	035734 marmota mon	P01375 homo sapien	. P06804 mus musculu	P16599 rattus norv	P01374 homo sapien	Q8hzd9 pan troglod	P13296 capra hircu
TNFA HORSE	TNFA SPAAU	TNFA BOVIN	TNFA PERLE	TNFB_BOVIN	TNFA MARMO	TNFA HUMAN	TNFA MOUSE	TNFA RAT	TNFB HUMAN	TNFA PANTR	TNFA_CAPHI
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
may be modulated by binding to the decoy receptors
TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Homotrimer.
SUBCELLULAR LOCATION: Type II membrane protein (Potential).
TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sung Y.C., Oh B.-H.; "2.8 A resolution crystal structure of human TRAIL, a cytokine with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          induce apoptosis.
COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per
                        X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
MEDLINES-20010764; PubMed=10549288;
Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M., Kelley R.F., Ashkenazi A., de Vos A.M.;
Krilgering cell death: the crystal structure of Apo2L/TRAIL in a complex with death receptor 5.";
Mol. Cell 4:563-571(1999).
                                                                                                                                                                                                                                                                                                                                                                                               Jones E.Y., Screaton G.R.; "Structure of the TRAIL-DR5 complex reveals mechanisms conferring specificity in apoptoric initiation."; Nat. Struct. Biol. 6:1048-1053(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
CYtokine; Apoptosis; Transmembrane; Signal-anchor; Metal-binding; Zinc; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99413670; PubMed=10485660;
Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,
Sung Y.C., Oh B.-H.;
                                                                                                                                                                                                                                                                                                                                                                Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the tumor necrosis factor family.
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GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005625; C:soluble fraction; TAS.
GO; GO:0005102; F:receptor binding; TAS.
GO; GO:0005102; F:receptor binding; TAS.
GO; GO:0005102; F:receptor binding; TAS.
GO; GO:0007102; P:cell-cell signaling; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR006983; TNF family.
InterPro; IPR009893; TNF like.
R Pfam; PF00229; TNF; 1.
R PRODOM; PD002012; TNF subf: 1.
R PRODOM; PD002012; TNF subf: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.
                                                                                                                                                                                                                                                                                              CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             selective antitumor activity.";
Immunity 11:253-261(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC032722; AAH32722.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U37518; AAC50332.1; -.
EMBL; U57059; AAB01233.1; -.
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PDB; 1D4V; 01-NOV-99.
PDB; 1D2Q; 11-FEB-00.
PDB; 1DG6; 26-SEP-01.
Genew, HGNC:11925; TNFSF10.
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121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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                                                                                                                                                                                                                                                                                                                                                                                                           1 MAMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96111955; PubMed=8777713; Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P., Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-007-1996 (Rel. 34, Created)
01-007-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family that induces apoptosis.";
Immunity 3:673-682(1995).
-!- FUNCTION: Cytokine that binds to INFRSF10A/TRAILRI,
INFRSF10B/TRAILR2, INFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
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                                                                                                                                                                                                                                                                                                                                                     Indels
           EXTRACELLULAR (POTENTIAL). ZINC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                              32509 MW; DDAAAF78DAAB2F6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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100.0%; Pred. No. 8e-115;
ive 0; Mismatches 0
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POTENTIAL)
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Best Local Similarity 100.
Matches 281; Conservative
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                                                                                                                                                                                                                                                                                              281 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWILERAT STANDARD; PRT; 318 AA.

OBESE2: O91219;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
7 tunor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TMF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF).

TNFSF11 OR RANKL OR TRANCE OR OPGL.
                  may be modulated by binding to the decoy receptors
TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
                                                                  SUBUNIT: Homotrimer (By similarity).
SUBCELLULAR LOCATION: Type II membrane protein (Potential).
TISSUB SPECIFICITY: WIDESPREAD.
SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 62.9%; Score 930; DB 1; Length 291; Best Local Similarity 65.6%; Pred. No. 1.4e-69; Matches 177; Conservative 37; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3FEACAB9F0D7D802 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 291 E
52 52 N
291 AA; 33477 MW;
                                                   induce apoptosis.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                               Marks S.C. Jr.;

"Evidence that the rat osteopetrotic mutation toothless (tl) is not in the TMSF11 (TRANCE, RANKL, ODF, OPGL) gene.";

Int. J. Dev. Biol. 45:853-859(2001).

Int. J. Dev. Biol. 45:853-859(2001).

"INFRSF11A/RANK. Osteoclast differentiation and activation factor. Augments the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral
Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEMBER 11, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
MEMBER 11, SOLUBLE FORM.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY

    similarity).
    TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.
    PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
    SIMILARITY: Belongs to the tumor necrosis factor family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypercalcemia of malignancy.
SUBUNIT: Homotrimer (By similarity).
SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
                                                                                                                                                                                                                                                                            MEDLINE=21662371; PubMed=11804028; Odgren P.R., Kim N., van Wesenbeeck L., MacKay C., Mason-Savas A., Safadi F.F., Popoff S.N., Lengner C., van-Hul W., Choi Y.,
                                                                                                      TIŠSUB=Tibial bone;
MEDLINE=20540945; PubWed=11092398;
Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytokine, Differentiation, Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLEAVAGE (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                          "Cloning, sequence and functional characterization of the rat homologue of receptor activator of NF-kB ligand."; J. Bone Miner. Res. 15:2178-2186 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
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EMBL; AF425669; AAL23963.1; -.
HSSP; P50591; 1D06.
InterPro; IFR006052; TNF family.
InterPro; IFR008983; TNF_like.
InterPro; IFR008566; TNF_subf.
ProDom; PD00229; TNF; 1.
ProDom; PD002012; TNF; 1.
SWART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                SEQUENCE OF 266-318 FROM N.A.
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140
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317
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                                                                                        SEQUENCE FROM N.A.
                                                       NCBI_TaxID=10116;
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                                                                                                                                                            Zheng M.H.;
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CONFLICT
SEQUENCE
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4B87A4D706AD098F CRC64;

35370 MW;

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                                                                                                                                                                                                                                                                                             43 PAASRFMFLALLGLGLGOVVCSIALFLYFRAQMD--PNRISEDSTRCFYRILRLRENTGL 100
                                                                                                                                                                                                                                                                                                                                                                                                  62 - DSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GAVORELOHIV-----GPO 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 R---VAAHITGT-----RGRS------NTLSSPNSKNEKALGRKINSWESSRSGH 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 SFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQXIYKYT-SYPDPI 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 AKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPADYLQLMVYVVKTSIKIPSSH 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 LLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 NLMKGGSTKNWSGNSEPHFYSINVGGFFKLRAGEEISVQVSNPSLLDPDDDDATYFGAFKV 314
                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TMIL MOUSE STANDARD; PRT; 316 AA.

035235; 035306; Q9JJK8; Q9JJK9; Q9RIX0;

16-CCT-2001 (Rel. 40, Last sequence update)

16-CCT-2003 (Rel. 42, Last annotation update)

10-CCT-2003 (Rel. 42, Last annotation update)

10-CCT-2003 (Rel. 42, Last annotation update)

10-CCT-2003 (Rel. 42, Last annotation update)

10-CCT-2003 (Rel. 42, Last annotation update)

10-CCT-2003 (Rel. 40, Last annotation update)

10-CCT-2003 (Rel. 40, Last annotation update)

11-CCT-2003 (Rel. 40, Last annotation update)

11-CCT-2003 (Rel. 40, Last annotation update)

11-CCT-2003 (Rel. 40, Last annotation update)

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11-CCT-2003 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Galibert L.; "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
                                                                                               Gaps
                                                                                                                                                                                                         ----LKED---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Hybridoma;
MEDLINE=97460112; PubMed=9312132;
Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                         57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Osteoprotegerin ligand is a cytokine that regulates osteoclast
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MEDLINE=98032977; PubMed=9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
IOmetsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
18.1%; Score 267.5; DB 1; Length 318;
                                                                                                                                                                                         10 PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF-
                                          ; Pred. No. 8e-15;
55; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 ODSTLESEDTEALPDSCRRMKQAFQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFSF11 OR RANKL OR TRANCE OR OPGL.
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                                                                                               82; Conservative
                                               Best Local Similarity
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Query Match
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Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.; "Crystal structure of the extracellular domain of mouse RANK ligand at
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J. Biol. Chem. 277:6631-6636(2002)
I Biol. Chem. 277:6631-6636(2002)
I FUNCTION: Cytokine that binds to TNPRSFILB/OPG and to
TNPRSFILA. OSteoclast differentiation and activation factor.
Augments the ability of dendritic cells to stimulate naive T-cell
proliferation. May be an important regulator of interactions
between T cells and dendritic cells and may play a role in the
regulation of the T cell-dependent immune response. May also play
an important role in enhanced bone-resorption in humoral
hypercalcemia of malignancy.
                                                                                                             Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M., Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E., Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.; "Osteoclast differentiation factor is a ligand for osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21464816; PubMed=11581298;
Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;
"Crystal structure of the TRANCE/RANKL cytokine reveals determinants
of receptor-ligand specificity.";
J. Clin. Invest. 108:971-979(2001).
                                                                                                                                                                                                                                                                                                                                      Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A., Ueda M., Higashio K.; "Cloning and characterization of the gene encoding mouse osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TNF-alpha)-converting enzyme-like protease in shedding of TRANCE, and family member involved in osteoclastogenesis and dendritic cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDILINE-21150053; PubMed=11250921;
Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
"Determination of three isoforms of the receptor activator of nucle factor-kappaB ligand and their differential expression in bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type II membrane protein and secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Erdjument-Bromage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument
Schloendorff J., Tempst P., Choi Y., Blobel C.P.,
"Evidence for a role of a tumor necrosis factor-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION
                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (isoforms 1 and 2); Cytoplasmic (isoform 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=3;
IsoId=035235-3; Sequence=VSP_006448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=035235-2; Sequence=VSP_006449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lsoId=035235-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 274:13613-13618(1999).
                                                                                                                                                                                                                                                                                                                   MEDLINE=99214075; PubMed=10196481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21839021; PubMed=11733492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endocrinology 142:1419-1426(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99240759; PubMed=10224132;
                                                    SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE-Bone marrow stroma;
MEDLINE-98188248; PubMed-9520411;
activation.";
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                    differentiation factor.";
Gene 230:121-127(1999).
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                Cell 93:165-176(1998)
                                                                                                                                                                                                                     to TRANCE/RANKL.
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-!- PTM: N-glycosylated.
-!- PTM: In-glycosylated.
-!- PTM: In-glycosylated.
-!- PTM: The soluble form of isoform 1 derives from the membrane form by proteolytic processing. The cleavage may be catalyzed by ADAMI7. A further shorter soluble form was observed.
-!- DISEASE: Deficiency in TRFSF11 results in failure to form lobulo-alveolar mammary structures during pregnancy. resulting in death of newborns. Trance-deficient mice show severe osteopetrosis, with on osteoclasts, marrow spaces, or tooth eruption, and exhibit profound growth retardation at several skeletal sites including the limbs, skull, and vertebrae and have marked chondrodysplasia, with think, irregular growth plates and a relative increase in hypertrophic chondrogytes.
-!- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT NOT IN NONYMHENDID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE TRABECULAR BONE AND LONG.
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PROSITE; PS00251; TNF 1; FALSE_NEG.
PROSITE; PS50049; TNF 2; TNF 2; TNF 2; TNF 2; TNF 2; TNF 2; TNF 3; TNF 2; TNF 3; TNF 3; TNF 4; TNF 4; TNF 4; TNF 4; TNF 4; TNF 4; TNF 4; TNF 4; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; TNF 5; 
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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G -> D (IN REF. 2).
MISSING (IN REF. 5)
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PDB; 11CA; 14-JAN-03.
MGD; MGI:1100089; Tnfsf11.
GO; GO:0009887; P:organogenesis; IMP.
GO; GO:0001503; P:ossification; IMP.
InterPro; IPR006052; TuP. family.
InterPro; IPR008983; TuP. like.
InterPro; IPR003636; TNF 20bf.
ProDom; PD002201; TNF; 1.
ProDom; PD002201; TNF; 1.
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EMBL; AF019048; AAB6612.1; --
EMBL; AF023713; AAC40113.1; --
EMBL; AB022034; BAA25425.1; --
EMBL; AB022035; BAA36970.1; --
EMBL; AB022037; BAA36970.1; --
EMBL; AB022037; BAA36970.1; --
EMBL; AB022037; BAA36970.1; JOINED.
EMBL; AB022771; BAA36970.1; JOINED.
EMBL; AB032771; BAA37257.1; --
EMBL; AB032772; BAA972581; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 -----VRERGPORVA--AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMK 224
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O14788; O14723; Q96Q17; Q9P2Q3;
116-OCT-2001 (Rel. 40, Created)
116-OCT-2001 (Rel. 40, Last annotation update)
110-OCT-2003 (Rel. 42, Last annotation update)
110-OCT-2003 (Rel. 42, Last annotation update)
110-OCT-2003 (Rel. 42, Last annotation update)
110-OCT-2003 (Rel. 42, Last annotation update)
110-OCT-2003 (Rel. 42, Last annotation update)
110-OCT-2003 (Rel. 42, Last annotation update)
110-OCT-2003 (Rel. 42, Last annotation (Receptor activator induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OFGL) (Osteoclast differentiation factor) (ODF).
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Nature 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                            51; Gaps
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MEDLINE=9822761; PubMed=9568710;
Lacey D.L., Timme B., Tan H.-L., Kelley M.J., Dunstan C.R.,
Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=98032977; PubMed=9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                                Length 316;
                                                                                                                                                                                                                                                                                                                         Query Match
17.5%; Score 258.5; DB 1; Length:
Best Local Similarity 26.4%; Pred. No. 4.4e-14;
Matches 78; Conservative 54; Mismatches 113; Indels
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Isochem. Biophys. Res. Commun. 269:532-536(2000).

Isochem. Biophys. Res. Commun. 269:532-536(2000).

TURRSFILA/RANK. Osteoclast differentiation and activation factor.

TURRSFILA/RANK. Osteoclast differentiation and activation factor.

Augments the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral hypercalcemia of malignancy.

-!- SUBCELTULAR LOCATION: Type II membrane protein (isoforms 1 and 3);

Secreted (isoform 2). A soluble form of isoform 1 arises by proteolytic processing (By similarity).

-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation her Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISOId=014786-3; Sequence=VSP_006446; ISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT WEAK IN SPLEEN, PERPHERAL BLOOD LENCOCYTES, BONE MARROW, HEART, PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.
                                                                                                                                                                                                                                           "TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells.";
J. Biol. Chem. 272:25190-25194 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION. PTM: The soluble form of isoform I derives from the membrane form by proteolytic processing (By similarity). The cleavage may be
                                                                                                                                                                               Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
                                                                                                                                                                                                                                                                                                                                                                                         Nagai M., Kyakumoto S., Sato N.;
"Cancer cells responsible for humoral hypercalcemia express mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding a secreted form of ODF/TRANCE that induces osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the tumor necrosis factor family.
                                                              "Determination of human RANKL isoforms.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event = Alternative splicing; Named isoforms = 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=014788-2; Sequence=VSP_006447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=014788-1; Sequence=Displayed;
[3] SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                        Kuroyama H., Hirokawa K.;
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20175237; PubMed=10708588;
                                                                                                                                                            MEDLINE=97460112; PubMed=9312132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; ARG52.-
EMBL; AB064269; BAB7760...
EMBL; AB064277; BAB71768.1; -
TWBL; AB064270; BAB79695.1; -
TMBL; AB07771; AAC51762.1; -
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF019047; AAB86811.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB064270; BAB79695.1;
EMBL; AF013171; AAC51762.1;
EMBL; AB037599; BAA90488.1;
HSSP; P50591; 1D0G.
                                                                                                                     SEQUENCE OF 73-317 FROM N.A.
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                                                                                                                                             TISSUE=Thymocytes;
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GO; GO:0005576; C:extracellular; NAS. GO; GO:0005887; C:integral to plasma membrane; NAS.

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160 LEAQPF-----AHLT-----INATDIPSGSHKVSL---SSWYHDR-GWAKISNM 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 QDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 QNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 HLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 PAASRSMFVALLGLGLGLGQVVCSVALFFYFRAQMD--PNRISEDGTHCIYRILRLHENADF 99
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                                                                                                                                                                                                                                                                                                                                                                                                             MEMBER 11, MEMBRANE FORM.

WHORN RECROSIS FACTOR LIGAND SUPERFAMILY
MEMBER 11, SOLUBLE FORM (BY SIMILARITY).

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 PSLGQTCVLIVIFTVLLOSLCVAVTYVYFTNELKQMQDKYSKSGIACF----LKED---
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                                                                                                                                                                                                                                                                                                                                                Signal anchor; Alternative splicing.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 RNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 STKYWSGNSEPHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                          Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
Missing (in isoform 3).
/FIId=VSP 006446.
/FIId=VSP 006447.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 317;
      GO:0005164; F:tumor necrosis factor receptor binding; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.0%; Score 251.5; DB 1; Length 24.1%; Pred. No. 1.7e-13; tive 61; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLEAVAGE (BY SIMILARITY)
                                                                differentiation; NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P41047; Q61217; Q9R1F2; 01-FRB-1995 (Rel. 31, Created) 15-FBE-1995 (Rel. 31, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> G (IN REF.
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GO; GO:0005164; F:tumor necrosis factor regol GO:0006955; P:immune response; NAS. GO; GO:001316; P:osteociast differentiat: InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF_like.
InterPro; IPR008983; TNF_like.
InterPro; IPR008983; TNF_subf.
ProDom; PD002012; TNF subf.
SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
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                                                                                                                                                                                                                                                             PROSITE; PS00251; TNF 1; FALSE NEG. PROSITE; PS50049; TNF 2; 1.
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SEQUENCE FROM N.A. (ISOFORM FASL).
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317 AA;
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SUBCELLULAR LOCATION: Type II membrane protein (isoform FASL);
                                                                                                          Secreted (isoforms FASL and FASLS).
           STRAIN=C57BL/6;
                                      STRAIN-BALB/c;
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Kayagaki N., Yamaguchi N., Nagao F., Matsuo S., Maeda H., Okumura K., the Fas-ligand and other members Suda T., Nagata S.;
"Generalized Lymphoproliferative disease in mice, caused by a point mutation in the Fas ligand.";
Cell 76:969-976 [1994]. Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G., SEQUENCE FROM N.A. (ISOFORM FASLS).
STRAIN=C3H; TISSUE-Spleen;
MEDLINE=20021684; PubMed=10552956,
Ayroldi E., D'Adamio F., Zollo O., Agostini M., Moraca R.,
Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;
"Cloning and expression of a short Fas ligand: A new alternatively
spliced product of the mouse Fas ligand gene."; CHARACTERIZATION OF VARIANT GLD.

WEDDLINE=96091722; PubMed=1495745;
Hahne M., Peitsch M.C., Irmler M., Schroeter M., Lowin B.,
Rousseau M., Bron C., Remno T., French L., Tschopp J.;
"Characterization of the non-functional Fas ligand of gld mice."; Fenner M.H., Shioda T., Isselbacher K.J., "Mus musculus Balb/c Fas ligand in Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E., Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K., "The mouse Fas-ligand gene is mutated in gld mice and is part of STRAIN=C57B1/6, C3H, MRL, SJL, NOD, NZB, NZW, BALB/c, DBA/1, and 'Polymorphism of murine Fas ligand that affects the biological SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING two amino acide.", Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases. Peitsch M.J., Tschopp J.J.; "Comparative molecular modelling of of the TNF family."; SEQUENCE FROM N.A. (ISOFORM FASL). SEQUENCE FROM N.A. (ISOFORM FASL). MEDLINE=95196085; PubMed=7889405; MEDLINE=97268671; PubMed=9108079; MEDLINE=95388076; PubMed=7544870; int. Immunol. 7:1381-1386(1995). dol. Immunol. 32:761-772 (1995). VARIANTS ALA-184 AND GLY-218. Blood 94:3456-3467(1999). INF family gene cluster." Immunity 1:131-136(1994). **Takahashi**

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37972E2728E0A1CA CRC64; Disease mutation, Polymorphism, Alternative splicing.

CHAIN 1 279 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 6, MEMBRANE FORM. TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 6, SOLUBLE FORM (BY SIMILARITY). CYTOPLASMIC (POTENTIAL). SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) Gaps lymphoproliferation disease phenotype (gld). Gld mice present lymphadenopathy and autoantibody production. The phenotype is recessively inherited. PRINTS; PRO1681; FASLIGAND.
PRINTS; PRO1234; TNECROSISFCT.
PRODOM; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
SMART; ES00221; TNF 1; 1.
PROSITE; PS50049; TNF 2; 1.
Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor; N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL). -> A (IN STRAINS BALB/C AND DBA; E -> G (IN STRAINS BALB/C AND DBA; ENHANCES CYTOTOXICITY). DB 1; Length 279; SIMILARITY: Belongs to the tumor necrosis factor family. 64; Indels Missing (in isoform FasLS) /FTId=VSP 006445. EXTRACELLULAR (POTENTIAL) POLY-PRO. CLEAVAGE (BY SIMILARITY). CYTOTOXICITY) 12.8%; Score 189.5; DB 1 25.8%; Pred. No. 1.9e-08; 50; Mismatches ENHANCES PRO-RICH MGD; MGT:99255; Thisefe.
InterPro; IPR008064; Fas_ligand.
InterPro; IPR006053; TWF abc.
InterPro; IPR006053; TWF family.
InterPro; IPR008983; TWF like.
InterPro; IPR008983; TWF like. EMBL; AF119335; AAD52106.1; -. PIR; A53062; A53062. 31442 MW; U10984; AAB19778.1; -. S76752; AAB33780.1; -. EMBL; U06948; AAA17800.1; -. U58995; AAB02915.1; -. 51; Conservative 279 218 273 Pfam; PF00229; TNF; 1. 279 AA; P01375; 4TSV Local Similarity 218 273 128 79 184 101 **TRANSMEM** DISULFID VARSPLIC SEQUENCE Query Match CARBOHYD CARBOHYD CARBOHYD CARBOHYD VARIANT VARIANT VARIANT DOMAIN NIAMOC DOMAIN DOMAIN EMBL; HSSP; CHAIN EMBL; EMBL; Matches g g ⋧ ਨੋ

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Isold=P41047-2; Sequence=VSP 006445; PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity). DISEASE: A deficiency in this protein is the cause of generalized

Event=Alternative splicing; Named isoforms=2; IsoId=P41047-1; Sequence=Displayed;

ALTERNATIVE PRODUCTS

Name=FasLS

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DKQMVQYIY-KYTSYPDPILLMKSAR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSV 260
                                         202 NQPLNHKVYMRNSKYPEDLVLMEEKRLNYCTT--GQIWAHSSYLGAVFNLTSADHLYVNI 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TNFRSPE/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR1 modulates its effects (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane, Glycoprotein, Signal-anchor.
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TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning, sequencing, and homology analysis of nonhuman primate Fas/Fas-ligand and co-stimulatory molecules."; Immunogenetics 53:315-328(2001).
-!- FUNCTION: Cytokine that binds to INFRSF6/FAS, a receptor that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey) Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae, Cercopithecinae, Cercoebus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Type II membrane protein and secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Lymphocytes;
MEDLINE=21383618; PubMed=11491535;
Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Weiss W.R., Ansari A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: The Soluble form derives from the membrane form by proteolytic processing (By similarity). SIMIDARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                    280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: Homotrimer (Probable).
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InterPro; IRR06053; TNF_abc.
InterPro; IRR06052; TNF family.
InterPro; IRR08983; TNF_like.
InterPro; IRR03636; TNF_subf.
Pfam; PF00229; TNF; 1.
                                                                                                                                261 TNEHLIDMDHEASFFGAF 278
                                                                                                                                                                                260 SOLSLINFEESKTFFGLY 277
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28-FEB-2003 (Rel. 41, Last seq.
28-FEB-2003 (Rel. 41, Last anno
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PRINTS; PRO1234; TNECROSISFCT.
ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF, 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CD95L protein).
TNFSF6 OR FASL OR CD95L.
                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 VYSKVYFRGQ-----SCTNLPLSHKVYMRNSKYPQDLVMMEGKMMS-YCTTGQMWAHSS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYY 183
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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
1Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
(Apoptosis antigen ligand) (APPL) (CD178 antigen).
TNFSF6 OR PASL OR APTILG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 MEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVVYFTNELKQMQDKXSKSGIACFLKEDDS
                           CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68; Gaps
MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Kominidae; Komo.
                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                         12.7%; Score 187; DB 1; Length 28
22.1%; Pred. No. 3e-08;
ive 56; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1). Schaetzlein C.E., Poehlmann R., Philippsen P., Eibel H.; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                     LINKED (GLCNAC. . .) (PU
729EA60067B7D398 CRC64;
                                                                                                                                                                    POLY-PRO. CLEAVAGE (BY SIMILARITY).
                                                                                                            EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 YLGAVENLTSTDHLYVNVSELSLVNFEESQTFFGLY 278
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                                                                                   POTENTIAL
                                                                                                                                                                                                                               POTENTIAL.
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MEDLINE=95105731; PubMed=7528780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=95127560; PubMed=7826947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     int. Immunol. 6:1567-1574(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                        31407 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61; Conservative
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249
259
280 AA;
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                        DOMAIN
TRANSMEM
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Best Local
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                                                                                                               DOMAIN
                                                                                                                                              DOMAIN
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Event=Alternative splicing; Named isoforms=2;
                                                                                                   ALTERNATIVE PRODUCTS:
                     Wilkinson J.;
                                                                                                      Name=1;
                                                                            PROCESSING
     infection.
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TISSUE=Blood,

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

METAUSEDER R.D., Feligold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchench D., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.B., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Girmwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Salska U., Smailus D.E.,

Beneration and initial analysis of more than 15,000 full-length transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development.

TNRRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6FDCR3 meduates its effects.

-!- SUBGNIT: Homotrimer (Probable).
-!- SUBGNIT: Homotrimer (Probable).
-!- SUBCELLUIAR LOCATION: Type II membrane protein. May be released into the extracellular fluid, probably by cleavage form the cell Zeytun A., Nagarkatti M., Nagarkatti P.S.;
"Isolation and characterization of a new naturally occuring variant of human Fas ligand that is expressed only in membrane bound form."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. Mita E., Hayashi N., Tio S., Takehara T., Hijioka T., Kasahara A., Fusamoto H., Kamada T., "Role of Fas ligand in apoptosis induced by hepatitis C virus MEDLINE=98087475; PubMed=9427603; Tanaka M., Itai T., Adachi M., Nagata S.; "Downregulation of Fas ligand by shedding."; Nat. Med. 4:31-36(1998) -!- FUNCTION: Cytokine that binds to INFRSF6/FAS, a receptor that CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TYR-218 AND PHE-275 MEDLINE=97373583; PubMed=9228058; Schneider P., Bedmer J.-L., Holler N., Mattmann C., Scuderi P., Terekikh A., Pettsch M.C., Tschopp J.; "Characterization of Fas (Apo-1, CD95)-Fas ligand interaction.", J. Biol. Chem. 272:18827-18833(1997). Matsumura M., Nakanishi Y., Ohba Y., Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases. Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). Biochem. Biophys. Res. Commun. 204:468-474(1994). MEDLINE=95071350; PubMed=7980502; SEQUENCE FROM N.A. (ISOFORM 2). SEQUENCE FROM N.A. (ISOFORM 1). human and mouse cDNA sequences. SEQUENCE OF 1-10 FROM N.A. TISSUE=Blood; SEQUENCE FROM N.A. TISSUE=Leukocyte;

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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEMBER 6, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                              -!- PTM: N-glycosylated.
-!- PTM: N-glycosylated.
-!- PTM: The soluble form derives from the membrane form by proteolytic processing to proteolytic processing the proteolytic processing the proteolytic processing the proteolytic processing the proteolytic processing the proteolytic area as cause of autoimmune lymphoproliferative syndrome (ALPS) [MIM:601859]; also known as Canale-Smith syndrome (CSS). ALPS is a childhood syndrome involving hemolytic anemia and thrombocytopenia with massive involving hemolytic anemia and thrombocytopenia with massive lymphagenopathy and splenomegaly.
-!- SIMILARITY: Belongs to the turn necrosis factor family.
-!- DATABASE: NAME=PROW; NOTE=PROW 2:59-69(2001); WWW.ncbi.nlm.nih.gov/prow/guide/333879674_g.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
STSQMHTASSL -> ATPVHPLKKRS (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
                                               [sold=P48023-2; Sequence=VSP_006443, VSP_006444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM) 601859; -
G0, G0008897; C:integral to plasma membrane; TAS.
G0, G0:0005102; F:receptor binding; TAS.
G0; G0:0007267; F:receptor binding; TAS.
G0; G0:0007267; F:receptor binding; TAS.
G0; G0:000717; F:induction of apoptosis; TAS.
G0; G0:0007165; F:signal transduction; TAS.
InterPro; IPR008064; FAS. ligand.
InterPro; IPR008065; TNF abc.
InterPro; IPR008983; TNF—Iike.
InterPro; IPR008983; TNF—Like.
FAM: PRO; IPR008983; TNF—Like.
PRINTS; PRO1681; FASLIGAND.
PRINTS; PR01281; FASLIGAND.
PRINTS; PR01281; TAF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012; TNF aubf: IPR0002012
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IsoId=P48023-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X89102; CAA61474.1; -. EMBL; U08137; AAC50071.1; -. EMBL; U11821; AAC50124.1; -.
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HSSP; P01375; 1TNF.
Genew; HGNC:11936; TNFSF6.
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DISULFID
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CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 ---AHLT---GKSNSRSMP------LEWEDT-YGIVLLSGVKYKKGGLVINETG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 FYXIYSQTYFRFQEEIKENTKNDKQMVQYIY-KYTSYPDPILLMKSARNS-----CWSK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 LYFVYSKVYFRGQ-----SCNNLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQMWAR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 MEVQGGPSLGQTCVLIVIFTVLLQSLCVAV---TYVYFTNELKOMODKYSKSGIACFLKE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kirii Y., Inoue T., Yoshino K., Submitted (MOV-1999) to the EMBL/Genbank/DDBJ databases.

-! FUNCTION: Cytokine that binds to TNRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TNRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3 modulates its effects (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                      /FTId=VSP_006444.
P-D,F.K: LOWERS BINDING TO THFRSF6 AND REDUCES CYTOTOXITY MORE THAN 100-FOLD.
Y->F,R: LOWERS BINDING TO THFRSF6 AND ABOLISHES CYTOTOXITY.
F->L: ABOLISHES BINDING TO THFRSF6 AND CYTOTOXITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca mulatta (Rhegus macaque),
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
Macaca nemestrina (Pig-tailed macaque).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning, sequencing, and homology analysis of nonhuman primate Fas/Fas-ligand and co-stimulatory molecules."; Immunogenetics 53:315-328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=M.mulatta; TISSUE=Lymphocytes;
MEDLINE=21383618; PubMed=11491535;
Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Weiss W.R., Ansari A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.6%; Score 186; DB 1; Length 281; 22.1%; Pred. No. 3.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----SSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFFGLY 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82; Indels
                                                                                                                                                                                                                                                                                                                                                               281 AA; 31485 MW; A8A6EB358246E9BB CRC64;
    (in isoform 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 OIGHPSPPPE-----KKELRKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54; Mismatches
         Missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 22.1 es 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CD95L protein).
TNFSF6 OR FASL OR CD95L.
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                                                                                                                                                                                  218
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                                                                                           206
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                                                                                           206
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128
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28-FEB-2003 (Re
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                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
VARSPLIC
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                                                                                                                                                                                  MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 YWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 AHITGTRGRSWTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYY 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 IYSQTYFRFQEEIKENTKNDKQMVQYIY-KYTSYPDPILLMKSARNSCWSKDABYGLYSI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                        TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 6, SOLUBLE FORM (BY SIMILARITY). CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 MEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
         SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68;
                                             proteolytic processing (By similarity).
                       similarity). PTM: The soluble form derives from the membrane form by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.5%; Score 185; DB 1; Length 280; 22.1%; Pred. No. 4.4e-08; Live 56; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F0B284D61A132EB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S -> P (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRO-RICH
Homotrimer (Potential)
                                                                                                                                                                                                                                          HSSP; PO1375; 4TSV.
InterPro; IPR008064; Fas ligand.
InterPro; IPR008063; TNF abc.
InterPro; IPR008053; TNF family.
InterPro; IPR008983; TNF limily.
InterPro; IPR008983; TNF limily.
InterPro; IPR008983; TNF limily.
PRIMTS; PR01681; FASLIGAND.
PRINTS; PR01681; FASLIGAND.
                                                                                                                                                                                          EMBL; AF344856; AAK37539.1; -.
                                                                                                                                                                                                       EMBL, AB035138; BAA90294.1; -. EMBL, AB035139; BAA90295.1; -. EMBL, AB035140; BAA90296.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 AA; 31367 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101
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129
232
183
249
259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
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                                                                                                                                                                                                                                                   28-FEE-2003 (Rel. 41, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-
                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 5, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 5, SOLUBLE FORM (BY SIMILARITY).
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                             proteolytic processing (By similarity).
-!- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM0207; TNF; I. PROSITE; PS00251; TNF 1; 1. PROSITE; PS50049; TNF 2; 1. CYtokine; Transmembrane; Glycoprotein; Signal-anchor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0016021; C:integral to membrane; ISS. GO; GO:0005174; F:CD40 receptor binding; ISS. GO; GO:0045174; F:CD40 receptor binding; ISS. GO; GO:0045106; F:D-cell proliferation; ISS. GO; GO:0005954; P:inflammatory response; ISS. GO; GO:0007159; P:leukocyte cell adhesion; ISS. GO; GO:0007159; P:platelet activation; ISS. GO; GO:0030168; P:platelet activation; ISS. InterPro; IPR003053; TNF 5.
InterPro; IPR003983; TNF family.
InterPro; IPR00383; TNF like.
Pfam; PF00229; TNF; 1.
PRINTS; PR01702; CD40LIGAND.
 243 YLGAVFNLTSADHLYVNVSELSLVNFEESQTFFGLY 278
                                                                 272 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD008600; TNF 5; 1.
ProDom; PD002012; TNF subf; 1.
                                                                                                                                        L) (CD154 protein).
TNFSF5 OR CD40LG OR CD40L.
                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272
111
229
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44
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111
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110
190
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                                                              CHICK
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DISULFID
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                                                TNF5_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 QVSF-----CTKAAASAPFTLYIYLYLPMEEDRLLMKGLDTHSTS-TALCELQSIREGG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 PÇWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGP------QRVAAHIT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 DCEKVLKGFQDLQCKD--RTASEELPKFEMHRGHEHPHLKSRNETSVAEEKROPIATHLA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTRGRSNTLSSPNSKNEKALGRKINSW-ESSRSGHSFLSNLHLRNGELVIHEKGFYYIYS 186
                                                                                                                                                                                                                                                                                                                          16 CVLIVIFTVLLQSLCVAVTYVYFTNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNS 75
                                                                                                                                                                                                                                                                                                                                                                                                             83
                                                                                                                                                                                                                                                                                                                                                                           26 CFLSVFMVV--QTIGTVLFCLYLHMKMDKMEEVLSLNEDYIFLRKVQKCQTGEDQKSTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tsuyuki S., Kono M., Bloom B.T.; "Cloning and potential utility of porcine Pas ligand: overexpression in porcine cells protects them from attack by human cytolytic cells."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 QTYPRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhu N., Young Y.; "Molecular cloning and characterization of porcine Fas ligand cDNA."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muneta Y., Shimoji Y., Inumaru S., Mori Y.;
"Molecular cloning, characterization, and expression of porcine Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. SEQUENCE TISSUE-THYMOCYTES; STAIN=LADAGRACE x Large Yorkshire white; TISSUE-THYMOCYTES; MEDLINE-21653191; PubMed=11792426; Motegi-1shiyama.Y., Nakajima Y., Hoka S., Takagaki Y.; Motegi-1shiyama.Y., Nakajima Y., Hoka S., Takagaki Y.; Motegi-1shiyama.Y., Borcine Fas-ligand gene: genomic sequence analysis and comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa (Pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Immunol. 38:581-586(2002).
-!- FUNCTION: Cytokine that binds to INFRSF6/FAS, a receptor that
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor necrosis factor ligand superfamily member 6 (FAS antigen
                                                                                                                                                                                     Length 272;
                                                                                                                                                                                                                                                         48; Mismatches 119; Indels
                                                                                                             30832 MW; 8CD0338A924E044B CRC64;
                                                                                                                                                                                 12.4%; Score 184; DB 1; 25.4%; Pred. No. 5.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 IFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9BEA8; Q95M04; Q95M10; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interferon Cytokine Res. 21:305-312(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       282 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Guanxi bama miniature pig;
                                                                                                                                                                                                                Local Similarity 25.4%
nes 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
   124 1
146 1
251 2
272 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with human gene.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFSF6 OR FASL.
   CARBOHYD
                                     CARBOHYD
                                                                       CARBOHYD
                                                                                                             SEQUENCE
                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 QLRQLVRKMILRISEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 NEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKN 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 DKQMVQYIYKYTS-YPDPILIMK-SARNSC-----WSKDAEYGLYSIYQGGIFELKENDR 255
transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TYRSPSF/FRS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TYRSF6B/DCR3 modulates its effects (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                      SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOLUBLE FORM (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00251; TNF 1; 1.
PROSITE; PS50049; TNF 2; 1.
Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL).

F-LINKED (GLCNAC. .) (POTENTIAL).

F -> L (IN REF. 4).

T -> P (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40;
                                                                                                                                                                     proteolytic processing (By similarity). SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                      PTM: The soluble form derives from the membrane form by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 182; DB 1; Length 282; Pred. No. 7.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31756 MW; 6743DAA1145671FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEMBER 6, MEMBRANE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; F01375; 4TSV.
InterPro; IPR008064; Fas ligand.
InterPro; IPR006052; TNF_abc.
InterPro; IPR006052; TNF_family.
InterPro; IPR008983; TNF_like.
PterPro; IPR008983; TNF_like.
Pfam; PF00229; TNF; I.
PRINTS; PR01681; FASLIGAND.
PRINTS; PR01234; TNECROSTSFCT.
ProDom; PD002012; TNF I.
SWART; SM00207; TNF; I.
                                                                                          SUBUNIT: Homotrimer (Probable)
                                                                                                                                                                                                                                                                                                                                      EMBL, AB027297, BAB40919.1; -.
EMBL, AR03834; AAK5649.1; -.
EMBL, AF397407, AAK84408.1; -.
EMBL, AB069764; BAB64291.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.3%;
27.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55; Conservative
                                                                                                                         similarity).
INDUCTION: By IL-18.
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103
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131
234
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251
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57
282 AA;
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Best Local Similarity
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TRANSMEM
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205 NQPLSHKVYTRNSRYPQDLVLMEGKMMNYCTTGQMWAR-----SSYLGAVFNLTSADH 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Of the tunner, the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of transfer of transfer of the transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of transfer of tra
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PROSITE; PS00251; TNF 1; 1.

PROSITE; PS50049; TNF 2; 1.

CYTCKING; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.

CHAIN 1 278 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY

MEMBER 6, MEMBRANE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES, KIDNEY AND LUNG.
-! INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.
-! PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
-! SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94084792; PubMed=7505205;
Suda T., Takahashi T., Golstein P., Nagata S.;
"Molecular cloning and expression of the Fas ligand, a novel member
                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Tumor necrosis factor ligand superfamily member 6 (FAS antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumor necrosis factor family.";
                                                         256 IFVSVTNEHLIDMDHEASFFGAF 278
                                                                                               258 LYVNVSELSLVNFEESKTFFGLY 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR008064, Fas_ligand.
InterPro; IPR006053; TNF abc.
InterPro; IPR006052, TNF family.
InterPro; IPR008993; TNF like.
InterPro; IPR003636; TNF like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO1259; TNF; 1.
PRINTS; PRO1261; FASLIGAND.
PRINTS; PRO1244; TNECROSISFOT.
SWART; SM002012; TNF; Subf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U03470; AAC52129.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ligand).
TNFSF6 OR FASL OR APTILG1.
                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P01375; 4TSV
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                                                                                                                                                                                                                                                                              RAT
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Cell 75
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TN15_HUMAN
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                                                                                                                                                            8
                                                                                                                                                                             100 ISTVQEKQQNISPLVRERGPQRVAAHITGT-RGRSNTLSSPNSKNEKALGRKINSWESSR 158
                                                                                                                                                                                             VSSFEKQIANPSTPSETKKPRSV-AHLTGNPRSRSIPL------EWEDT- 162
                                                                                                                                                                                                                                163 YGTALISGVKYKKGGLVINEAGLYFVYSKVYFRGQ-----SCNSQPLSHKYYMRNFKYP 216
                                                                                                                                                                                                                                                                        217 GDLVLMEEKKLNYCTT--GQIWAHSSYLGAVFNLTVADHLYVNISQLSLINFEESKTFFG 274
                                                                                                                                                                                                                    159 SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY-KYTSYP 217
                                                                                                                                                                                                                                                           218 DPILLMKSAR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276
                                                                                                                                                                                                                                                                                                                                                                  TIMES BOVIN STANDARD; PRT; 261 AA.

F91749;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-FEB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (TNF-related activation protein) (TRAP) (T cell antigen GP39).

TNFSF5 OR CD40LG OR CD40L.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLUAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).
         CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                            Gaps
SOLUBLE FORM (BY SIMILARITY).
                                                                                  POLINIAL GLUNAC. ..) (POTENTIAL).
N-LINKED (GLUNAC. ..) (POTENTIAL).
N-LINKED (GLUNAC. ..) (POTENTIAL).
                                                                                                                                                           29;
                                                                                                                                       Score 177.5; DB 1; Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteolytic processing (By similarity). SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                           64; Indels
                                                       POLY-PRO.
CLEAVAGE (BY SIMILARITY).
POTENTIAL.
                                                                                                        N-LINKED (GLCNAC. . .) (PC
2898E18A862CEAC6 CRC64;
                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                  Pred. No. 1.8e-07;
                                                                                                                                                          39; Mismatches
                                                PRO-RICH
                                                                                                                    31140 MW;
                                                                                                                                      12.0%; 27.5%;
                                                                                                                                                          50; Conservative
                                    278
69
58
127
230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovidae; Bovinae; Bos.
                                                                 126
199
116
247
257
278 AA;
                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                 277 AF 278
                                                                                                                                                                                                                                                                                                                     275 LY 276
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                                                                  SITE
DISULFID
                                                                                     CARBOHYD
CARBOHYD
                                                                                                                                                                                                 121
                TRANSMEM
                                                                                                                  SEQUENCE
                                                                                                                                     Query Match
                                                                                                          CARBOHYD
                                                                                                                                                 Local
                                     DOMAIN
                                                        DOMAIN
                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 YWDPNDEESMNS--PCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 VAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSN--LHLRNG-ELVIHE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 KGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: SMOOZO1; TNF 1.

PROSITE: PSSO049; TNF 1; 1.

PROSITE; PSSO049; TNF 2; 1.

Cytokine; Transmembrane; Glycoprotein; Signal-anchor.

Cytokine; Transmembrane; Glycoprotein; Signal-anchor.

MEMBER 5, MEMBRANE FORM.

MEMBER 5, MEMBRANE FORM.

MEMBER 5, MEMBRANE FORM.

MEMBER 5, MEMBRANE FORM.

MEMBER 7, MEMBRANE FORM.

MEMBER 7, MEMBER 1, MEMBRANE FORM.

MEMBER 7, MEMBER 1, MEMBER 1, MEMBER 1, MEMBER 1, MEMBER 1, MEMBER 1, MEMBER 2, MEMBER 3, MEMBER 1, MEMBER 1, MEMBER 1, MEMBER 2, MEMBER 1, MEMBER 2, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER 3, MEMBER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 IORCHKGEGSLSLINCEEIRSRFEDLV-KDIMQNKE-----VKKKEKNFEMHKGDQEPQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 15 (Vascular endothelial cell growth inhibitor) (TNF ligand-related molecule 1).
TNFSF15 OR VEGI OR TL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
11.1%; Score 164; DB 1; Length 26
Best Local Similarity 25.9%; Pred. No. 2.2e-06;
Matches 72; Conservative 52; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLEAVAGE (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 QQSIHLGGVFELQSGASVFVNVTDPSQVSHGTGFTSFG 257
                                                                                                                                                                                                                                               HSSP: P29965; JALY.

GO; GO:0016021; C:integral to membrane; ISS.
GO; GO:0015174; F:CD40 receptor binding; ISS.
GO; GO:000174; F:CD40 receptor binding; ISS.
GO; GO:000159; P:inflammatory response; ISS.
GO; GO:000159; P:inflammatory response; ISS.
GO; GO:000168; P:platelet activation; ISS.
GO; GO:000168; P:platelet activation; ISS.
InterPro; IPR006052; TNF 5.
InterPro; IPR006052; TNF 5.
InterPro; IPR008983; TNF 1ike.
InterPro; IPR008983; TNF 1ike.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 AA.
         and this statement is not removed.
modified and this statement is not removentities requires a license agreement (Soor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 N-
29242 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD008600; TNF 5; 1.
PD002012; TNF subf; 1.
                                                                                                                                                                              EMBL; Z48469; CAA88363.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01702; CD40LIGAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261
113
218
                                                                                                                                                                                                                        PIR; S53090; S53090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TN15 HUMAN 095150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom;
ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
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us-10-662-429-2.rsp

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IN14 HUMAN
                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license egreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 TVVITKVTDSYPEPTQLLMGTKSVC----EVGSNWFQPIYLGAMFSLQEGDKLMVNVSD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 WESSRSGHSFLSN-LHLRNGELVIHEKGFYYIYSQTYFRFQ----EEIKENTKUDK--QM 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 WE-HELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDSI 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 VQYIYKYT-SYPDPILLMKSARNSCWSKDAEYG---LYSIYQGGIFELKENDRIFVSVTN 262
                                                       SEQUENCE FROM N.A.
TISSUB-SUMBALIZED vein;
MEDLINE-99091541; PubMed-9872942;
Zhai Y., Ni J., Jiang G.-W., Lu J., Xing L., Lincoln C., Carter K.C.,
Zhai Y., Ni J., Yu G.-W., Lu J., Aggarwal B.B., Ruben S.,
Li L.-Y., Gentz R., Yu G.-L.,
"VEGI, a novel cyrckine of the tumor necrosis factor family, is an angiogenesis inhibitor that suppresses the growth of colon carcinomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Type II membrane protein (Probable).
IISSUE SPECIFICITY: Specifically expressed in endothelial cells.
                                                                                                                                                                  FASEB J. 13:181-189(1999).
-!- FUNCTION: Inhibits vascular endothelial growth and angiogenesis
                                                                                                                                                                                                                                          Detected in placenta, lung, kidney, skeletal muscle, pancreas, spleen, prostate, small intestine and colon. SIMILARITY: Belongs to the tumor necrosis factor family.
          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL.)
N-LINKED (GLCNAC. . .) (POTENTIAL.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCB83BA7EE673B98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 604052; -.

GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:00051102; F:receptor binding; TAS.
GO; GO:0000074; P:regulation of cell cycle; TAS.
InterPro; IPR006053; TNF abc.
InterPro; IPR008083; TNF_family.
InterPro; IPR008983; TNF_family.
InterPro; IPR008983; TNF_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.8%; Score 160; DB 1; 35.3%; Pred. No. 2.7e-06; tive 24; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                      -!- SUBUNIT: Homotrimer (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 EHLIDMDHE-ASFFGAFLV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 ISLVDYTKEDKTFFGAFLL 174
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF039390; AAD08783.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR01234; TNECROSISFCT.
ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20131 MW;
                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:11931; TNFSF15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125
56
152
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Homo sapiens (Human)
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85 1
56
152 1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      P50591; 1D0G.
                                NCBI_TaxID=9606;
                                                                                                                                                                                            (in vitro)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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**X. TESUBLE-EXTAIN;

**REDLIFE-22388257; PubMed=12477932;

**REDLIFE-22388257; PubMed=12477932;

**RIAUSE-22388257; PubMed=12477932;

**RIAUSE-R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

**Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

**Stapleton M., Soares M.E., Bonaldo M.F., Carninci P., Prange C.,

**Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

**Richards S., Worley K.C., Hale S., Garcina A.M., Gay L.J., Hulyk S.W.,

**Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

**Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

**Altkring M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

**Altkring M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

**Altkring M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

**Altkring M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

**Altkring M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

**Altkring M., Schein J.E., Jones S.J.M., Marra M.A.,

**Achriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

**A Cherertion and initial analysis of more than 15,000 full-length

**Thuman and mouse CoNA sequences.",

**Althuman and mouse CoNA sequences.",

**Althuman and mouse CoNA sequences.",

**Althuman and mouse CoNA sequences.",

**Althuman and mouse CoNA sequences.",

**Althuman and mouse CoNA sequences.",

**Althuman and mouse CoNA sequences.",

**Althuman and mouse CoNA sequences.",

**Althuman and mouse CoNA sequences.",

**Althuman and mouse CoNA sequences.",

**Althuman and mouse CoNA sequences.",

**Althuman and mouse CoNA sequences.",

**Althuman and mouse CoNA sequences.",

**Althuman and mouse CoNA sequences.",

**Althuman and mouse CoNA sequences.",

**Althuman and mouse CoNA sequences.",

**Althuman and mouse CoNA sequences.",

**Althuman and mouse CoNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "LIGHT, a new member of the TNF superfamily, and lymphotoxin alpha are
ligands for herpesvirus entry mediator.";
Immunity 8:21-30(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=98122340; PubMed=9462508;
Mauri D.N., Ebner R., Montgomery R.I., Kochel K.D., Cheung T.C.,
Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.G.,
TN14 HUMAN STANDARD;
043557; 075476; Q8WVF8; Q96LD2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor ligand superfamily member 14 (Herpesvirus entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Granger S.W., Butrovich K.D., Houshmand P., Edwards W.R., Ware C.F., "Genomic characterization of LIGHT reveals linkage to an immune response locus on chromosome 19913.3 and distinct isoforms generated by alternate splicing or proteolysis.", Immunol. 167:5122-5128(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Truneh A., Young P.R.;
"Herpesvirus entry mediator ligand (HVEM-L), a novel ligand for
HVEM/TR2, stimulates proliferation of T cells and inhibits HT29 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98438532; PubMed=9765287;
Harrop J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J., Tan K.B., Dede K., Spampanato J., Silverman C., Hensley P., Difrinzio R., Emery J.G., Deen K., Eichman C., Chabot-Fletcher M., Truneh A., Young P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Cytokine that binds to TNFRSF9/LTBR. Binding to the decoy receptor TNFRSF6B modulates its effects. Activates NFRS, stimulates the proliferation of T cells, and inhibits growth of the adenocarcinoma HT-29. Acts as a receptor for Herpes simplex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 2), AND PROCESSING. MEDLINE=21528948; PubMed=11673523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cowth.";
. Biol. Chem. 273:27548-27556(1998).
                                                                                                                                                                                                                                                                                                                                                                                                             TNFSF14 OR LIGHT OR HVEML. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                  mediator-ligand) (HVEM-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ware C.F.;
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SUBUNIT: Homotrimer.
SUBCELLULAR LOCATION: Type II membrane protein and secreted (isoform 1); Cytoplasmic (isoform 2).
ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

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                                                                                                  Isoid-043557-1; Sequence=Displayed;
Name=2; Synonyms=LiGHT delta-TM;
Isoid-043557-2; Sequence=VSP 006452;
Isoid-043557-2; Sequence=VSP 006452;
FOUND IN THE BRAIN: WEADOMINATILY EXPRESSED IN THE SPLEEN BUT ALSO FOUND IN THE BRAIN: WEACHY EXPRESSED IN PERIPHERAL LYMPHOID INSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND KIDNEY, AND NO EXPRESSION SEEN IN FETAL TISSUES, ENDOCRINE GLANDS, OR
                                                                                                                                                                                                                                         PTM: N-glycosylated.
PTM: The soluble form of isoform 1 derives from the membrane form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.8%; Score 159.5; DB 1; Length 240;
23.8%; Pred. No. 4.6e-06;
tive 41; Mismatches 66; Indels 63; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 14, SOLUBLE FORM.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                       by proteolytic processing.
SIMILARITY: Belongs to the tumor necrosis factor family.
CAUTION: Ref. 4 sequence differs from that shown due to a frameshift in position 178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49D0BF67E1390B39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.

N-LINKED (GLCNAC. .).

Missing (in isoform 2).

/FIId=VSP 006452.

L -> V (IN REF. 4).

E -> K (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEMBER 14, MEMBRANE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane, Glycoprotein; Signal-anchor;
                                                                                                                                                                                                           NONHEMATOPOIETIC TUMOR LINES.
INDUCTION: UPREGULATED AFTER T-CELL ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLEAVAGE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 604520; ...
GO; GO:0005102; F:receptor binding; TAS.
GO; GO:0006917; P:induction of apoptosis; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR006053; TNF abc.
InterPro; IPR006053; TNF family.
InterPro; IPR008983; TNF family.
InterPro; IPR008983; TNF family.
Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF036581; AAC39563.1; -.
EMBL; AF064090; AAC25169.1; -.
EMBL; AY02861; AAX028610.1; -.
EMBL; BC018058; AAX18058.1; ALT_FRAME.
HSSP; P01375; 4TSV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01234; TNECROSISFCT.
ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF 1; FALSE_NEG.
PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26351 MW;
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187
102
73
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58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
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53; Conservative

Best Local Similarity Matches 53; Conserv

Query Match

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79 QVKWQLRQLVRKMILRTSEETISTVQEKQQN-ISPLVRERGPQRVAAHITGTRGRSNTLS 137
                           138 SPNSKNEKALGRKINSWESSRSGHSFLSNIHLRNGELVIHEKGFYYIYSQTYFRFQEEIK 197
                                                                                                                                                                           198 ENTKNDKOMVQY------IYKYT-SYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                 147 ------VQLGGVGCPLGLASTITHGLYKRTPRXPEELELLVSQQSPCGRATSSSRVW 197
                                                                                                                             -----LLWE-TQLGLAFLRGLSYHDGALVVTKAGYYIISK------
                                                                                                                                                                                                                                                                                   198 WDSSFLGGVVHLEAGEEVVVRVLDERLVRLRDGTRSYFGAFWV 240
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Search completed: March 23, 2004, 09:05:48 Job time : 18 secs us-10-662-429-2.rspt

Page 1

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1 MAWKEVQGGPSLGQTCVLIV.....NEHLIDMDHEASFFGAFLVG 281
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                    - protein search, using sw model
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2: sp_bacteria:*
3: sp_tungi:*
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5: pp_nwan:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

δī	Description	Q8k3q0 rattus norv	O7t1f2 gallus gall	07zyx9 brachydanio	090wt9 gallus gall	09ddz5 brachydanio	O7tmv9 mus musculu	Q8k3y8 mus musculu	0861w5 felis silve	O9wv90 marmota mon	Q80yz0 mus musculu	08k3v7 rattus norv	OBnfe9 homo sapien	O8mj19 macaca mula	07t2d3 cyprinus ca	O70332 memocricetu	Q8aw02 cyprinus ca
SUMMARIES	ID	Q8K3G0	Q7T1F2	6XXZLO	Q90WT9	09DDZ5	Q7TMV9	QBK3Y8	Q861W5	09WV90	QBOYZO	Q8K3Y7	Q8NFE9	Q8MJ19	Q7T2Q3	070332	Q8AW02
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	Query Match Length DB	287	304	317	287	214	279	252	280	169	252	252	251	154	227	216	231
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	Result No.	н	71	Ю	4	'n	φ	7	80	σ	10	11	12	13	14	15	16

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Ouery Match 65.2%; Score 963; DB 11; Length 287; Best Local Similarity 67.7%; Pred. No. 2.7e-72; Matches 189; Conservative 29; Mismatches 51; Indels 10; Gaps

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111 113 113 113 113 113 113 113 113	1. 22, [. 22,]. 25, [. 22,]. 25, [. 25,]. 26, [. 26,]. 26, [. 26,]. 26, [. 26,]. 26, [. 26,]. 26, [. 26,]. 26, [. 26,]. 26, [. 26,]. 27, [. 26,].
11522 22222 22222 22222 22222 22222 2222 2222	ELIMINARY; TEMBLE-1. 22, Cr. TEMBLE-1. 22, La. PEMBLE-1. 25, La. PEMBLE-1. 25, La. PEMBLE-1. 25, La. PEMBLE-1. 25, La. Tazoa, Chordata; Tazoa, Chordata; Total Rodentia; N.A. N.A. N.A. Giegerich G.; Giegerich G.; Giegerich G.; Giegerich G.; Giegerich G.; AAM89797.1; " Total Tare S. P.; tumor necrosis P.; Futuor necrosis P.; Futuor necrosis P.; Futuor necrosis P.; Tumel Lamilian Tur;
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                                                                        68 N----DEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQ-EKQQNISPLVRERGPQ- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYI 184
                                                                                                         185 YSQTYFRFQE--EIKENTKND----KQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYG 238
                                                                                                                               189 YSQTYYRFKEAKEASKTVSKDGGRIKQMVQYIYKYTSYPDPILLMKSARNSCWSREAEYG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIH 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 EKGFYYIYSQTYFRFQEE----IKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCW 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 QTGFYYIYSQTYFRFRENEDEDSGLLERIKNPKQLVQYIYKLTNYPDPILLMKSARTSCW 241
            WDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 GGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDSYWDP 67
                                                                                                                                                                                                                                                                                                                                                                                                              TISSTE=Spleen;
Sayed A.A., Horluchi H.H., Furusawa S., Matsuda H.;
Sayed A.A., Horluchi H.H., Furusawa S., Matsuda H.;
Sayed A.A., Horluchi and Charachterization of Chicken TWF-Superfamily
Lidentification and Charachterization of Chicken TWF-Superfamily
Lidentification and Grandential of Twor Necrosis Factor Related Apoptosis
Inducing Ligand TRAIL).";
Submitted (JUL-2003) to the EWBL/GenBank/DDBJ databases.
EMBL; ABI14678; BAC79267.1;
SEOUENCE 304 AA; 34658 MW; DFC128B517747C96 CRC64;
                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 SKKAEYGLYSVYQGGVFQLKREDRIFVSVSNSDIVDMDKEASFFGAFMI 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 809.5; DB 13; Length 304;
; Pred. No. 1.9e-59;
45; Mismatches 65; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
                                                                                                                                                                                                                                                                                                        Tumor necrosis factor related apoptosis inducing ligand.
                                                                                                                                                                       249 LYSIXQGGLFELKENDRIFVSVTNEHLMDLDHEASFFGA 287
                                                                                                                                                         239 LYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGA 277
                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                             304 AA.
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01-JUN-2003 (TrEMBLrel. 24, Created)
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Best Local Similarity 55.4%;
Matches 160; Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
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01-0CT-2003
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                                                                                                                                                                                                                                             O7T1F2
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Q7ZYX9
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Q7T1F2
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98 LFGEPCMKLAEGIKAYISKVTDSIISKQTLHAARTRTHSYNTTGSKFMTTV-----MQ 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 RVAAHITGTRGRSNT----LSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 IHEKGFYYIYSQTYFRF-QEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKD 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 VPQDGRYYLYSQVYFRYPSPSDSDQSSVSHQLVQCIYKKTSYLNPIQLLKGVGTKCWAPD 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
1TMF-related apoptosis inducing ligand.
Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves; Neognathae, Galliformes; Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 LIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF----LKEDDSYMDPND-EE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 MVIVVVIQIASTTGLFVYLNMSLSQVKSQGVTEELRČLGLLNVLGKDQDI -- PEDLAQ
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annoctation update)
51-OCT-2003 (TrEMBLrel. 25, Last annoctation update)
Similar to tumor necrosis factor (Ligand) superfamily, member 10.
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Bridgham J.T., Johnson A.L.,
"TNF-related apoptosis inducing ligand (TRAIL) expression in the hen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13; Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0016020; C:membrane; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:000655; P:immune response; IEA.
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF_like.
InterPro; IPR008636; TNF_aubf.
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HSSP; O35235; IIQA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.6%; Score 334.5; DB 13; Length
29.2%; Pred. No. 8.7e-20;
ive 55; Mismatches 113; Indels
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                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317 AA; 35465 MW; 68F76BC1A40DCE9F CRC64;
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ProDom; PD002012; TNF; 1.
SMART; SM00207; TNF; 1.
SROSTE; PS50049; TNF 2; 1.
SEQUENCE 317 AA; 35465 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; BC044336; AAH44336.1;
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ses 83; Conservative
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124 GKPSAHLIFRPQNPAQDGSSRRFGNLS-----QSCRHALTRWEDS-TIHSHLQNITYR 175
                                                                                                                                                                                                                                                                                                                                                        67 PNDEESM-NSPCWQVKWQLRQLVRKMILRTSEETI--STVQEKQQ---NISP-LVRERGP 119
                                                                                                                                                                                                                                                                                                                                                                                         68 SNLEELISNOSC----LKLANTIKAYVATVTENVISRSVVNEAOKSYFNISEGOVATKTL 123
                                                                                                                                                                                                                                                                                                                                                                                                                             120 QRVAAHI------TGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 NGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 DGRLRVNQAGKYYVYSQIYFRYSRDGARASVPQLVQCINWKTSYSQPILLLKGVGTKC 235
                                                                                                                                                                                                                                                                                 18 LIVIFTVLLQ--SLCVAVTYVYFT-----NELKQM--QDKYSKSGIACFLKEDDSYWD 66
                                                                                                                                                                                                                                                                                                                     8 LLHAFSLELÖLLPLCTAPEWAEGTWSQALQGNAFPRLKAQSQGSSEELRCLQLINQQQEG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Danio rerio)
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                  39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bobe J., Goetz F.W.;
"Molecular cloning and expression of a TNF receptor and two TNF ligands in the fish ovary.";
Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).
ENBL; AF250041; AAG47640.1; -.
ENBL; AF25091; 1D20.
ZFIN; ZDB-6501; LD20.
ZFIN; ZDB-6501; LD20.
                                                                                                                                                                                                                DB 13; Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0016020; C:membrane; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 WSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 307.5; DB 13; Length
; Pred. No. 1.4e-17;
46; Mismatches 110; Indels
                                                                                                                                                          150049; TNF 2; 1.
287 AA; 32092 MW; DB06E1C95087B108 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24093 MW; 98C002474FF691AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0006955; P:immune response; IEA.
InterPro; IPR006652; TNF family.
InterPro; IPR008983; TNF like.
InterPro; IPR003636; TNF subf.
Pfam; PF00229; TNF; 1.
ProDom; PD002012; TNF subf.
PR051TE; SM0207; TNF; 1.
GO; GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
                InterPro; IPR006053; TNF abc:
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF like.
InterPro; IPR008983; TNF like.
PRAM; PF00229; TNF; 1.
PRAM; PF00229; TNF; 1.
SMART; SW01234; TNEROSISFT.
ProDom; PD002012; TNF aubf; 1.
SMART; SW00207; TNF; 2; 1.
SROSITE; PS50049; TNF; 2; 1.
SEQUENCE 287 AA; 3Z092 MW; DB00
                                                                                                                                                                                                              ch 20.8%;
1 Similarity 32.3%;
93; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 16, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRAIL-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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20.7%; Score 305.5; DB 13; Length 214;

Query Match

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RECENTE RECORDING: TISSUE=Hematopoietic Stem Cell;

KRAIN-GSTBL/GNCT; TISSUE=Hematopoietic Stem Cell;

KRAIN-GSTBL/GNCT; TISSUE=Hematopoietic Stem Cell;

KRAIN-GSTBL/GNCT; TISSUE=Hematopoietic Stem Cell;

KRAUSHER R.D., Colling F.S., Magner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Jenger C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R Richards S., Wolfer W., Sodergen B.J., Lu X., Gibbs R.A.,

R Richards S., Wolfer W., Sodergen B.J., Lu X., Gibbs R.A.,

R Hilalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

RA Blakeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Marra M.J.,

R Marra M.A.,

Nobes S.J., Marra M.A.,

R Menneration and initial analysis of more than 15,000 full-length human
                                                                                                   106 RVPQDGRYXLYSQVYFRYPSPSDSDQSSVSHQLVQCIXKKTSYLNPIQLLKGVGTKCWAP 165
                                                                                                                                                              175 VIHEKGFYYIYSQTYFRF-QEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 OLROLVRKMILRTSEETISTVQEKQQNISPLVRERGPORVAAHITGTRGRSNTLSSPNSK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 DKQMVQYIY-KYTSYPDPILLMKSAR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 QRVAAHITGTRGRSNT----LSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 NEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 SIPL-----EWEDI-YGTALISGVKYKKGGLVINETGLYFVYSKVYFRGQ-----SCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse),
Sukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.5%; Score 184.5; DB 11; Length 279; llarity 25.3%; Pred. No. 2.4e-07; Conservative 51; Mismatches 64; Indels 33;
                                                                                                                                                                                                                                                                                        166 DAEYALHSVYQGGLFELRAGDEVFVSVSSPTWVYGEDSSSYFGAF 210
                                                                                                                                                                                                                                                               234 DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 279 AA; 31416 MW; C2972E2728FBBB7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=CS7BL/6NCr; TISSUE=Hematopoietic Stem Cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
37.6%; Pred. No. 1.4e-17;
ive 37; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                              279 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Matches 50; Conserv
  Best Local Similarity
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                        Matches
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08K3Y8; **Q8K3Y8**

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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                NCBI_TaxID=9685;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NE-KALGRKINSWESSRSGHSFLSN-LHLRNGELVIHEKGFYYIYSQTYFRFQEEI---- 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 NQPLNHKVYMRNSKYPEDLVLMBEKRLNYCTT--GQIWAHSSHLGAVFNLTSADHLYVNI 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 OLRVPGKDCMLRAITEERSE-PSPOOVYSP---PRGKPR--AHLT----IKKQTPAPHLK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 NOLSAL-----HWEHD-LGMAFTKNGMKYINKSLVIPESGDYFIYSOITFRGTISVCGDI 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 ---KENTKNDKQMVQYIYKYTSYPDPILLMKSARNSC-----WSKDAEYGLYSIYQGGIF 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Migone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S., Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakaraj P., Carrell J., Boyd E., Olsen H.S., Hu G., Pukac L., Liu D., Ni J., Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P., "TilA is a TNF-like ligand for DR3 and TR6/DcR3 and functions as a T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunity 16:479-492(2002).

EMBL; AF520786; AAM77367.1; -

MGD; MG1:2180140; Tnfsf15.

MGO; G0:001640; Tnfsf15.

G0; G0:001620; C:membrane; IEA.

G0; G0:0005164; F:tumor necrosia factor receptor binding; IEA.

G0; G0:0006955; P:immune response; IEA.

InterPro; IPR006053; TNF abc.

InterPro; IPR008093; TNF family.

InterPro; IPR008093; TNF family.

InterPro; IPR0080936; TNF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.2%; Score 180; DB 11; Length 252; Best Local Similarity 32.4%; Pred. No. 5.1e-07; Matches 69; Conservative 26; Mismatches 80; Indels 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO1234; TNECROSISFCT.

ProDom; PD002012; TNF subf; 1.

SMART; SM00207; TNF, 1.

PROSITE; PSS0049; TNF 2; 1.

SEQUENCE 252 AA; 27723 MW; BB901C9350119E0F CRC64;
                                                                                                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 ELKENDRIFVSVTNEHLIDMDHE-ASFFGAFLV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 SLEEGDRLMVNVSDISLVDYTKEDKTFFGAFLL 252
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                                                                                                                                                                                                          252 AA.
                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21909416; PubMed=11911831;
                                                                                                   260 SQLSLINFEESKTFFGLY 277
                                                                           261 TNEHLIDMDHEASFFGAF 278
                                                                                                                                                                                                                                                                                                   TNF superfamily ligand TLIA.
                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel, 22, 01-OCT-2002 (TrEMBLrel, 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell costimulator.";
                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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Q861W5 Q861W5;

RESULT 8 Q861W5

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73 MNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGR 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 CLLVMFFMVLVALVGLGLGMFQLFHLQKELAELRESTSQKHVASSLEKQIGQLNPPSEK- 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 -----KPNSRSIPL------EWEDT-YGIALVSGVKXKKGGLVINDTGMYFVYSKVNFRG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 QEEIKENTKNDKQMVQYIY-KYTSYPDPILLMK-SARNSC-----WSKDAEYGLYSIYQG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 CVLIVIFTVLLQSLCVAV---TYVYFTNELKQMQDKYSKSGIACFLKEDDSYMDPNDEES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 -----RKVAHLTG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85; Gaps
                                                                                                                                                                                                                                                                            WEDUINE=99053606; PubMed=9839871;

WEDUINE=99053606; PubMed=9839871;

WEDUINE=99053606; PubMed=9839871;

WEDUINE=99053606; PubMed=9839871;

WALSENDER TIME TIME TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TENDER TO THE TEN
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Sciuridae, Sciurinae,
Felis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
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12.1%; Score 178.5; DB 6; Length
Best Local Similarity 21.2%; Pred. No. 7.7e-07;
Matches 58; Conservative 53; Mismatches 77; Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 AVFNLTSADHLYVNVSELSLVSFEESKTFFGLY 278
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                              83 OLROLVRKMILRISEETISTVOEKOONISPLVRERGPORVAAHITGTRGRSNTLSSPNSK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 NEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKN 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 DKOMVOYIY-KYTSYPDPILLAMK-SARNSC-----WSKDAEYGLYSIYQGGIFELKENDR 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 NQPLSHKVYVKNSKYPQDLVLMEGKMMYCTTGQMMAR-----SYLGAVFNFTSNDH 153
                                                                                                                                                                                                                                                                                                                                                                                                                                           43; Gaps
                                                                                                                           R GO; GO:0005575; C:extracellular; IEA.

R GO; GO:0005575; C:extracellular; IEA.

R GO; GO:0016520; C:membrane; IEA.

R GO; GO:0016516; F:tumor necrosis factor receptor binding; IEA.

R GO; GO:0006915; P:papoptosis; IEA.

R GO; GO:000695; P:immune response; IEA.

R GO; GO:0007165; P:signal transduction; IEA.

R InterPro; IPR008664; Fas ligand.

R InterPro; IPR008664; Fas ligand.

R InterPro; IPR008664; Fas ligand.

R InterPro; IPR008863; INF_1ixe.

R InterPro; IPR008863; INF_1ixe.

R Pfam; PR00229; INF_1.

R PRINTS; PR01681; FASIIGAND.

R Probom; PD00201; TNF subf; 1.

SMART; SM00207; TNF; 1.

R PROSITE; PS00251; TNF 1: 1.

R PROSITE; PS00251; TNF 1: 1.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                        Hodgson P.D., Grant M.D., Michalak T.I.;
"Perforin and Fas/Fas ligand-mediated cytotoxicity in acute and chronic woodchuck viral hepatitis.";
Clin. Exp. Immunol. 118:63-70(1999).
EMBL, AFISCAS, AAD3887.1;
HSSP, P50591; 104V.
                                                                                                                                                                                                                                                                                                                                                                               11.9%; Score 175.5; DB 11; Length 169; 27.8%; Pred. No. 7.2e-07;
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-07N-2003 (TrEMBLrel. 24, Created)
01-07N-2003 (TrEMBLrel. 24, Last sequence update)
01-07N-2003 (TrEMBLrel. 25, Last annotation update)
BM20KL3.3 (Tumor necrosis factor (Ligand) superfamily, member
                                                                                                                                                                                                                                                                                                                                                                                                      39; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                      169 AA; 19274 MW; FDE395B014717B6B CRC64;
                                             MEDLINE=20010026; PubMed=10540161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::|:|: ||: : 154 LYVNVSELSLINFE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IFVSVTNEHLIDMD 269
                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 27.88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 OLROLVRKMILRISEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 NE-KALGRKINSWESSRSGHSFLSN-LHLRNGELVIHRKGFYYIYSQTYFRFQEEI---- 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 NOLSAL-----HWEHD-LGMAFTKNGMKYINKSLVIPESGDYFIYSOITFRGTTSVCGDI 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 SRGRRPNKPDSITMVITKVADSYPEPARLLTGSKSVCEISNNW-----FOSLYLGATF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 ---KENTKNDKOMVQYIYKYTSYPDPILLMKSARNSC----WSKDAEYGLYSIYQGGIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Sprague-Dawley,
MEDLINE=21909416; PubMed=11911831;
Migone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,
Migone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Kanakaraj P.,
Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakaraj P.,
Carrell J., Boyd E., Olsen H.S., Hu G., Pukac L., Liu D., Ni J.,
Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P.,
"TLIA is a TNF-like ligand for DR3 and TR6/DcR3 and functions as a T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENEL, AFSIOTAT, ANTITAGE 11.

GO; GO: 0016020; C: membrane; IEA.
GO; GO: 0016050; F: tumor necrosis factor receptor binding; IEA.
GO; GO: 005655; F: tumor necrosis factor receptor binding; IEA.
GO; GO: 005655; F: tumoune response; IEA.
InterPro; IPR066053; TNF abc.
InterPro; IPR0606052; TNF family.
InterPro; IPR060898; TNF like.
InterPro; IPR060898; TNF Bubf.
Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                11.8%; Score 175; DB 11; Length 252; 31.9%; Pred. No. 1.3e-06; tive 26; Mismatches 81; Indels 36
GO; GO:0006955; P:immune response; IEA.
InterPro; IPRO06053; TNF_family.
InterPro; IPRO06053; TNF_family.
InterPro; IPRO0365; TNF_like.
A InterPro; IPRO0365; TNF_like.
R InterPro; IPRO0365; TNF_like.
Pfam; PF00229; TNF_10.
R PKINTS; PRO0224; TNF Subf: 1.
R PROMITS; PRO0207; TNF Subf: 1.
SMART; SMO0207; TNF 1.
RPOSITE; PSSO049; TNF 2: 1.
SEQUENCE 252 AA; 27725 MW; A63ABDCC9E969E0F CRC64;
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28029 MW; 7789E6556D46F293 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 ELKENDRIFVSVTNEHLIDMDHE-ASFFGAFLV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 SLEEGDRLMVNVSDISLVDYTKEDKTFFGAFLL 252
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ProDom; PD002012; TNF subf; 1.
SWART; SM00207; TNF; 1.
PROSITE; PS50049; TNF 2; 1.
SEQUENCE 252 AA; 28029 MW;
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datches 68; Conservative
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Length 252;

DB 11;

11.7%; Score 173;

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Query Match
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                                  RESULT 13
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                                                            149 FIYSQITFRGTTSECGDISRVRRPKKPDSITVVITKVADSYPEPAHLLIGTKSVCEISSN 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 QONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNE-KALGRKINSWESSRSGHSFLS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSN-LHLRNGELVIHEKGFY 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 N-LHLRNGELVIHEKGFYYIYSQTYFRFQ----EEIKENTKNDK--QMVQYIYKYT-SYP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPILLIMKSARNSCWSKDAEYG---LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHE-AS 273
                                                                                          183 YIYSQTYFRFQ-----EEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSC----
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21909416; PubMed=11911831; Migone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S., Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakaraj P., Zerrell J., Boyd E., Olsen H.S., Hu G., Pukac L., Liu D., Ni J., Kim S., Gentz R., Feng Pe., Moore P.A., Ruben S.M., Wei P., "TLIA is a TNF-like ligand for DR3 and TR6/DcR3 and functions as a T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                       231 WSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHE-ASFFGAFLV 280
                                                                                                                                                             209 W-----FQPIYLGAMFSLEEGDRLMVNVSDISLVDYTKEDKTFFGAFLI 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AFS20765; AAM77366.1; -.
GO; GO:001620; C:membrane; IEA.
GO; GO:0005164; F:tumor necroais factor receptor binding; IEA.
GO; GO:000555; P:tumor response; IEA.
InterPro; IPR06655; TNP abc.
InterPro; IPR06652; TNF family.
InterPro; IPR06893; TNF—IME.
InterPro; IPR06893; TNF—IME.
InterPro; IPR06859; TNF—IME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.2%; Score 166; DB 4; Length 251; 33.2%; Pred. No. 7.4e-06; ive 30; Mismatches 65; Indels
Pred. No. 1.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 AA; 28087 MW; 65ED70E367E3446D CRC64;
                                                                                                                                                                                                                                                         (TrEMBLrel. 22, Last sequence update) (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                       251 AA.
       32.7%; Pred. wo.
                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01234; TNECROSISFCT.
ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                01-OCT-2003 (TrEMBLrel. 25,
TNF superfamily ligand TLIA.
TNFSF15.
                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunity 16:479-492(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62; Conservative
                      Conservative
                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50049; TNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 FFGAFLL 251
                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                               cell costimulator.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                 QBNFE9;
                                                                                                                                                                                                                       Q8NFE9
                    Matches
                                                                                                                                                                                               RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
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95 TSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : | | | : : | | | | : | | | | : | | | 53 EDT-YGIVILSGVKYYKKGGLVINETGLYFVYSKVYFRGQ-----SCTNLPLSHKVYMRN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Caspase-dependent and -independent cell death pathways characterize pathogenic Simian Immunodeficiency Virus infection. Relationship with disease evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exign Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

REBL, AF53076; AAM95636.1; -...

ROJ GO.0005576; Crextracellular; IEA.

ROJ GO.0016020; Crembrane; IEA.

ROJ GO.0006915; Prapoptosis; IEA.

ROJ GO.0006915; Prapoptosis; IEA.

ROJ GO.0006915; Pramour response; IEA.

ROJ GO.0006915; Pramour response; IEA.

ROJ GO.0006915; Pramour response; IEA.

ROJ GO.0006915; Pramour response; IEA.

ROJ GO.0006915; Pramour response; IEA.

ROJ GO.0007165; Pramour response; IEA.

ROJ GO.0007165; Pramour response; IEA.

ROJ GO.0007165; Pramour response; IEA.

RINTERPO; IPR00893; TNF like.

RINTERPO; IPR00893; TNF like.

R PRINTS; PR01691; FASLIGAND.

R PRODOM; PR02011; TNF subf; I.

R RSART; SM00201; TNF; I.
                                                                                                                                                                           Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cyprinus carpio (Common carp).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Petit F., Arnoult D., Lelievre J.-D., Lecossier D., Hance A.J., Monceaux V., Ho Tsong Fang R., Hurtrel B., Ameisen J.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 TSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 SKYPQDLVWPMEGKMMS-YCTTGQMWAHSSYLGAVFNLTSADHLYVNVS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 AA; 17410 MW; 971A43779E029449 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Tumor necrosis factor-3 alpha.
                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.6%; Score 157; DB 6; 27.4%; Pred. No. 2.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Mismatches
      154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 AA
                                                             Created)
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   PRT;
                                                                                                                                                        (Fragment).
                                                      01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00251; TNF_1; 1. PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 27.4% tes 46; Conservative
PRELIMINARY;
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                                                                                                                                                                                                                                                                               Cercopithecinae; Macaca.
NCBI TaxID=9544;
                                                                                                                                                    Fas ligand CD178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Estaquier J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNF-3ALPHA.
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67 -LSKENVISKVAIHLSGA------YEPDVSKNNIDWKQNQDGAFVSGGLKLVD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD-----PILLMKS 225
                                                                                                                                                                                                                                                                                                                                                                52 SGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNIS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                     112 PLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 REIIIPNDGIYFIYSQVSFHI--SCKNDMTEDQEVMHVSHAVFHYSDFFGIYKP--LIRA 168
                                                                                                                                                                                                                                                                                      3 MMEVQGGP-----SLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSK 51
                                                                                                                                                                                                                                                                                                                        1 MMDLESQPLPQEMVSRRNASSSKSAVWWVCGVLLAVALCAAAAVCFTLNK------ 50
                                                                                                                                                                                                                                                                                                                                                                                                    -------NNQEGGNE-------6RLTLKDN-------66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 ARNSCW----SKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHL--IDMDHEASFFGAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Spleen;
MEDLINE=98234044; PubMed=9573100;
MEDLINE=98234044; PubMed=9573100;
MEDLINE=98234044; PubMed=9573100;
Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
"Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and analysis of cytokine mRNA expression in experimental visceral leisthaniasis.";
Infect. Immun. 66:2135-2142(1998).
EMBL; AF046215; AAC40100.1; -.
HSSP; P06804; ZTNF.
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprinus.
NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Cricetinae;
                                                                                                                                                                                                                                                           97;
                                                                                                                                                                                                                       DB 13; Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO, GO:0016020; C:membrane; IEA.
GO, GO:0016020; C:membrane; IEA.
GO, GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO, GO:0006955; P:immune response; IEA.
InterPro; IPR006053; TNF abc.
InterPro; IPR006052; TNF amily.
InterPro; IPR008993; TNF like.
InterPro; IPR008093; TNF like.
                                                                                                                                                                                                                   10.4%; Score 153.5; DB 13; Length 20.1%; Pred. No. 7.2e-05; Live 50; Mismatches 92; Indels
                                                                SEQUENCE FROM N.A.
TISSUE=Head kidney;
Savan R., Sakai M.,
"Cloning of tumor necrosis factor 3 alpha in carp.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AB112424; BAC77690.1; -.
SEQUENCE 227 AA, 25226 MW; 010BC2B1E8D7265E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Tumor necrosis factor-alpha (Fragment).
Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00229; TNF; 1. PRINTS; PR01234; TNECROSISFCT. ProDom; PD0020012; TNF; 1. SMART; SMO02207; TNF; 1. PROSITE; PS00251; TNF_1; 1.
                                                                                                                                                                                                                                                       60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                   Query Match
Best Local Similarity
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49 GPÖREEKFPNPIIGSMGOTLTLRSSSONSNDKPVGHVVANHQVEEQLEWLSHRANALLAN 108
                                                                                                                                                           118 GPQRVAAH---ITGTRGRSNTL-SSPNSKNEKALGRKINS------WESSRSGHSFLS 165
                                                                                                                                                                                                                                                    166 NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK-----YTSYPD 218
                                                                                                                             63; Indels 37; Gaps
                                                                                                                                                                                                                                                                                                  219 PILLMKSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLID 267
                                                                                                                                                                                                                                                                                                                       DB 11; Length 216;
                                      216 216
216 AA; 23793 MW; BADAE3F83F45B533 CRC64;
                                                                                        'Match 9.8%; Score 144.5; DB J
Local Similarity 26.9%; Pred. No. 0.00038.
Les 47; Conservative 28; Mismatches 63
PROSITE; PS50049; INF 2; 1.
                   NON TER
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SEQUENCE
                                                                                        Query Match
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Search completed: March 23, 2004, 09:06:47
Job time: 47 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

March 23, 2004, 09:04:02; Search time 60 Seconds (without alignments) 1323.264 Million cell updates/sec Run on:

US-10-662-429-2
1478
1 MANNARVQGGPSLGQTCVLIV.....NEHLIDMDHEASFFGAFLVG 281 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_29Jan04:* 1: geneseqp1980s:* 2: geneseqp1990s:* Database :

geneseqp2000s:* geneseqp2001s:* geneseqp2001s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMARIES	ID Description	AAW19777 Aaw19777 Novel Cut	4 Aaw27134 Human	Human	Нишап	Aaw56760 Human	Human	Protei	~	6 Human	Human	Aab08545 Amino	1 Human	7 Human	3 Human	Human	Human	Human	O Human	Human	Human	Human	Check		
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	Score	1478	1478	1478	. 1478	1478	1478	1478	1478	1478	1478	1478	1478	1478	1478	1478	1478	1478	1478	1478	1478	1478	1478	1478	0 5 5
Result	No.	ч	61	e	4	D.	ø	7	80	o,	10	I,	12	13	14	15	16	17	18	19	50	21		23	

281 6 ABU71443 281 6 AAG72738 281 6 AAG72738 281 6 ABG72738 281 6 ABG72135 281 6 ABG71905 281 6 ABG71905 281 6 AAG71151 281 7 ADG71512 281 7 ADG714080 281 7 ADG714080 281 7 ADG714080 281 7 ADG714080 281 7 ADG714080 281 7 ADG714080 281 7 ADG714080 281 7 ADG714080 281 7 ADG714080 281 7 ADG714080 281 7 ADG714080 281 7 ADG714080 281 7 ADG714080 281 7 ADG714080	Abu71443 Human neo Abg72738 Human TNA Ab08558 Human TNR Abr42313 Human TNR Abg71905 Human TNR Abg71905 Human TRA Abg71515 Human TRA Abg1151 Human TRA Abo25125 Human TNR Ado31515 Human TNR Ado31517 Human TNR Add61471 Native hu Add35202 Human TNF Add4080 Human TNF	
77787877770000000000000	ABU71443 AAG72738 AAO29543 ABG72738 ABG72958 ABG71905 ABF60546 AAE36258 AAC31151 AAC3625125 ADSG1471 ADSG1471	ADD19010 ADB76953 ADB76953 ABG72257 ADB61478 ADB61477
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1000 1000 1000 1000 1000 1000 1000 100	1 4 4 7 8 8 8 4 7 4 7 8 8 8 4 7 4 7 8 8 8 4 7 4 7	1478 1478 1475 1473 1473 1473
	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	W 4 4 4 4 4 4 4 6 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

ALIGNMENTS

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Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy.
                                                                                                                                                                                                                 /label= Glycosylation
/note= "putative N-linked glycosylation site"
                                                                                                                                                                              41. .281
/note= "Claim 2"
41. .281
/label= Extracellular_region
                                                                                                                                                             15. .40
/label= Transmembrane_region
                                                                                                                                 1. .14
/label _ Cytoplasmic_region
                                                                                                                                                                                                                                                                                                                                     Ashkenazi AJ, Chuntharapai A, Kim KJ;
                                                                                                          Location/Qualifiers
              AAW19777 standard; protein; 281 AA.
                                                                                                                  1. .281
/note= "Claim 4"
                                                                                                                                                                                                                                 114. .281
/note= "Claim 1"
                                                                                                                                                97WO-US000272.
                                                                                                                                                                                                                                                                                                      96US-00584031.
                                                             Novel cytokine Apo-2 ligand.
                                              22-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-372867/34.
N-PSDB; AAT72796.
                                                                                                                                                                                                           Modified-site
                                                                                            Homo sapiens
                                                                                                                                                                                                                                                         WO9725428-A1.
                                                                                                                                                                                                                                                                                      08-JAN-1997;
                                                                                                                                                                                                                                                                                                      09-JAN-1996;
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                              AAW19777;
                                                                                                          Key
Peptide
                                                                                                                                                                                                                                  Protein
                                                                                                                                                Protein
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                                                                                                                                Region
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                                                                                                                                                                                            Region
RESULT 1
        AAW1977
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                                                                                        A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian cell apoptosis. It is belived to be a member of the tumnour necrosis factor cytokine family. Its amino acid sequence was deduced from a cDNA clone (AAT72796) isolated from a human placental cDNA library. Apo-2 ligand polypeptides, esp. those corresponding to amino acids 114-281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells transformed or transfected with a vector contg. Apo-2 ligand nucleic pathological conditions such as cancer (esp. breast or colon cancer) or to raise antibodies useful in diagnostic assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLIMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FYYIYSQTYFRFQEEIKENTKNDKQMVQXIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSCHSFLSNLHLRNGELVIHEKG 180
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                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apoptosis inducing molecule-I; AIM-I; autoimmune disorder; tumour necrosis factor ligand superfamily; AIM-I altered expression; neoplasia inhibition; anti-inflammatory agent.
       00-2 ligand and corresponding DNA - used to induce treatment of breast and colon cancer.
                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                               100.0%; Score 1478; DB 2; Length 281; 100.0%; Pred. No. 2.6e-137; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Apoptosis inducing molecule-I (AIM-I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW27134 standard; protein; 281 AA
accent cytokine, Apo-2 ligand and apoptosis for the treatment of hy
                                                         Claim 4; Fig 1a; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
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hes 281; Conservative
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N-PSDB; AAT85210.
                                                                                                                                                                                                                                                                                 Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-SEP-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                   Matches
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The present sequence represents a human Apoptosis inducing molecule-I (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand superfamily. The products can be used in the diagnosis and treatment of disorders related to under-expression, over-expression or altered expression of AIM-I. AIM-I or agonists can be used for treating autoimmune disorders including systemic lupus erythematosus, immunoproliferative disease lymphadenopathy (IPI), rheumatoid arthritis, angioimmunoproliferative lymphadenopathy (AIL), rheumatoid arthritis, cliabetes, and multiple sclerosis, graft versus host disease, to inhibit neoplasia such as tumour cell growth, to treat restenosis, to regulate haematopolesis in endothelial cell development, to stimulate peripheral tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be to used for treating cachexia, cerebral malaria, rheumatoid arthritis or osteoporosis, for preventing graft-host rejection, and as anti-coll ammatory agents, for treating endotoxic shock or to prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
             New isolated apoptosis inducing molecule-I - used to develop products for the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft versus host disease or inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumour necrosis factor related apoptosis inducing ligand, TRAIL, cytokine; cancer; leukaemia; lyphoma; melanoma; viral infection; thrombotic microangioplasty; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1478; DB 2; 100.0%; Pred. No. 2.6e-137;
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/label= Transmembrane_domain
39. .281

    18
    label= Cytoplasmic_domain

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW19787 standard; protein; 281 AA.
                                                                                          Claim 2; Fig 1; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             activation of HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 281 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FYXIXSQTYFREQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRISEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected cells - useful for treating thrombotic microangiopathy, cancer and viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human tumour necrosis factor related apoptosis inducing ligand (TRAIL)
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/label= Extracelular domain
/note= "contains a receptor-binding region"
                                                                           note= "potential KEX2 protease processing
                                                                                                                                                                                         /note= "potential KEX2 protease processing
                                                                                                  109. .111
/note= "potential N-glycosylation site"
149. .150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Page 43-44; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection and for use in assays.
                                                                                                                                                                                                                                                                                                                                                             96WO-US010895
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                                                      89. .90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goodwin RG;
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                                                      Cleavage-site
                                                                                                                                                               Cleavage-site
                                                                                                        Modified-site
                                                                                                                                                                                                                                             WO9701633-A1
                                                                                                                                                                                                                                                                                                                                                                                                               29-JUN-1995;
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                                                                                                                                                                                                                                                                                                      16-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wiley SR,
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Best Local S
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SIYQGGIFELKENDRIFVSVINEHLIDMDHEASFFGAFLVG 281

AAW76829 standard; protein; 281 AA

RESULT 4 AAW76829

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AAW76829;

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                                                                                              inflammation, arthritis, septicaemia, autoimmune disease, restenosis, transplant rejection, infection, ischaemia, brain injury, bone disease, acute respiratory disease syndrome, acquired autoimmune disease syndrome, AIDS, cancer, atherosclerosis, Alxheimers disease, TRAIL, TNF, TL2. tumour necrosis factor-related apoptosis-inducing ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor, TL2 (also known as tumour necrosis factor-related apoptosis-inducing ligand, TRALI). This protein is used in a method resulting in the isolation of the novel human TNF related receptor, TR6. TR6 polypeptides and polynucleotides can be used in the treatment of chronic and acute inflammation, arthritis, septicaemia, autoimmune diseases (e.g. inflammatory bowel disease, isochaemia, acute respiratory disease syndrome, restenois, brain injury, (acquired autoimmune disease syndrome, restenois, brain injury, (acquired autoimmune disease diseases), atherosclevosis and Alzheimers disease
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                                                                               tumour necrosis factor related receptor; human; treatment; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the human tumour necrosis factor (TNF)-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1478; DB 2;
100.0%; Pred. No. 2.6e-137;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TR6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding tumour necrosis factor receptor TR6 polypeptide, antibody, agonist, antagonist, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 32-33; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                    97US-0041230P.
97US-00853684.
97US-00916625.
                                                                                                                                                                                                                                                                                                    97EP-00310562.
              (first entry)
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Best Local Similarity 100.
Matches 281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-523156/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Deen KC, Young PR;
                                               Human TL2 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 281 AA;
                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                  23-DEC-1997;
                                                                                                                                                                                                                                                                                                                                    14-MAR-1997;
09-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                      22-AUG-1997;
               25-JAN-1999
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                                                                                                                                                                                                                                                                    14-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDSYWDPNDEESWASPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prosis factor related apoptosis ligand; TRAIL; research; human; therapy; leukaemia; lymphoma; melanoma; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding cytokine TNF-related apoptosis ligand polypeptides - useful for producing recombinant polypeptides for research and therapy of leukaemia, lymphoma, melanoma and viral infections.
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                                                                                                                                                                                                                                                    "N-terminal cytoplasmic domain"
                                                                                                                                                                                                                                                                                  "transmembrane region"
                                                                                                                                                                                                                                                                                                              /note= "extracellular domain"
                                                                                                                                                                                                                          Location/Qualifiers
                            AAW56760 standard; protein; 281 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Col 33-36; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     96US-00670354
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95US-00548368,
                                                                                       (first entry)
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                                                                                                                                                                                                                                      /note= "
                                                                                                                   Human TRAIL polypeptide
                                                                                                                                                                                                                                                                     19. .38
                                                                                                                                                necrosis factor
                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goodwin RG, Wiley SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMY ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-347322/30.
N-PSDB; AAV29518.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 281 AA;
                                                                                                                                                                                            Homo sapiens
                                                                                       05-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUN-1995;
                                                                                                                                                                                                                                                                                                                                        US5763223-A.
                                                                                                                                                                                                                                                                                                                                                                       09-JUN-1998
                                                                                                                                                                cytokine;
                                                           AAW56760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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RESULT 5
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The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis factor (TNF) related protein, involved in inflammation, myelopoiesis and bone resorption. It has the ame nucleic acid and animo acid (aa) sequences as the TNF-related apoptosis-induced ligand (TRAIL) described in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay caequences for detecting AGP-1 expression. Nucleic acid complementary to AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are used to treat inflammation (e.g. rheumatoid anthritis, systemic lupus carythematics, pooriasis, scleroderma, infection-related inflammation) or bone resorption diseases (e.g. osteoporosis, osteomyelitis, hypercalcaemia, Paget's disease). AGP-1 can be used to treat home accordated with reduction in the number of bone marrow cells, particularly neutrophils and lymphocytes, e.g. where caused by disease, injury or exposure to myelosuppressive agents. Host cells, containing AGP-1 DNA, are used to
   240
                 FYXIYSQTYFRFQEEIKENTKODKQMVQYIYKYTSYPDPIILMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                            tumour necrosis factor-related protein; TNF; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein - useful for treating inflammation, bone resorption and haematopoietic
FYYIYSQTYFREQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                               SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 1478; DB 2;
; Pred. No. 2.6e-137;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                             bone resorption; haematopoietic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Danilenko DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 36-37; 54pp; English.
                                                                                                                                                                              AAW44354 standard; protein; 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johnson MJ, Simonet WS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1998-042194/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                           Human; AGP-1;
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                         WO9746686-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1996;
                                                                                                                                                                                                                                           28-MAY-1998
                                                                                                                                                                                                                                                                            Human AGP-1
                                                                                                                                                                                                              AAW44354;
                              181
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181
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The specification describes the use a polypeptide corresponding to at disast the primary sequence of part of the present sequence to produce a diagnostic, prophylactic or therapeutic composition useful in cases of degenerative, autoimmune and inflammatory diseases. The polypeptides can be used in treatment of neurodegenerative disease, The polypeptides can rhuematoid arthritis, and SBP. The polypeptides are apoptotic in central nervous system cells, antigenci and specifically recognise the surface receptor of the TRAIL protein. The polypeptide is a marker of disease and a therapeutic target, e.g. its apoptotic activity can be blocked with an anti-TRAIL antibody or a TRAIL equivalent that binds to specific
                                                         FYYIYSQIYFRFQEEIKENTKNDKQMVQXIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                  RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                        FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 240
DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of polypeptide derived from TRAIL protein for diagnosis of degenerative disease - autoimmunity and inflammation, also useful in prevention or treatment, and similar use of corresponding ligand and nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurodegenerative disease; autoimmune disease; inflammatory disease; lupus erythematosus; rhuematoid arthritis; SEP; apoptotic; surface receptor; TRAIL protein.
                                                                                                                                                                                                                                                                                                                                                                                                                     Protein associated with neurodegenerative and autoimmune diseases.
                                                                                                                                                                                                   SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                               SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                            AAY01517 standard; peptide; 281 AA
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                                                                                                                                                                                                                                                                                                                                                                                 27-MAY-1999
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61
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                                                                                                        181
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                                                                                                                                                                       240
                                                                  DDSYMDPNDEESMNSPCWQVKWQLRQLVRXMILRTSETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                            121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHIRNGELVIHEKG 180
                                                                                                                                                                                            RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             designated Apo-2 ligand, useful for inducing apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder; lupus; immune-mediated glomerular nephritis; human.
                                                                                                                                                                         FYY1YSQTYFRFQEEIKENTKNDKQMVQY1YKYTSYPDPILLMKSARNSCWSKDAEYGLY
                 MAMMEVOGGPSLGOTCVLIVIFTVLLOSLCVAVTYVYFTNELKOMODKYSKSGIACFLKE
                                                  DDSYMDPNDEESMNSPCWQVKWQLRQLVRKM1LRTSEET1STVQEKQQN1SPLVRERGPQ
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schwall RH;
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                                                                                                                                                                                                                                                     SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Apo-2 ligand (Apo-2L) polypeptide.
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                                                                                                                                                                                                                                                                                                                                              AAY27012 standard; protein; 281
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98US-00060533.
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                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-444397/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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15-APR-1998;
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Matches 281;
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Query Match Best Local Similarity

Length 281;

Length 281;

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                                       DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEFTISTVQEKQQNISPLVRERGPQ 120
                                                         DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRISEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                 Apo-2 ligand; human; monoclonal antibody; hybridoma cell line; diagnosis;
                   9
           MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                        181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                              RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                     FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                        SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                                                                                                                                                           Human Apo-2 ligand protein sequence.
                                                                                                                                                                                                                                 AAY81956 standard; protein; 281 AA
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                                                                                                                                                                                                                                                                                                                             therapy; apoptosis; cancer.
                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                       61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                    61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
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                                                            1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                             Gaps
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                             Indels
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100.0%; Score 1478; DB 3;
100.0%; Pred. No. 2.6e-137;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PRO1096 protein sequence SEQ ID NO:51.
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAB24038 standard; protein; 281 AA.
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              Local Similarity 100.
1es 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC
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This sequence is the human Apo-2 ligand protein, which is recognised by monoclonal antibodies produced by the hybridoma cell lines of the invention. The Mybridoma cell lines are deposited under the American Type Culture Collection Accession Numbers. ATCC HB-12256, HB-12257, HB-12258 and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic assays for Apo-2 ligand, e.g. detecting its expression in specific cells, tissues, or serum. The antibodies may also be employed as therapeutics. For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand activity, like Apo-2 ligand antibodies which block Apo-2 ligand activity, like Apo-2 ligand-induced apoptosis, may be employed to treat activity, like Apo-2 ligand-induced apoptosis, may be applosed from recombinant cell culture or natural sources. The Apo-2 ligand from recombinant cell culture or natural sources. The Apo-2 ligand itself may be used to treat diseases e.g. cancer, by inducing apoptosis in cells.

Sequence 281 AA;

New isolated monoclonal antibodies having antigen specificity for Apo-2 ligand, e.g. 2G6, 2E11 or 5C2, useful for detecting the expression of Apo -2 ligand serum, and for treating diseases associated with increased

Claim 9; Fig la; 46pp; English.

apoptosis.

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diagnose tumours. Agents which inhibit the activity of (I), especially the antibodies, or an antisense oligomuclectide which hybridises to genes encoding (I), can be used to inhibit tumour growth, preferably by inducing cell death. Methods from the present invention can be used to identify compounds which inhibit the biological activity of (I). AAC58019 to AAC58102 represent PCR primers and hybridisation probes used in examples from the present invention for human PRO sequences. AAC58103 to AAC58122 and AAB24021 to AAB24040 represent human PRO polymucleotide and protein sequences given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                       DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 FYYIYSQTYFRFQEEIKENTKNDKQMVQXIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                             1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
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                                                                                                                                                                                                                                     Length 281;
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                                                                                                 100.0%; Score 1478; DB 3;
100.0%; Pred. No. 2.6e-137;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of a human TRAIL polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-small cell lung carcinoma.
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Matches 281; Conservative
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                                                                                                                                                                                               Sequence 281 AA;
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                                            (TNF) related apoptosis-inducing ligand) polypeptide. The specification describes a method for enhanced killing of tumour cells. The method comprises contacting a susceptible tumour cell with a synergistic mixture of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined dosage to kill at least 50 % of the cells. This mixture is synergistic, and so is active at lower doses and against otherwise resistant cell lines. The method is used for killing tumour cells, especially solid tumours or carcinomas (especially mammary carcinoma or non-small cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
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                               present sequence represents a human TRAIL (tumour necrosis factor
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                                                                                                                                                                                                                                                  100.0%; Score 1478; DB 3;
100.0%; Pred. No. 2.6e-137;
ive 0; Mismatches 0;
Disclosure; Page 23-24; 29pp; English.
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N-PSDB; AAC67831.
                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                      Sequence 281 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200063253-A1.
                                                                                                                                                                                      lung carcinoma)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-FEB-2001
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                                                                                                                                                                                                                                                                                        Matches 281;
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                                                                                                                                                                                                                                                      Query Match
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The present sequence is human AGP-1, a type II transmembrane protein. Fusion proteins comprising an FC immunoglobulin region fused to the N-terminal portion of the AGP-1 protein have been produced. The fusion proteins can be used to induce apoptosis in a tissue, and to treat proliferative disorders, immune disorders, or virally-induced disorders. The proliferative disorders include cancers, such as breast, prostate, lung or colon cancer. The viral infections include hepatitis, and acquired immunodaficiancy syndrome (AIDS), and the immune disorders may be autoimmune disorders or transplant rejection. Cardiovascular diseases such as arteriosclerosis may also be treated. The AGP-1 containing fusion proteins have increased biological activity compared to the soluble AGP-1 proteins used in prior art therapies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, PRO; cytostatic; nootropic; neuroprotective; respiratory general; antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant; PRO agonist; cancer; inflammatory disorder; immunological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
Fusion protein of AGP-1 protein and an Fc region, used to treat proliferative disorders, immune disorders, and virally-induced disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
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                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1478; DB 3;
100.0%; Pred. No. 2.6e-137;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB50977 standard; protein; 281 AA.
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99US-0140650P.
99US-0141037P.
99US-0144758P.
99WO-US020111.
                                                      Claim 3; Fig 2; 93pp; English
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                   Sequence 281 AA;
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23-JUN-1999;
20-JUL-1999;
01-SEP-1999;
08-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                             281;
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Twenty eight nucleic acids encoding PRO polypeptides which are useful for treating various tumors, e.g. breast cancer, and other inflammatory, angiogenic and immunological disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FYYIYSQTYFRFQEBIKENTKNDKQMVQXIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is one of twenty eight novel PRO polypeptides. The PRO polypeptides and their agonists, including antibodies, peptides, and small molecule agonists, may be used to treat various tumours, e.g., cancers such as breast cancer, ovarian cancer, renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer, central nervous system cancer, melanoma or leukaemia. They are also useful for treating other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandlar, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1478; DB 4;
100.0%; Pred. No. 2.6e-137;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                    Hebert C,
Wood WI;
                                                                                                                                                                                                                                                                                                                    Watanabe CK,
                                                                                                                                                                                                                                                                                                      Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 31; Fig 54; 188pp; English.
                                                                                                                                 2000WO-US004341.
2000WO-US004342.
                                                                                                                                                                 2000WO-US005841.
                                                                                                                                                                                                            2000WO-US006884
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2000WO-US013705
                                                       99US-0170262P
99WO-US030095
                                                                                                    2000WO-US000376
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                                            99WO-US028551
                                                                                      99WO-US030999
                                                                                                                    2000WO-US003565
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                                                                                                                                                                                                                                                                                                    Goddard A,
                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                    2001-016509/02.
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Matches 281, Conserv
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                                                                                                                   11-FEB-2000;
18-FEB-2000;
18-FEB-2000;
                                                      09-DEC-1999;
16-DEC-1999;
20-DEC-1999;
                                                                                                                                                                                                            15-MAR-2000;
                                                                                                                                                                                                                                          17-MAY-2000;
                                                                                                      06-JAN-2000;
                                                                                                                                                                 02-MAR-2000;
                                                                                                                                                                               03-MAR-2000;
                                                                                                                                                                                              10-MAR-2000;
                                                                                                                                                                                                                                                                                                                    Shelton DL,
                            01-DEC-1999
02-DEC-1999
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                                                                                                                                                                                                                                                                                                       Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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AAB67243 standard; protein; 281 AA.

AAB67243 ID AAB6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a formulation comprising Apo-2 ligand and divalent metal ions. Apo-2 ligand and the formulation are useful for treating cancers and viral infections. Addition of divalent metal ions for making Apo-2 ligand and formulations containing Apo-2 ligand results in increased yield and stability of Apo-2 ligand trimers
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                                                                                                                                                                                                                                                                                                                                                                     Use of divalent metal ions for making Apo-2 ligand and in formulations containing Apo-2 ligand for increasing yield and stability of ligand trimers, useful for therapeutic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FYYIYSQIYFREQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                 divalent metal ions; viral infection; cancer
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                                                                                                                                                                                                                                                                                                   RF, Koumenis I,
Simmons L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1478; DB 4;
100.0%; Pred. No. 2.6e-137;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                 Hymowitz S, Kelley
                                                                                                                                                                                                                                                                                                                                                                                                                             6; Fig 1; 60pp; English.
                                                                                                                                                                                                               26-JUN-2000; 2000WO-US017579
                                                                                                                                                                                                                                            99US-0141342P
                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity 100.
281; Conservative
                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                               Pai R,
                                                                                               Human; Apo2 ligand:
                                                                                                                                                                                                                                                                                                                                          WPI; 2001-123012/13.
                                                                    Human Apo2 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 281 AA;
                                                                                                                                                      WO200100832-A1
                                                                                                                                                                                                                                                                                                 Ashkenazi AJ,
O'connell M,
                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                            28-JUN-1999;
                                         18-APR-2001
                                                                                                                                                                                   04-JAN-2001
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The invention relates to a cytokine designated as tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis of certain target cells, including cancer cells and virally infected cells. The TRAIL polypeptides are useful in killing cancer cells, in treating viral infections (e.g. bovine viral diarrhoea or human minumunodeficiency virus (HIV)) and cancers (e.g. lenkaemia, lymphoma and melanoma), as a research reagent useful in studying apoptosis including the regulation of programmed cell death. TRAIL DNA sequences may be employed in developing a gene therapy approach to treating disorders mediated by defective or insufficient amounts of TRAIL, in the production of TRAIL polypeptides and as probes or primers in polymerase chain reactions (PCR). The present sequence is human TRAIL protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New tumor necrosis factor related apoptosis inducing ligand polypeptides for treating viral infections (e.g. bovine viral diarrhea or human immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
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                              Human, tumour necrosis factor, TNF; cytokine; cytostatic; virucide; TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection; human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
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Human TNF related apoptosis inducing ligand (TRAIL) protein.
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/label= N_terminal_cytoplasmic_domain
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                 and searchable
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             MARCH 5 CURRENT WINDOWS VERSION IS V7.00A, CURRENT
              MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
              AND CURRENT DISCOVER FILE IS DATED 3 MARCH 2004
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=> s human Fas ligand L1 370 HUMAN FAS LIGAND

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L3 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN

1996:61419 Document No. 124:115474 Use of Fas ligand to suppress T
lymphocyte-mediated immune responses. Bellgrau, Donald; Duke, Richard C.
(University of Colorado, USA). PCT Int. Appl. WO 9532627 Al 19951207, 50
pp. DESIGNATED STATES: W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ,
DE, DK, ES, FI, GB, GE, HU, JP, KE, KG, KP, KR, KZ, LK, LT, LU, LV, MD,
MG, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SI, SK, TJ, TT, UA, US,
UZ, VN; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FR, GA, GB,
GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English).
CODEN: PIXXD2. APPLICATION: WO 1995-US6742 19950526. PRIORITY: US
1994-250478 19940527; US 1995-378507 19950126.

AB Soluble mouse and human Fas ligand polypeptides and methods are useful for inhibiting T-lymphocyte-mediated immune responses, treating inflammation or preventing transplant rejection. The Fas ligand may be provided to the recipient mammal by a variety of means, including by direct administration of the Fas ligand or by providing the gene encoding the Fas ligand to a subject such that Fas ligand is synthesized by the subject. Also, antibody and monoclonal antibody against the mouse and human Fas ligand epitopes are claimed.

- 1996:402030 Document No. 125:84664 Novel mammalian Fas ligands and cDNAs encoding them and their use in the therapeutic regulation of apoptosis. Nagata, Shigekazu; Suda, Takashi; Takahashi, Tomohiro; Nakamura, Norio (Mochida Pharmaceutical Co., Ltd., Japan; Osaka Bioscience Institute). Eur. Pat. Appl. EP 675200 Al 19951004, 175 pp. DESIGNATED STATES: R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE. (English). CODEN: EPXXDW. APPLICATION: EP 1994-117761 19941110. PRIORITY: JP 1993-305975 19931110; JP 1993-342526 19931213; JP 1994-74344 19940318; JP 1994-180955 19940708; JP 1994-239363 19940907; JP 1994-278378 19941018.
- AB Novel polypeptide ligands for the Fas antigen are identified, purified and characterized and cDNAs encoding them are cloned and expressed. These proteins may be manufactured for regulation of apoptosis by expression of the cloned cDNA for therapeutic use or in the preparation of antibodies. These proteins have a cytoplasmic domain, a transmembrane domain and extracellular domain and takes part in apoptosis. CDNAs for these ligands were cloned by panning of an expression library in COS-7 cells. Monoclonal antibodies to the ligand were prepared and shown to inhibit Fas ligand-induced apoptosis. Antisense oligonucleotides to the Fas gene were able to inhibit gene expression.
- MEDLINE on STN DUPLICATE 1 L3ANSWER 3 OF 3 PubMed ID: 7980502. Role of Fas ligand in apoptosis induced by 95071350. hepatitis C virus infection. Mita E; Hayashi N; Iio S; Takehara T; Hijioka T; Kasahara A; Fusamoto H; Kamada T. (First Department of Medicine, Osaka University School of Medicine, Japan.) Biochemical and biophysical research communications, (1994 Oct 28) 204 (2) 468-74. Journal code: 0372516. ISSN: 0006-291X. Pub. country: United States. Language: English. To investigate the role that Fas ligand plays in the apoptosis of AΒ hepatocytes induced by hepatitis C virus infection, we isolated a cDNA clone for human Fas ligand and examined the expression of Fas ligand in liver-infiltrating mononuclear cells obtained from patients with chronic hepatitis C. The amino acid sequence of human Fas ligand showed 76% and 77% identity with those of rat and mouse Fas ligand,

respectively. When the expression of Fas ligand transcripts was tested by reverse transcription-polymerase chain reaction, the amplified signal was detected in liver-infiltrating mononuclear cells and peripheral blood mononuclear cells, whereas only a weak signal or none at all was detected in liver tissues. These findings suggest that the Fas ligand-Fas antigen system may play an important role in liver cell injury by hepatitis C virus infection.

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L6 14 DUP REMOVE L5 (7 DUPLICATES REMOVED)

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L6 ANSWER 1 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
2004:39584 Document No. 140:87695 A new member of the TNF ligand superfamily
and its use in treating immune disorders. Ebner, Reinhard; Yu, Guo-Liang;
Ruben, Steven M.; Zhai, Yifan; Ullrich, Stephen (Human Genome
Sciences, Inc., USA). U.S. Pat. Appl. Publ. US 2004009147 Al 20040115,
189 pp., Cont.-in-part of U.S. 6,635,743. (English). CODEN: USXXCO.
APPLICATION: US 2003-375680 20030228. PRIORITY: US 1996-PV13923 19960322;

- US 1996-PV30157 19961031; US 1997-822953 19970321; US 1998-3886 19980107; US 1998-27287 19980220; US 1998-PV75409 19980220; US 1999-252656 19990219; US 1999-PV124041 19990311; US 1999-PV137457 19990604; US 1999-PV142657 19990706; US 1999-PV148326 19990811; US 1999-PV168380 19991202; US 2000-523323 20000310; US 2002-PV360234 20020301.
- An ew member of the human TNF-Ligand superfamily, Apoptosis Inducing Mol. II (AIM II) is identified by sequence homol. for use in the treatment of immune disorders. The protein is a ligand for the TNF receptor TR6 and so may be used for the therapeutic induction of apoptosis or as a target for new drugs for the therapeutic inhibition of apoptosis. The invention further relates to screening methods for identifying agonists and antagonists of AIM II activity. Also provided are therapeutic methods for treating lymphadenopathy, aberrant bone development, autoimmune and other immune system diseases, graft vs. host disease, rheumatoid arthritis, osteoarthritis and to inhibit neoplasia, such as tumor cell growth.
- L6 ANSWER 2 OF 14 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN DUPLICATE 1
- 2003:537115 Document No.: PREV200300537649. Apoptosis inducing molecule II and methods of use. Ebner, Reinhard [Inventor, Reprint Author]; Yu, Guo-Liang [Inventor]; Ruben, Steven M. [Inventor]; Ullrich, Stephen [Inventor]; Zhai, Yifan [Inventor]. Guilford, CT, USA. ASSIGNEE: Human Genome Sciences, Inc.. Patent Info.: US 6635743 October 21, 2003. Official Gazette of the United States Patent and Trademark Office Patents, (Oct 21 2003) Vol. 1275, No. 3. http://www.uspto.gov/web/menu/patdata.html.e-file.
 - ISSN: 0098-1133 (ISSN print). Language: English.
- The present invention relates to a novel member of the TNF-Ligand superfamily. More specifically, isolated nucleic acid molecules are provided encoding a human Apoptosis Inducing Molecule II (AIM II). AIM II polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of AIM II activity. Also provided are therapeutic methods for treating lymphadenopathy, aberrant bone development, autoimmune and other immune system diseases, graft versus host disease, rheumatoid arthritis, osteoarthritis and to inhibit neoplasia, such as tumor cell growth.
- L6 ANSWER 3 OF 14 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN 2003:70974 Document No.: PREV200300070974. Apoptosis Inducing Molecule II and methods of use. Ebner, Reinhard [Inventor, Reprint Author]; Yu, Guo-Liang [Inventor]; Ruben, Steven M. [Inventor]; Zhang, Jun [Inventor]; Ullrich, Stephen [Inventor]; Zhai, Yifan [Inventor]. Rockville, MD, USA. ASSIGNEE: Human Genome Sciences, Inc.. Patent Info.: US 6495520 December 17, 2002. Official Gazette of the United States Patent and Trademark Office Patents, (Dec 17 2002) Vol. 1265, No. 3. http://www.uspto.gov/web/menu/patdata.html. e-file. ISSN: 0098-1133 (ISSN print). Language: English.
- The present invention relates to a novel member of the TNF-Ligand superfamily. More specifically, isolated nucleic acid molecules are provided encoding a human Apoptosis Inducing Molecule II (AIM II). AIM II polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of AIM II activity. Also provided are therapeutic methods for treating lymphadenopathy, aberrant bone development, autoimmune and other immune system diseases, graft versus host disease, rheumatoid arthritis, osteoarthritis and to inhibit neoplasia, such as tumor cell growth.

- 2003:42575 Document No.: PREV200300042575. Apoptosis inducing molecule II. Ebner, Reinhard [Inventor, Reprint Author]; Yu, Guo-Liang [Inventor]; Ruben, Steven M. [Inventor]. ASSIGNEE: Human Genome Sciences, Inc.. Patent Info.: US 6479254 November 12, 2002. Official Gazette of the United States Patent and Trademark Office Patents, (Nov 12 2002) Vol. 1264, No. 2. http://www.uspto.gov/web/menu/patdata.html. e-file. ISSN: 0098-1133 (ISSN print). Language: English.
- The present invention relates to a novel member of the TNF-Ligand superfamily, Apoptosis Inducing Molecule II (AIM II). In particular, isolated nucleic acid molecules are provided encoding the human AIM II protein. AIM II polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of AIM II activity. Also provided are therapeutic methods for treating lymphadenopathy, autoimmune disease, graft versus host disease, and to inhibit neoplasia, such as tumor cell growth.
- L6 ANSWER 5 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
 2002:488138 Document No. 137:57591 Apoptosis inducing Molecule II and methods of use. Ebner, Reinhard; Yu, Guo-liang; Ruben, Steven M.; Zhang, Jun; Ullrich, Stephen; Zhai, Yifan (Human Genome Sciences, Inc., USA). U.S. Pat. Appl. Publ. US 2002081647 A1 20020627, 96 pp., Cont.-in-part of U.S. Ser. No. 27,287. (English). CODEN: USXXCO. APPLICATION: US 1999-252656 19990219. PRIORITY: US 1996-PV13923 19960322; US 1996-PV30157 19961031; US 1997-822953 19970321; US 1998-3886 19980107; US 1998-27287 19980220; US 1998-PV75409 19980220.
- The present invention relates to a novel member of the TNF-Ligand superfamily. More specifically, isolated nucleic acid mols. are provided encoding a human Apoptosis Inducing Mol. II (AIM II).

 AIM II polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of AIM II activity. Also provided are therapeutic methods for treating lymphadenopathy, aberrant bone development, autoimmune and other immune system diseases, graft vs. host disease, rheumatoid arthritis, osteoarthritis and to inhibit neoplasia, such as tumor cell growth.
- L6 ANSWER 6 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
 2002:409195 Document No. 137:1567 Human apoptosis inducing molecule II and its cDNA and use thereof in drug screening and therapy. Ebner, Reinhard; Yu, Guo-liang; Ruben, Steven M.; Ullrich, Stephen (Human Genome Sciences, Inc., USA). U.S. Pat. Appl. Publ. US 2002064869 A1 20020530, 79 pp., Cont.-in-part of U.S. Ser. No. 822,953, abandoned. (English). CODEN: USXXCO. APPLICATION: US 1998-27287 19980220. PRIORITY: US 1996-PV13923 19960322; US 1996-PV30157 19961031; US 1997-822953 19970321.

 AB The present invention relates to a novel member of the TNF-Ligand
 - The present invention relates to a novel member of the TNF-Ligand superfamily, Apoptosis Inducing Mol. II (AIM II). In particular, isolated nucleic acid mols. are provided encoding the human AIM II protein. AIM II polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. The effect of AIM II on the cell growth are tested in breast cancer cell line or xenograft human breast carcinoma cell MDA in nude mice. Soluble AIM II can mediate cytotoxicity in HT-29 cell and stimulate secretion of IFNγ in human PBL cells. Cell surface expression of β-lymphokine receptor fusion protein LTβR-Fc or TR2-Fc fusion protein can block soluble AIM II-mediated cytotoxicity in HT-29 cells and AIM II can bind to LTβR specifically. The invention further relates to screening methods for identifying agonists and antagonists of AIM II activity. Also provided are therapeutic methods for treating lymphadenopathy, autoimmune disease, graft vs. host disease, and to inhibit neoplasia, such as tumor cell growth.

- ANSWER 7 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN Document No. 133:242574 Apoptosis-inducing molecule II and for 2000:645884 antitumor, antiarthritic, antiautoimmune, and other therapeutic use. Ebner, Reinhard; Yu, Guo-liang; Ruben, Steven M.; Zhai, Yifan; Ullrich, Stephen (Human Genome Sciences, Inc., USA). PCT Int. Appl. WO 2000053223 A1 20000914, 388 pp. DESIGNATED STATES: W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 2000-US6332 20000310. PRIORITY: US 1999-PV124041 19990311; US 1999-PV137457 19990604; US 1999-PV142657 19990706; US 1999-PV148326 19990811; US 1999-PV168380 19991202.
- The present invention relates to a novel member of the TNF-Ligand superfamily. More specifically, isolated nucleic acid mols. are provided encoding a human Apoptosis Inducing Mol. II (AIM II).

 AIM II polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of AIM II activity. Also provided are therapeutic methods for treating lymphadenopathy, aberrant bone development, autoimmune and other immune system deseases, graft vs. host desease, rheumatoid arthritis, osteoarthritis and to inhibit neoplasia, such as tumor cell growth.
- L6 ANSWER 8 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
 2000:628154 Document No. 133:236828 Tumor necrosis factor receptors 6α and 6β. Gentz, Reiner L.; Ni, Jian; Ebner, Reinhard; Yu, Guo-liang; Ruben, Steven M.; Feng, Ping (Human Genome Sciences, Inc., USA).

 PCT Int. Appl. WO 2000052028 A1 20000908, 332 pp. DESIGNATED STATES: W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 2000-US5686 20000303. PRIORITY: US 1999-PV121774 19990304; US 1999-PV124092 19990312; US 1999-PV131279 19990427; US 1999-PV131964 19990430; US 1999-PV146371 19990802; US 1999-PV168235 19991201.
- The present invention relates to novel Tumor Necrosis Factor Receptor proteins. In particular, isolated nucleic acid mols. are provided encoding the human TNFR-6 α and -6 β proteins. TNFR-6 α and -6 β polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of TNFR-6 α and -6 β activity. Also provided are diagnostic methods for detecting immune system-related disorders and therapeutic methods for treating immune system-related disorders.
- L6 ANSWER 9 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
 1999:549380 Document No. 131:180813 Apoptosis-inducing molecule II, its
 encoding cDNA sequence, and therapeutic and clinical uses. Ebner,
 Reinhard; Yu, Guo-Liang; Ruben, Steven M.; Zhang, Jun; Ullrich,
 Stephen; Zhai, Yifan (Human Genome Sciences, Inc., USA). PCT Int. Appl.
 WO 9942584 Al 19990826, 224 pp. DESIGNATED STATES: W: AL, AM, AT, AU,
 AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD,
 GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
 LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE,

SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 1999-US3703 19990219. PRIORITY: US 1998-PV75409 19980220; US 1998-27287 19980220.

- The present invention relates to a member of the TNF-Ligand superfamily. AB More specifically, isolated nucleic acid mols. are provided encoding a human Apoptosis-Inducing Mol. II (AIM II). The nucleic acid was discovered in a cDNA library derived from human macrophage ox LDL, and shown to contain an open reading frame encoding a protein of 240 amino acid residues. AIM II polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. AIM II is highly expressed in activated lymphocytes but not in cancer cells. The protein has potent antitumor activity in vivo and in vitro and both lymphotoxin β receptor and TR2 are required for AIM II-induced growth inhibition of cancer cells. The invention further relates to screening methods for identifying agonists and antagonists of AIM II activity. Also provided are therapeutic methods for treating lymphadenopathy, aberrant bone development, autoimmune and other immune system diseases, graft vs. host disease, rheumatoid arthritis, osteoarthritis and to inhibit neoplasia, such as tumor cell growth.
- ANSWER 10 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN Document No. 131:86868 Cloning and cDNA sequence encoding human 1999:451368 apoptosis-inducing molecule II. Ebner, Reinhard; Ruben, Steven M. ; Yu, Guo-liang; Ullrich, Stephen (Human Genome Sciences, Inc., USA). Int. Appl. WO 9935262 A2 19990715, 165 pp. DESIGNATED STATES: W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 1999-US242 19990107. PRIORITY: US 1998-3886 19980107; US 1998-27287 19980220. The present invention relates to a member of the tumor necrosis factor AΒ ligand superfamily, apoptosis-inducing mol. II (AIM II). In particular, isolated nucleic acid mols. are provided encoding the human

ligand superfamily, apoptosis-inducing mol. II (AIM II). In particular, isolated nucleic acid mols. are provided encoding the human AIM II protein. AIM II polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. AIM II is highly expressed in activated lymphocytes but not in cancer cells, and demonstrates enhanced apoptosis and potent in vivo anti-tumor activities. Both lymphotoxin β receptor and TR2 are required for AIM II-induced growth inhibition of cancer cells. The invention further relates to screening methods for identifying agonists and antagonists of AIM II activity. Also provided are therapeutic methods for treating lymphadenopathy, autoimmune disease, graft vs. host disease, and to inhibit neoplasia, such as tumor cell growth.

L6 ANSWER 11 OF 14 MEDLINE on STN DUPLICATE 2
1999123371. PubMed ID: 9924296. Vertical cup/disc ratio in relation to optic disc size: its value in the assessment of the glaucoma suspect.

Garway-Heath D F; Ruben S T; Viswanathan A; Hitchings R A.

(Glaucoma Unit, Moorfields Eye Hospital, London.) British journal of ophthalmology, (1998 Oct) 82 (10) 1118-24. Journal code: 0421041. ISSN: 0007-1161. Pub. country: ENGLAND: United Kingdom. Language: English.

AB AIMS: The vertical cup/disc ratio (CDR) has long been used in the assessment of the glaucoma suspect, though the wide range of CDR values in the normal population limits its use. Cup size is related physiologically to disc size and pathologically to glaucomatous damage. Disc size can be measured at the slit lamp as the vertical disc diameter

- (DD). The ability of the CDR, in relation to DD, to identify glaucomatous optic discs was investigated. METHODS: 88 normal, 53 early glaucoma, and 59 ocular hypertensive subjects underwent stereoscopic optic disc photography and clinical biometry. Photographs were analysed in a masked fashion by computer assisted planimetry. The relation between vertical cup diameter and DD was explored by linear regression, and expressed in terms of CDR. The upper limit of normal was defined by the 95% prediction intervals of this regression (method 1) and by the upper 97.5 percentile for CDR (method 2). The sensitivity and specificity of CDR to identify an optic disc as glaucomatous was tested with these disc size dependent and disc size independent cut offs in small, medium, and large discs. RESULTS: The CDR was related to DD by the equation CDR = $(-1.31 + (1.194 \times 1.00))$ DD))/DD. The sensitivity in small, medium, and large discs was 80%, 60%, and 38% respectively for method 1 and 33%, 67%, and 63% respectively for method 2. Specificity was 98.9% (method 1) and 97.7% (method 2). CONCLUSIONS: The CDR, relative to disc size, is useful clinically, especially to assist in identifying small glaucomatous discs.
- ANSWER 12 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN Document No. 127:288196 Apoptosis-inducing molecule II. Ebner, 1997:640681 Reinhard; Ruben, Steven M.; Yu, Guo-Liang (Human Genome Sciences, Inc., USA; Ebner, Reinhard; Ruben, Steven M.; Yu, Guo-Liang). PCT Int. Appl. WO 9734911 Al 19970925, 89 pp. DESIGNATED STATES: W: AM, AU, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IL, JP, KG, KP, KR, KZ, LT, LV, MD, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TR, UA, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE. (English). CODEN: PIXXD2. APPLICATION: WO 1996-US16966 19961031. PRIORITY: US 1996-13923 19960322. The present invention relates to a novel member of the TNF-Ligand AΒ superfamily, Apoptosis-Inducing Mol. II (AIM II). In particular, isolated nucleic acid mols. are provided encoding the human AIM II protein. AIM II polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of AIM II activity. Also provided are therapeutic methods for treating lymphadenopathy, autoimmune disease,
- L6 ANSWER 13 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
 1997:623179 Document No. 127:315580 Apoptosis-inducing molecule I and its
 encoding cDNA from human tissues. Ruben, Steven M. (Human
 Genome Sciences, Inc., USA; Ruben, Steven M.). PCT Int. Appl. WO 9733899
 A1 19970918, 83 pp. DESIGNATED STATES: W: AM, AU, BG, BR, BY, CA, CN,
 CZ, EE, FI, GE, HU, JP, KG, KP, KR, KZ, LT, LV, MD, MN, MX, NO, NZ, PL,
 RO, RU, SG, SI, SK, TJ, TM, UA, US, UZ, VN; RW: AT, BE, CH, DE, DK, ES,
 FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE. (English). CODEN: PIXXD2.
 APPLICATION: WO 1996-US3773 19960314.

graft vs. host disease, and to inhibit neoplasia, such as tumor cell

growth.

The invention relates to apoptosis-inducing mol. I (AIM-I) AΒ polypeptides, polynucleotides encoding the polypeptides, methods for producing the polypeptides, in particular by expressing the polynucleotides, and agonists and antagonists of the polypeptides. AIM-I cDNA was discovered in a cDNA library derived from cells of a human pancreatic tumor and shown to contain an open reading frame encoding 281 amino acid residues with 48.6% similarity and 22.9% identity to human Fas ligand. Northern blot anal. shows that AIM-I mRNA is abundant in human heart, bone marrow, CD4+ and CD19+ peripheral blood lymphocytes, and less so in lung and kidney tissue. Cloning of human AIM-I cDNA was demonstrated by expression in Escherichia coli using the bacterial expression vector pQE9, expression in a baculovirus expression system using the pA2 vector, expression in COS cells using the pcDNAI/Amp vector, and gene therapeutic expression. The invention further relates to methods for utilizing such polynucleotides, polypeptides,

agonists and antagonists for applications, which relate, in part, to research, diagnostic and clin. arts.

L6 ANSWER 14 OF 14 MEDLINE on STN DUPLICATE 3
95260771. PubMed ID: 7742276. Pattern electroretinogram and peripheral colour contrast thresholds in ocular hypertension and glaucoma: comparison and correlation of results. Ruben S T; Arden G B; O'Sullivan F; Hitchings R A. (Electrodiagnostic Department, Moorfields Eye Hospital, London.) British journal of ophthalmology, (1995 Apr) 79 (4) 326-31. Journal code: 0421041. ISSN: 0007-1161. Pub. country: ENGLAND: United Kingdom. Language: English.

AIMS--Both pattern electroretinogram and peripheral colour AΒ contrast thresholds have been shown to be abnormal in glaucoma and ocular hypertension. This study evaluates each of these tests as tools for the early diagnosis of glaucoma, compares and contrasts the results, and examines the relation between the two tests in a large cohort of ocular hypertensive patients. METHODS--Transient and steady state pattern electroretinograms and peripheral colour contrast thresholds were performed in 45 normal, 37 glaucomatous, and 206 ocular hypertensive eyes. The results were analysed using receiver operating characteristic curves, together with evaluation of sensitivity and specificity of the tests. The relation between the two tests was examined by direct statistical correlation of the results. RESULTS--All tests showed high sensitivity and specificity for discriminating between normal and glaucomatous eyes. However, there was a significant difference between the two tests for the number of ocular hypertensives considered as abnormal. Forty per cent of ocular hypertensives had abnormal pattern electroretinogram compared with 30% with abnormal peripheral colour vision. Peripheral colour contrast thresholds showed a significant correlation with both transient and steady state pattern electroretinogram. CONCLUSION--Both of these tests have been shown to be promising new tools for the early detection of glaucoma but the number of ocular hypertensive patients showing abnormal results is rather higher than expected considering the natural history of the condition. Sensitivity in ocular hypertension may be increased by using a combination of both tests. The significant correlation between these psychophysical and electrophysiological tests is discussed.

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